

**Methods and Compositions for Reducing Screening in
Oligonucleotide-Directed Nucleic Acid Sequence Alteration**

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. provisional applications nos.
5 60/453,360, filed March 7, 2003, and 60/416,983, filed October 7, 2002, the disclosures of which are
incorporated herein by reference in their entireties.

FIELD OF THE INVENTION

[0002] The technical field of the invention relates to oligonucleotide-directed alteration
10 of nucleic acid sequence.

BACKGROUND OF THE INVENTION

[0003] A number of methods have been developed to alter specific nucleotides within
both isolated DNA molecules and DNA present within intact cells of bacteria, plants, fungi and animals,
15 including humans.

[0004] In one approach, genomic sequences are targeted for alteration by homologous
recombination using duplex fragments. The duplex fragments are large, having several hundred
basepairs. See, e.g., Kunzelmann et al., *Gene Ther.* 3:859-867 (1996).

[0005] In another approach, oligonucleotides are used to effect targeted genetic
20 changes.

[0006] In early experiments, oligonucleotide-directed sequence changes were typically
effected in yeast, Moerschell *et al.*, 1988, *Proc. Natl. Acad. Sci.* 85:524 and Yamamoto *et al.*, *Yeast* 8:935

(1992), which among eukaryotes are known to have high recombinogenic activity, although one series of experiments were attempted in human cells, Campbell et al., *The New Biologist* 1: 223-227 (1989).

[0007] More recently, a number of different types of polynucleotides and oligonucleotides have been described that permit targeted alteration of genetic material in cells of higher eukaryotes, including (i) triplex-forming oligonucleotides; (ii) chimeric RNA-DNA oligonucleotides that are internally duplexed, notably in the region containing the nucleotide that directs the sequence alteration; and (iii) terminally modified single-stranded oligonucleotides having an internally unduplexed DNA domain and modified ends.

[0008] Sequence-altering triplexing oligonucleotides are described, for example, in U.S. Pat. Nos. 6,303,376, 5,962,426, and 5,776,744.

[0009] Triplex-forming oligonucleotides require a structural domain that binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide. The binding domain must typically target polypurine or polypyrimidine tracts. These sequence requirements limit the usefulness of triplex-forming oligonucleotides for targeted sequence alteration, requiring that the target sequence to be modified be situated in proximity to such polypurine or polypyrimidine tract. Triplex-forming oligonucleotides may also require an additional DNA reactive moiety, such as psoralen, to be covalently linked to the oligonucleotide, in order to stabilize the interactions between the triplex-forming domain of the oligonucleotide and the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Patent 5,422,251. Such DNA-reactive moieties can, however, be indiscriminately mutagenic.

[0010] In more recent work with sequence-altering triplexing oligonucleotides, the triplex-forming domain is linked or tethered to a domain that effects targeted alteration, Culver et al., *Nat. Biotechnology* 17: 989-93 (1999), relaxing somewhat the permissible distance between target sequence and polypurine/polypyrimidine stretch.

[0011] Internally duplexed, hairpin- and double-hairpin-containing chimeric RNA-DNA oligonucleotides are described, *inter alia*, in U.S. Pat. Nos. 6,573,046; 5,888,983; 5,871,984; 5,795,972; 5,780,296; 5,760,012; 5,756,325; 5,731,181, and 5,565,350. Such chimeric RNA-DNA oligonucleotides are reportedly capable of directing targeted alteration of single base pairs, as well as introducing frameshift alterations, in cells and cell-free extracts from a variety of host organisms, including bacteria, fungi, plants and animals. The oligonucleotides are reportedly able to operate on almost any target sequence.

[0012] Such chimeric molecules have significant structural requirements, however, including a requirement for both ribonucleotides and deoxyribonucleotides, and typically also a requirement that the oligonucleotide adopt a double-hairpin conformation. Even when such double hairpins are not required, however, significant structural constraints remain.

5 [0013] Single-stranded oligonucleotides having modified ends and an internally unduplexed DNA domain that directs sequence alteration are described in copending international patent applications published as WO 03/027265; WO 02/10364; WO 01/92512; WO 01/87914; and WO 01/73002, as well as in U.S. Pat. Nos. 6,479,292 and 6,271,360, the disclosures of which are incorporated herein by reference in their entireties.

10 [0014] These single-stranded oligonucleotides have fewer structural requirements than chimeric oligonucleotides and are capable of directing sequence alteration, including introduction of frameshift mutations, in cells and cell-free extracts from a variety of host organisms, including bacteria, fungi, plants and animals, in episomal and in chromosomal targets, often at alteration efficiencies that exceed those observed with hairpin-containing, internally duplexed, chimeric oligonucleotides.

15 [0015] The usefulness of oligonucleotide-mediated nucleic acid sequence alteration — as a means, for example, for manipulating cloned DNA, for generating agricultural products with enhanced traits, for generating cellular models for laboratory use, or for generating animal models or animals with desired traits — is affected by its frequency. The usefulness of oligonucleotide-mediated nucleic acid sequence alteration as an *ex vivo* or *in vivo* therapeutic method would also be enhanced by increasing its
20 efficiency.

[0016] A need exists, therefore, for methods to enhance the efficiency of targeted alteration of genetic material.

SUMMARY OF THE INVENTION

25 [0017] The invention provides methods, compositions and kits for enhancing oligonucleotide-directed nucleic acid sequence alteration by reducing the number of target nucleic acid molecules required to be screened during oligonucleotide-directed targeted nucleic acid sequence alteration. The methods, compositions and kits involve using at least two oligonucleotides, where at least one of the oligonucleotides directs alteration of a selectable target.

30 [0018] In one aspect, the invention provides methods for reducing the number of target nucleic acid molecules required to be screened during oligonucleotide-directed nucleic acid sequence alteration comprising combining a nucleic acid molecule in the presence of repair proteins with at least two

oligonucleotides capable of directing alteration in at least two nucleic acid targets, where alteration by at least one oligonucleotide confers a selectable phenotype which is selected for, and selecting or screening for a nucleic acid molecule having the alteration directed by the other oligonucleotide in a composition having the selectable phenotype.

5 **[0019]** In other aspects, the invention provides compositions and kits for oligonucleotide-directed nucleic acid sequence alteration comprising at least two oligonucleotides, where at least one of the oligonucleotides directs an alteration which confers a selectable phenotype.

[0020] Other embodiments of the invention are set forth in the following numbered items:

10 **[0021]** 1. A method for reducing the number of target nucleic acid molecules required to be screened during oligonucleotide-directed nucleic acid sequence alteration of a first nucleic acid target in a composition comprising said first nucleic acid target and a second nucleic acid target,

[0022] wherein alteration of said first nucleic acid target is effected by combining, in the presence of cellular repair proteins, a nucleic acid molecule comprising said first nucleic acid target with a
15 first oligonucleotide and a second oligonucleotide,

[0023] wherein said first oligonucleotide is capable of effecting alteration of said first nucleic acid target and said second oligonucleotide is capable of effecting alteration of said second nucleic acid target, and wherein alteration of said second nucleic acid target confers a selectable phenotype,

20 **[0024]** said method comprising:

[0025] (a) selecting for alteration of said second nucleic acid target and

[0026] (b) screening for a nucleic acid molecule comprising an alteration of said first nucleic acid target.

25 **[0027]** 2. A method for targeted alteration of a first nucleic acid target in a composition comprising said first nucleic acid target and a second nucleic acid target, comprising:

[0028] (a) combining, in the presence of cellular repair proteins, a nucleic acid molecule comprising said first nucleic acid target with a first oligonucleotide and a second oligonucleotide,

[0029] wherein said first oligonucleotide is capable of effecting alteration of said first
30 nucleic acid target and said second oligonucleotide is capable of effecting alteration of said second nucleic acid target, and wherein alteration of said second nucleic acid target confers a selectable phenotype; and

[0030] (b) identifying a nucleic acid molecule comprising an alteration of said first nucleic acid target in a composition in which alteration of the second nucleic acid target has occurred.

[0031] 3. The method of item 1 or 2, wherein alteration of the selectable phenotype is selected from the group consisting of: antibiotic resistance, prototrophy, expression of a fluorescent protein, presence of an epitope and resistance to an apoptotic signal.

[0032] 4. The method of any one of items 1-3, wherein the alteration of the first nucleic acid target is a substitution, deletion or insertion of at least one base.

[0033] 5. The method of item 4, wherein the alteration of the second nucleic acid target is a substitution, deletion or insertion of at least one base.

[0034] 6. The method of any one of items 1-5, wherein the nucleic acid molecule comprising the first nucleic acid target does not comprise the second nucleic acid target.

[0035] 7. The method of any one of items 1-5, wherein the nucleic acid molecule comprising the first nucleic acid target comprises the second nucleic acid target.

[0036] 8. The method of any one of items 1-7, wherein the nucleic acid molecule comprising the first nucleic acid target is a DNA molecule.

[0037] 9. The method of item 8, wherein the DNA molecule is selected from the group consisting of: a chromosome, a plasmid, a YAC, a BAC, a PLAC, a MAC, and a PAC.

[0038] 10. The method of item 8 or 9, wherein the DNA molecule is present in a cell.

[0039] 11. The method of item 10, wherein the cell is selected from the group consisting of: a prokaryotic cell, a fungal cell, a plant cell, and an animal cell.

[0040] 12. The method of item 11, wherein the cell is prokaryotic cell.

[0041] 13. The method of item 12, wherein the prokaryotic cell is an *Escherichia coli* cell.

5 [0042] 14. The method of item 11, wherein the cell is a fungal cell.

[0043] 15. The method of item 14, wherein the fungal cell is selected from the group consisting of: a *Saccharomyces cerevisiae* cell, an *Ustilago maydis* cell, a *Neurospora crassa* cell and a *Candida albicans* cell.

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[0044] 16. The method of item 11, wherein the cell is a plant cell.

[0045] 17. The method of item 16, wherein the plant cell is selected from the group consisting of: an angiosperm cell, a gymnosperm cell and a moss cell.

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[0046] 18. The method of item 16, wherein the cell is a *Chlamydomonas reinhardtii* cell.

[0047] 19. The method of item 17, wherein the angiosperm cell is an *Arabidopsis thaliana* cell.

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[0048] 20. The method of item 17, wherein the moss cell is a *Physcomitrella patens* cell.

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[0049] 21. The method of item 11, wherein the cell is an animal cell.

[0050] 22. The method of item 21, wherein the animal cell is a mammalian cell.

[0051] 23. The method of item 22, wherein the mammalian cell is selected from the group consisting of: a human cell, a rodent cell, a mouse cell, a hamster cell, a rat cell, and a monkey cell.

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[0052] 24. The method of item 23, wherein the human cell is selected from the group consisting of: a liver cell, a lung cell, a colon cell, a cervical cell, a kidney cell, an epithelial cell, a blood cell, a cancer cell, and a stem cell.

5 **[0053]** 25. The method of any one of items 1-24, wherein the first oligonucleotide has a region that is fully complementary in sequence to the first nucleic acid target, but for one or more mismatches as between the sequences of the first oligonucleotide and its complement on the first nucleic acid target, and wherein the first oligonucleotide has at least one terminal modification.

10 **[0054]** 26. The method of item 25, wherein the at least one terminal modification is selected from the group consisting of: at least one terminal locked nucleic acid (LNA), at least one terminal 2'-O-Me base analog, and at least three terminal phosphorothioate linkages.

15 **[0055]** 27. The method of item 26, wherein the first oligonucleotide is a single-stranded oligonucleotide 15 - 121 nucleotides in length, has an internally unduplexed domain of at least 8 contiguous deoxyribonucleotides, and wherein the one or more mismatches are positioned exclusively in the oligonucleotide DNA domain and at least 7 nucleotides from said oligonucleotide's 5' and 3' termini.

20 **[0056]** 28. The method of item 27, wherein the first oligonucleotide has at least one terminal locked nucleic acid (LNA).

[0057] 29. The method of item 1 or 2, wherein the first oligonucleotide is at least 25 nucleotides in length.

25 **[0058]** 30. The method of item 1 or 2, wherein the first oligonucleotide is no more than 121 nucleotides in length.

[0059] 31. The method of item 30, wherein the first oligonucleotide is no more than 74 nucleotides in length.

30 **[0060]** 32. A composition for targeted alteration of a first nucleic acid target, comprising:

[0061] a first oligonucleotide and a second oligonucleotide, wherein the oligonucleotides are capable, in the presence of cellular repair proteins, of effecting targeted alteration of a first nucleic target and a second nucleic acid target, respectively; and

[0062] wherein alteration of the second nucleic acid target confers a selectable phenotype.

[0063] 33. The composition of item 32 further comprising cellular repair proteins.

[0064] 34. The composition of item 33, wherein said cellular proteins are purified.

[0065] 35. The composition of item 33, wherein said cellular proteins are present in a cell-free protein extract.

[0066] 36. The composition of item 33, wherein said cellular proteins are present within an intact cell.

[0067] 37. The composition of any one of items 33 – 36, wherein the cell is selected from the group consisting of: a prokaryotic cell, a fungal cell, a plant cell, and an animal cell.

[0068] 38. The composition of any one of items 33 – 37, further comprising lambda beta protein.

[0069] 39. The composition of any one of items 33 – 37, wherein the cellular proteins are derived from a cell prior-contacted with hydroxyurea.

[0070] 40. The composition of any one of items 33 – 37, wherein the cellular proteins are derived from a cell prior-contacted with a histone deacetylase inhibitor.

[0071] 41. The composition of item 37, wherein the cell is prokaryotic cell.

[0072] 42. The composition of item 41, wherein the prokaryotic cell is an *E. coli* cell.

[0073] 43. The composition of item 37, wherein the cell is a fungal cell.

[0074] 44. The composition of item 43, wherein the fungal cell is selected from the group consisting of: a *Saccharomyces cerevisiae* cell, an *Ustilago maydis* cell, a *Neurospora crassa* cell and a *Candida albicans* cell.

[0075] 45. The composition of item 37, wherein the cell is a plant cell.

[0076] 46. The composition of item 45, wherein the plant cell is selected from the group consisting of: an angiosperm cell, a gymnosperm cell and a moss cell.

[0077] 47. The composition of item 45, wherein the cell is a *Chlamydomonas reinhardtii* cell.

[0078] 48. The composition of item 46, wherein the angiosperm cell is an *Arabidopsis thaliana* cell.

[0079] 49. The composition of item 46, wherein the moss cell is a *Physcomitrella patens* cell.

[0080] 50. The composition of item 37, wherein the cell is an animal cell.

[0081] 51. The composition of item 50, wherein the animal cell is a mammalian cell.

[0082] 52. The composition of item 51, wherein the mammalian cell is selected from the group consisting of: a human cell, a rodent cell, a mouse cell, a hamster cell, a rat cell, and a monkey cell.

[0083] 53. The composition of item 52, wherein the human cell is selected from the group consisting of: a liver cell, a lung cell, a colon cell, a cervical cell, a kidney cell, an epithelial cell, a blood cell, a cancer cell, and a stem cell.

[0084] 54. The composition of any one of items 32 - 53, wherein the first oligonucleotide is fully complementary in sequence to the first nucleic acid target, but for one or more mismatches as between the sequences of the first oligonucleotide and its complement on the first nucleic acid target, and wherein the first oligonucleotide has at least one terminal modification.

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[0085] 55. The composition of item 54, wherein the at least one terminal modification is selected from the group consisting of: at least one terminal locked nucleic acid (LNA), at least one terminal 2'-O-Me base analog, and at least three terminal phosphorothioate linkages.

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[0086] 56. The composition of item 55, wherein the first oligonucleotide is a single-stranded oligonucleotide 15 - 121 nucleotides in length, has an internally unduplexed domain of at least 7 contiguous deoxyribonucleotides, and wherein the one or more mismatches are positioned exclusively in the oligonucleotide DNA domain and at least 8 nucleotides from said oligonucleotide's 5' and 3' termini.

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[0087] 57. The composition of item 55, wherein the first oligonucleotide has at least one terminal locked nucleic acid (LNA).

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[0088] 58. The composition of any one of items 32 - 57, wherein said oligonucleotide is at least 25 nucleotides in length.

[0089] 59. The composition of any one of items 32 - 57, wherein said oligonucleotide is no more than 121 nucleotides in length.

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[0090] 60. The composition of item 59, wherein said oligonucleotide is no more than 74 nucleotides in length.

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[0091] 61. A kit for targeted alteration of nucleic acid sequence comprising:
[0092] a first oligonucleotide and a second oligonucleotide, wherein the oligonucleotides are capable, in the presence of cellular repair proteins, of effecting targeted alteration of a first nucleic target and a second nucleic acid target, respectively; and

[0093] wherein alteration of the second nucleic acid target confers a selectable phenotype.

[0094] 62. The kit of item 61 further comprising a cellular repair protein.

5 [0095] 63. The kit of item 62, wherein the cellular repair protein is from a cell precontacted with an HDAC inhibitor; hydroxyurea or lambda phage beta protein.

[0096] 64. The kit of item 62, wherein the cellular repair protein is selected from the group consisting of: RAD10, RAD51, RAD52, RAD54, RAD55, MRE11, PMS1 and XRS2.

10 [0097] 65. The kit of any one of items 61 - 64 further comprising an HDAC inhibitor; hydroxyurea or lambda phage beta protein.

[0098] 66. The kit of item 65 further comprising a cell.

15 [0099] 67. The kit of item 66, wherein the cell has increased levels or activity of at least one protein selected from the group consisting of: RAD10, RAD51, RAD52, RAD54, RAD55, MRE11, PMS1 and XRS2.

20 [0100] 68. The kit of item 66 or 67, wherein the cell has decreased levels or activity of at least one protein selected from the group consisting of: RAD10, RAD51, RAD52, RAD54, RAD55, MRE11, PMS1 and XRS2.

25 [0101] 69. The kit of any one of items 66 – 68, wherein the cell comprises a target nucleic acid sequence, wherein alteration of said target nucleic acid sequence by said second oligonucleotide confers a selectable phenotype.

[0102] 70. The kit of any one of items 61-69, wherein the kit further comprises instructions for performing the method of item 1 or item 2.

30 BRIEF DESCRIPTION OF THE DRAWINGS

[0103] Figure 1. *Diagram of pAURHYG(x)eGFP target plasmids.* Sequences are shown for the normal hygromycin resistance allele (SEQ ID NO:) and the mutant alleles present in

pAURHYG(rep)eGFP (SEQ ID NO: __), pAURHYG(ins)eGFP (SEQ ID NO: __) and pAURHYG(Δ)eGFP (SEQ ID NO: __).

[0104] FIG. 2. *Dual targeting protocol*. (A) Schematic diagram of the generalized strategy for dual targeting. (B) Sequences of the hygromycin-resistance gene and its mutation. (C) Schematic of the YAC containing the human β -globin locus and the β Thal1 and β Thal2 sequences that are changed by the corresponding oligonucleotides.

[0105] FIG. 3. *Dual targeting results*. (A) Efficiency of gene editing of hygromycin mutation using the dual targeting protocol. For these experiments, YAC-containing LSY678IntHyg(rep) β cells are grown in the presence of HU, electroporated with the selectable and nonselectable oligonucleotides, and allowed to recover in the presence of TSA. (B) Gene editing of the human β -globin gene directed by the β Thal1 oligonucleotide, including the sequence of the altered segment before (SEQ ID NO: __) and after (SEQ ID NO: __) the conversion.

[0106] FIG. 4. *Dual targeting and Rad51*. (A) Efficiency of gene editing of hygromycin mutation using the dual targeting protocol in combination with overexpression of yeast Rad51. For these experiments, YAC-containing LSY678IntHyg(rep) β cells are grown in the presence of HU, electroporated with the selectable and nonselectable oligonucleotides, and allowed to recover in the presence of TSA. (B) Gene editing of the human β -globin gene directed by the β Thal2 oligonucleotide, including the sequence of the altered segment before (SEQ ID NO: __) and after (SEQ ID NO: __) the conversion.

DETAILED DESCRIPTION

[0107] We have discovered, surprisingly, that the frequency of oligonucleotide-directed sequence alterations at a first nucleic acid target site is higher in a population of cells that has been selected for concurrent alteration at a second nucleic acid target site, as compared to a population of cells that has not been selected for concurrent alteration at a second nucleic acid target site.

[0108] Accordingly, in a first aspect the invention provides a method for identifying cells having a desired oligonucleotide-directed sequence alteration at a first nucleic acid target site within the cell. The method comprises identifying the desired sequence alteration in cells that have been selected for the presence of a selectable phenotype conferred upon the cell by a concurrent oligonucleotide-directed sequence alteration at a second nucleic acid target site within the cell.

[0109] In a second aspect, the invention provides a method for effecting a desired sequence alteration at a first nucleic acid target site within a cell, the method comprising concurrently targeting first and second nucleic acid sites within the cell for sequence alteration with respective first and

second sequence-altering oligonucleotides, the second alteration conferring a selectable phenotype upon the cell; selecting cells having the selectable phenotype; and then identifying among the selected cells those having the desired sequence alteration at the first nucleic acid target site.

[0110] The methods of the present invention increase the efficiency with which
5 bacteria, plant, fungi and animal cells having a desired genotypic change at the first target site may be identified. In related aspects, the invention provides compositions and kits for effecting or facilitating practice of the methods of the present invention.

[0111] Either or both of the first and second nucleic acid target sites within the cell may be in genomic double-stranded DNA.

[0112] The targeted genomic DNA can be normal, cellular chromosomal DNA;
10 organellar DNA, such as mitochondrial or plastid DNA; or extrachromosomal DNA present in cells in different forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), BiBACS, as well as episomal DNA, including episomal DNA from an exogenous source such as
15 a plasmid or recombinant vector. Many of these artificial chromosome constructs containing human DNA can be obtained from a variety of sources, including, e.g., the Whitehead Institute, and are described, e.g., in Cohen et al., *Nature* 336: 698-701 (1993) and Chumakov, et al., *Nature* 377: 175-297 (1995).

[0113] The first targeted nucleic acid site may be in a part of the DNA that is transcriptionally silent or transcriptionally active; typically, the second targeted nucleic acid site will be in a
20 part of the DNA that is transcriptionally active so as to confer a selectable phenotype upon the cell. The first and second targeted sites may be in any part of a gene including, for example, an exon, an intron, a promoter, an enhancer or a 3'- or 5'- untranslated region, and may be in intergenic regions, with the second targeted site typically being in an exon so as to confer a selectable phenotype upon the cell.

[0114] In some embodiments, the first and/or second sequence-altering oligonucleotide
25 is designed to direct alteration of the transcribed strand of the target sequence; in other embodiments, the first and/or second oligonucleotide is designed to direct alteration of nucleic acid sequence targeting the non-transcribed strand of the target sequence. The targeted strand may differ as between first and second target sites.

[0115] The first and second oligonucleotides may independently be selected from any
30 type of sequence-altering oligonucleotide known in the art, including (i) triplex-forming oligonucleotides; (ii) chimeric RNA-DNA oligonucleotides that are internally duplexed, notably in the region containing the

nucleotide that directs the sequence alteration; and (iii) terminally modified single-stranded oligonucleotides having an internally unduplexed DNA domain and modified ends.

[0116] Sequence-altering triplexing oligonucleotides useful in the methods, compositions, and kits of the present invention are described, for example, in U.S. Pat. Nos. 6,303,376, 5,962,426, and 5,776,744, the disclosures of which are incorporated herein by reference in their entireties. Bifunctional oligonucleotides having a triplex-forming domain linked or tethered to a domain that effects targeted alteration, useful in the methods, compositions, and kits of the present invention, are described in Culver et al., *Nat. Biotechnology* 17: 989-93 (1999), the disclosure of which is incorporated herein by reference in its entirety.

[0117] Internally duplexed, hairpin- and double-hairpin-containing chimeric RNA-DNA oligonucleotides useful in the methods, compositions, and kits of the present invention are described, *inter alia*, in U.S. Pat. Nos. 6,573,046; 5,888,983; 5,871,984; 5,795,972; 5,780,296; 5,760,012; 5,756,325; 5,731,181, and 5,565,350, the disclosures of which are incorporated herein by reference in their entireties.

[0118] In preferred embodiments, at least one of the first and second oligonucleotides is a single-stranded oligonucleotide having modified ends and an internally unduplexed DNA domain that directs sequence alteration.

[0119] Such oligonucleotides are further described in copending international patent applications published as WO 03/027265; WO 02/10364; WO 01/92512; WO 01/87914; and WO 01/73002, as well as in U.S. Pat. Nos. 6,479,292 and 6,271,360, the disclosures of which are incorporated herein by reference in their entireties.

[0120] In typical embodiments, the oligonucleotide is 17 - 121 nucleotides in length and has an internally unduplexed domain (that is, a nonhairpin domain) of at least 8 contiguous deoxyribonucleotides. The oligonucleotide is fully complementary in sequence to the sequence of a first strand of the respective nucleic acid target, but for one or more mismatches as between the sequences of the oligonucleotide internally unduplexed deoxyribonucleotide domain and its complement on the target nucleic acid first strand. Each of the mismatches is positioned at least 8 nucleotides from each of the oligonucleotide's 5' and 3' termini. The oligonucleotide has at least one terminal modification.

[0121] In some embodiments, the at least one terminal modification may be selected from the group consisting of 2'-O-alkyl, such as 2'-O-methyl, residue; phosphorothioate internucleoside linkage; and locked nucleic acid (LNA) residue. The basic structural and functional characteristics of LNAs and related analogues are disclosed in various publications and patents, including WO 99/14226, WO 00/56748, WO 00/66604, WO 98/39352, United States Patent No. 6,043,060, and United States

Patent No. 6,268,490, the disclosures of which are incorporated herein by reference in their entireties. In some embodiments, the terminal modification comprises a plurality of adjacent phosphorothioate internucleoside linkages, such as three phosphorothioate linkages at the 3' terminus of the oligonucleotide.

5 **[0122]** In certain preferred embodiments, both of the first and second sequence-altering oligonucleotides are single-stranded oligonucleotides having modified ends and an internally unduplexed DNA domain that directs sequence alteration.

[0123] In some embodiments, a plurality of single-stranded oligonucleotides having modified ends and an internally unduplexed DNA domain that directs sequence alteration can be used to effect either or both of the first and second sequence alterations. Use of such plural oligonucleotides is described in copending U.S. patent application no. 10/623,107, filed July 18, 2003 ("Targeted Nucleic Acid Sequence Alteration Using Plural Oligonucleotides"), the disclosure of which is incorporated herein by reference in its entirety.

10 **[0124]** In the methods, compositions, and kits of the present invention, at least the second oligonucleotide directs a sequence alteration that produces a selectable phenotype. Although the first oligonucleotide may also direct an alteration that produces a selectable phenotype, generally the first oligonucleotide directs an alteration that must be identified by screening, *e.g.*, by determining the corresponding nucleic acid sequence or by assaying a non-selectable phenotype that is generated by the alteration event.

15 **[0125]** The selectable phenotype chosen will depend on the host cell chosen and whether the selection is effected *in vitro* or *in vivo*. As is well known in the art, exemplary selectable phenotypes include, *e.g.*, antibiotic or other chemical resistance, ability to use a nutrient source, expression of a fluorescent protein, presence of an epitope or resistance to an apoptotic signal. The selectable phenotype chosen may be selectable based on preferential growth of a cell with the desired sequence alteration. Examples of such selectable phenotypes include, *e.g.*, the ability to grow in the presence of a compound that either kills or prevents the growth of the cell such as an apoptotic signal or an antibiotic, the ability to grow in the absence of a nutrient that is required prior to the sequence alteration, or the ability to utilize a particular resource that is not usable prior to the sequence alteration. The selectable phenotype may also be selected mechanically. Examples of phenotypes that may be selected mechanically include, *e.g.*, expression of a fluorescent protein or a particular epitope. Mechanical selection may be by any means known to one of skill in the art including, *e.g.*, FACS (directly in the case of a fluorescent protein or using a labeled antibody for an epitope), column chromatography,

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or using paramagnetic beads produced by, e.g., Miltenyi Biotec. Selection also does not require intact cells. For example, a single nucleotide change (SNP) in a nucleic acid molecule may be detected and isolated *in vitro* using methods such as are described in WO 03/027640. In such cases, the first oligonucleotide effects a change in the selected molecule.

5 **[0126]** The methods, compositions and kits of the invention typically reduce the number of cells required to be screened by at least about two-fold relative to the number that must be screened in a population of targeted cells that has not previously been selected for an oligonucleotide-directed nucleic acid sequence alteration that confers a selectable phenotype. The reduction can be by at least about two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold.

10 **[0127]** The methods, compositions and kits of the invention may be used with any oligonucleotide that directs targeted alteration of nucleic acid sequence. In the examples and in Tables 5 to 42 herein, correcting oligonucleotides of defined sequence are provided for alteration of human genes, including correction of genes mutated in human diseases, and for directing specific alterations in plant genes. Each of these oligonucleotides may be a first sequence-altering oligonucleotide as defined herein.

15 Certain of these oligonucleotides may also be a second sequence-altering oligonucleotide as defined herein, e.g., where the oligonucleotide effects a nucleic acid sequence alteration that confers a selectable phenotype such as herbicide resistance. In the tables of these examples, the oligonucleotides are not limited to the particular sequences disclosed. The oligonucleotides include extensions of the appropriate sequence of the longer 121 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Some oligonucleotides may be 15 or 16 bases which can be obtained by subtraction or one or two bases from the smallest disclosed oligonucleotides of 17 bases.

20 Thus the representative oligonucleotides include for each correcting change, oligonucleotides of length 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. These

25 oligonucleotide sequences can be used to design first oligonucleotides, or, where the oligonucleotide directs an alteration that confers a selectable phenotype, first and/or second oligonucleotides. Moreover, 30 the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides designed using the sequences of oligonucleotides disclosed in the various tables for correction of human diseases or for directing specific alterations in plant genes

comprise structures or modifications that enable them to effect oligonucleotide-directed nucleic acid sequence alteration, such as, e.g., phosphorothioate linkages, LNA residues or chimeric RNA-DNA internally duplexed structure.

[0128] Efficiency of conversion is defined herein as the percentage of recovered substrate target molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. an extrachromosomal element in a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be analyzed, e.g. by sequencing, allele-specific PCR or comparable techniques, to determine the percentage that have acquired the desired change. This latter method of determining efficiency is most frequently applied where the phenotype conferred by the alteration is a non-selectable phenotype.

[0129] Each of the first and second oligonucleotides can direct any kind of alteration, including, for example, deletion, insertion or replacement of 1, 2 or 3 nucleotides in the target sequence. These altered nucleotides may be contiguous or non-contiguous to each other. Multiple alterations can be directed to each of the first and second target sites by a single oligonucleotide or by 1, 2 or 3 separate oligonucleotides. In some embodiments, the multiple alterations are directed by a single oligonucleotide. In some embodiments, the multiple alterations are within 1 to 10 nucleotides of each other.

[0130] The methods, compositions and kits of the invention can be combined with one or more other methods of enhancing the efficiency of oligonucleotide-directed alteration of nucleic acid sequence known in the art.

[0131] Such methods are described, e.g., in copending International patent applications published as WO 02/10364 ("Methods for Enhancing Targeted Gene Alteration Using Oligonucleotides,"); WO 03/027265 ("Composition and Methods for Enhancing Oligonucleotide-Directed Sequence Alteration"); and WO 03/075856 ("Methods, Compositions, and Kits for Enhancing Oligonucleotide-Mediated Nucleic Acid Sequence Alteration Using Compositions Comprising a Histone Deacetylase Inhibitor, Lambda Phage Beta Protein, or Hydroxyurea"), the disclosures of which are incorporated herein by reference in their entireties.

[0132] For example, in typical embodiments of this aspect of the invention, the methods comprise treating a cell or tissue from a bacterium, a fungus, a plant, or an animal with a histone deacetylase (HDAC) inhibitor or hydroxyurea (HU), and then administering to the treated cell or tissue at least first and second oligonucleotides having nucleic acid sequence alteration activity. In other

embodiments, the HDAC inhibitor or hydroxyurea, respectively, may be added contemporaneously with oligonucleotide addition or even following oligonucleotide addition.

[0133] The HDAC inhibitor can be trichostatin A.

[0134] One of skill in the art will appreciate, however, that other HDAC inhibitors may be suitable for these purposes. For example, U.S. Patent Application Publication No. 2002/0143052, which is hereby incorporated by reference in its entirety, discloses compounds having HDAC inhibitor activity due to the presence of a zinc-binding moiety. Other examples of HDAC inhibitors suitable for purposes of the invention include butyric acid, MS-27-275, suberoylanilide hydroxamic acid (SAHA), oxamflatin, trapoxin A, depudecin, FR901228 (also known as depsipeptide), apicidin, *m*-carboxy-cinnamic acid bishydroxamic acid (CBHA), suberic bishydroxamic acid (SBHA), and pyroxamide. See Marks *et al.*, *J. Natl. Canc. Inst.* 92(15):1210-1216 (2000), which is hereby incorporated by reference in its entirety. Yet other examples of suitable HDAC inhibitors are chlamydocin, HC-toxin, Cyl-2, WF-3161, and radicicol, as disclosed in WO 00/23567, which is hereby incorporated by reference in its entirety.

[0135] When administering an HDAC inhibitor or HU to cells or cell extracts, the dosage to be administered and the timing of administration will depend on various factors, including cell type.

[0136] In the case of TSA, the dosage may be 10 nM, 100 nM, 1 μ M, 10 μ M, 100 μ M, 1 mM, 10 mM, or even higher, or as little as 1 nM, 100 μ M, 10 μ M, 1 μ M, 100 nM, 10 nM, 1 nM, or even lower. In the case of HU, the dosage may be 100 nM, 1 μ M, 10 μ M, 100 μ M, 1 mM, 10 mM, 100 mM, 1 M or even higher, or as little as 100 nM, 10 mM, 1 mM, 100 μ M, 10 μ M, 1 μ M, 100 nM, 10 nM, or even lower.

[0137] In the case of HU, treatment may be with 100 mM, 75 mM, 50 mM, 40 mM, 20 mM, 10 mM, 2 mM, 1 mM, 100 microM, 10 microM, 1 microM, 100 nM, 10 nM or lower. The dosage is preferably from about 4 to 100 mM for yeast cells and from about 0.05 mM to 3 mM for mammalian cells. The dosage may be at least 0.05 mM, 0.10 mM, 0.15 mM, 0.20 mM, 0.25 mM, 0.30 mM, 0.35 mM, 0.40 mM, 0.50 mM or more, including at least 0.55 mM, 0.60 mM, 0.65 mM, 0.70 mM, 0.75 mM, 0.80 mM, 0.85 mM, 0.90 mM, 0.95 mM or even 1 mM, 1.1 mM, 1.2 mM, 1.3 mM, 1.4 mM, 1.4 mM, 1.5 mM, 1.6 mM, 1.7 mM, 1.8 mM, 1.9 mM, 2.0 mM, 2.5 mM, 3 mM, or more. Typically, the dosage for mammalian cells is less than about 3.0 mM, and can be less than 2.5 mM, 2.0 mM, 1.5 mM, 1.0 mM, even less than 0.90, 0.85, 0.80, 0.75, 0.70, 0.65, 0.60, 0.55, 0.50, 0.45, 0.40, and even less than about 0.35 or 0.30 mM.

[0138] Cells may be grown in the presence of an HDAC inhibitor or HU, and cell extracts may be treated with the HDAC inhibitor or HU, for various times prior to combination with a sequence-altering oligonucleotide. Growth or treatment may be as long as 1 h, 2 h, 3 h, 4 h, 6 h, 8 h, 12

h, 20 h, or even longer, including up to 28 days, 14 days, 7 days, or shorter, or as short as 12 h, 8 h, 6 h, 4 h, 3 h, 2 h, 1 h, or even shorter. Alternatively, treatment of cells or cell extracts with HDAC inhibitor or HU and the sequence-altering oligonucleotide may occur simultaneously, or the HDAC inhibitor or HU, respectively, may be added after oligonucleotide addition.

5 **[0139]** Cells may further be allowed to recover from treatment with an HDAC inhibitor or HU by growth in the absence of the HDAC inhibitor or HU for various times prior to treatment with a sequence-altering oligonucleotide. Recovery may be as long as 10 min, 20 min, 40 min, 60 min, 90 min, 2 h, 4 h, or even longer, or as short as 90 min, 60 min, 40 min, 20 min, 10 min, or even shorter. Cells may also be allowed to recover following their treatment with a sequence-altering oligonucleotide. This
10 recovery period may be as long as 1 h, 2 h, 4 h, 6 h, 8 h, 12 h, or even longer, or as short as 8 h, 6 h, 4 h, 2 h, 1 h, or even shorter. The HDAC inhibitor or HU may either be present in or absent from the cell medium during the recovery period.

[0140] Optimum dosages and the timing and duration of administration of HDAC inhibitors and HU to cells or cell extracts can be determined by routine experimentation. For example,
15 optimized dosage and timing of treatment with an HDAC inhibitor, such as TSA, can be determined using the assay system described in WO 03/075856.

[0141] Cultured cells (such as yeast cells) are treated with varying concentrations of HDAC inhibitor for a varying number of hours prior to electroporation with the sequence altering oligonucleotide. After recovery for varying periods, the cells are plated and tested for efficiency of
20 sequence alteration. Parameters are then selected that provide the highest efficiency of correction. The method may then be repeated, as necessary, further to optimize dosage, duration of pretreatment, duration of recovery period, if any, and the like.

[0142] A similar approach for HU can be determined using the assay system set forth in WO 03/075856.

25 **[0143]** The methods, compositions, and kits of the instant invention comprising either an HDAC inhibitor, such as trichostatin A, or HU typically increase nucleic acid sequence alteration efficiency by at least two fold relative to the same method respectively lacking the HDAC inhibitor or HU. The increase in nucleic acid sequence alteration efficiency can also be about three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold. The methods, compositions, and kits
30 of the instant invention comprising beta protein increase the efficiency of altering a DNA sequence, as compared to the same method lacking beta protein, typically at least 2 fold, and can increase the efficiency 5 fold, 10 fold, 15 fold, 20 fold, 25 fold, 30 fold, 40 fold, 50 fold, 60 fold, 70 fold, 80 fold, 90 fold,

100 fold, 250 fold, 500 fold, 1000 fold, or more; in certain embodiments, the methods, compositions, and kits of the instant invention that comprise beta protein increase efficiency less than two-fold as compared to comparable methods lacking beta protein, such as 1.9 fold, 1.5 fold, or even by 10%, 20%, 30%, 40%.

[0144] The cells in which targeted nucleic acid sequence alterations may usefully be made according to the methods of the present invention include mammalian cells, including human cells, such as liver, lung, colon, cervix, kidney, and epithelium cells.

[0145] Cultured mammalian cells that usefully may be targeted for desired sequence alteration according to the methods of the present invention include HT1080 cells (human epithelial fibrosarcoma), COS-1 and COS-7 cells (African green monkey), CHO-K1 cells (Chinese hamster ovary), H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C127I (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma) cancer cells as well as PC12 cells (rat pheochromocytoma).

[0146] Alterations in cultured mammalian cells may usefully be made to create coisogenic cell collections, as described in copending international patent application published as WO 03/027264 and U.S. patent application no. 10/260,638, the disclosures of which are incorporated herein by reference in their entireties. Genes usefully targeted in such coisogenic collections include loci affecting drug resistance (equivalently, drug sensitivity) or drug metabolism, including: CYP1A2, CYP2C17, CYP2D6, CYP2E, CYP3A4, CYP4A11, CYP1B1, CYP1A1, CYP2A6, CYP2A13, CYP2B6, CYP2C8, CYP2C9, CYP11A, CYP2C19, CYP2F1, CYP2J2, CYP3A5, CYP3A7, CYP4B1, CYP4F2, CYP4F3, CYP6D1, CYP6F1, CYP7A1, CYP8, CYP11A, CYP11B1, CYP11B2, CYP17, CYP19, CYP21A2, CYP24, CYP27A1, CYP51, ABCB1, ABCB4, ABCC1, ABCC2, ABCC3, ABCC4, ABCC5, ABCC6, MRP7, ABCC8, ABCC9, ABCC10, ABCC11, ABCC12, EPHX1, EPHX2, LTA4H, TRAG3, GUSB, TMPT, BCRP, HERG, hKCNE2, UDP glucuronosyl transferase (UGT), sulfotransferase, sulfatase, glutathione S-transferase (GST) -alpha, glutathione S-transferase -mu, glutathione S-transferase -pi, ACE, and KCHN2.

[0147] In other embodiments, cells within which targeted alterations may usefully be effected according to the methods of the present invention include progenitor and stem cells — both embryonic (ES) stem cells and non-ES cells such as hematopoietic progenitor or stem cells, including CD34⁺CD38⁻ hematopoietic progenitor and stem cells and muscle-derived stem cells.

[0148] ES cells can be mammalian ES cells, either non-human mammalian ES cells or human ES cells; human ES cells may, e.g., be from a cell line approved for use in the jurisdiction in which

the methods, compositions and kits of the present invention are to be used. For example, for use in the United States, any human stem cell line that does not violate state or federal law may be used, such as those cell lines that meet United States federal funding criteria; the National Institutes of Health is currently compiling a list of these existing stem cell lines (<http://escr.nih.gov>) which includes those held by the following: BresaGen, Inc., Athens, Georgia (4 lines); CyThera, Inc., San Diego, California (9 lines); Karolinska Institute, Stockholm, Sweden (5 lines); Monash University, Melbourne, Australia (6 lines); National Center for Biological Sciences, Bangalore, India (3 lines); Reliance Life Sciences, Mumbai, India (7 lines); Technion-Israel Institute of Technology, Haifa, Israel (4 lines); University of California, San Francisco, California (2 lines); Göteborg University, Göteborg, Sweden (19 lines); Wisconsin Alumni Research Foundation, Madison, Wisconsin (5 lines).

[0149] In yet other embodiments, the cells within which targeted alterations are made are plant cells.

[0150] Particularly useful plants from which the cells to be used may be drawn include, for example, experimental model plants such as *Chlamydomonas reinhardtii*, *Physcomitrella patens*, and *Arabidopsis thaliana* in addition to crop plants such as cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), fruits such as apples (*Malus*, e.g. *domesticus*), mangoes (*Mangifera*, e.g. *indica*), banana (*Musa*, e.g. *acuminata*), berries (such as currant, *Ribes*, e.g. *rubrum*), kiwifruit (*Actinidia*, e.g. *chinensis*), grapes (*Vitis*, e.g. *vinifera*), bell peppers (*Capsicum*, e.g. *annuum*), cherries (such as the sweet cherry, *Prunus*, e.g. *avium*), cucumber (*Cucumis*, e.g. *sativus*), melons (*Cucumis*, e.g. *melo*), nuts (such as walnut, *Juglans*, e.g. *regia*; peanut, *Arachis hypogaeae*), orange (*Citrus*, e.g. *maxima*), peach (*Prunus*, e.g. *persica*), pear (*Pyrus*, e.g. *communis*), plum (*Prunus*, e.g. *domestica*), strawberry (*Fragaria*, e.g. *moschata* or *vesca*), tomato (*Lycopersicon*, e.g. *esculentum*); leaves and forage, such as alfalfa (*Medicago*, e.g. *sativa* or *truncatula*), cabbage (e.g. *Brassica oleracea*), endive (*Cichoreum*, e.g. *endivia*), leek (*Allium*, e.g. *porrum*), lettuce (*Lactuca*, e.g. *sativa*), spinach (*Spinacia*, e.g. *oleraceae*), tobacco (*Nicotiana*, e.g. *tabacum*); roots, such as arrowroot (*Maranta*, e.g. *arundinacea*), beet (*Beta*, e.g. *vulgaris*), carrot (*Daucus*, e.g. *carota*), cassava (*Manihot*, e.g. *esculenta*), turnip (*Brassica*, e.g. *rapa*), radish (*Raphanus*, e.g. *sativus*), yam (*Dioscorea*, e.g. *esculenta*), sweet potato (*Ipomoea batatas*); seeds, including oilseeds, such as beans (*Phaseolus*, e.g. *vulgaris*), pea (*Pisum*, e.g. *sativum*), soybean (*Glycine*, e.g. *max*), cowpea (*Vigna unguiculata*), mothbean (*Vigna aconitifolia*), wheat (*Triticum*, e.g. *aestivum*), sorghum (*Sorghum* e.g. *bicolor*), barley (*Hordeum*, e.g. *vulgare*), corn (*Zea*, e.g. *mays*), rice (*Oryza*, e.g. *sativa*), rapeseed (*Brassica napus*), millet (*Panicum* sp.), sunflower (*Helianthus annuus*), oats (*Avena sativa*), chickpea (*Cicer*, e.g. *arietinum*); tubers, such as kohlrabi (*Brassica*, e.g. *oleraceae*), potato (*Solanum*, e.g.

tuberosum) and the like; fiber and wood plants, such as flax (*Linum* e.g. *usitatissimum*), cotton (*Gossypium* e.g. *hirsutum*), pine (*Pinus* sp.), oak (*Quercus* sp.), eucalyptus (*Eucalyptus* sp.), and the like and ornamental plants such as turfgrass (*Lolium*, e.g. *rigidum*), petunia (*Petunia*, e.g. *x hybrida*), hyacinth (*Hyacinthus orientalis*), carnation (*Dianthus* e.g. *caryophyllus*), delphinium (*Delphinium*, e.g. *ajacis*), Job's tears (*Coix lacryma-jobi*), snapdragon (*Antirrhinum majus*), poppy (*Papaver*, e.g. *nudicaule*), lilac (*Syringa*, e.g. *vulgaris*), hydrangea (*Hydrangea* e.g. *macrophylla*), roses (including Gallicas, Albas, Damasks, Damask Perpetuals, Centifolias, Chinas, Teas and Hybrid Teas) and ornamental goldenrods (e.g. *Solidago* spp.).

[0151] Generally, the oligonucleotides are administered to isolated plant cells or protoplasts according to a method of the present invention and the resulting cells are used to regenerate whole plants according to any method known in the art.

[0152] Relatively few specific plant mutations that produce desirable phenotypes have been described for plant species or cultivars.

[0153] However, the methods, compositions and kits of the instant invention may be used to identify a desirable mutation in one species, for example an experimental model plant, and the desirable mutation can then be introduced in the homologous genes of other species using the kits, compositions and methods of the invention. Further, the methods, compositions and kits of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying glutamine can be modified at a specific site to TAA; a AAG codon specifying lysine can be modified to TAG at a specific site; and a CGA codon for arginine can be modified to a TGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a truncated protein shortened at the site of the stop codon, which truncated protein may be defective or have an altered function. Alternatively, frameshift additions or deletions can be directed at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

[0154] Desirable phenotypes that may be obtained in plants by known nucleic acid sequence alterations include, for example, herbicide resistance; male- or female-sterility; salt, drought, lead, freezing and other stress tolerances; altered amino acid content; altered levels or composition of starch; altered levels or composition of oils; and elimination of epitopes in gluten that are known to instigate autoimmune responses in individuals with celiac disease.

[0155] The cells within which targeted alterations are effected according to the methods of the present invention can be primary isolated cells, selectively enriched cells, cultured cells, or tissue explants.

[0156] In certain *ex vivo* embodiments of the methods of the present invention, in which
5 targeted sequence alterations are made in non-human cells, such as non-human mammalian ES cells or plant cells, the sequence-altered cells can be used to generate intact organisms, which can thereafter be propagated.

[0157] For example, the methods of the present invention can be used to create
10 genetically altered animals, including livestock — such as cattle, bison, horses, goats, sheep, pigs, chickens, geese, ducks, turkeys, pheasant, ostrich and pigeon — to enhance expression of desirable traits, and/or decrease expression of undesirable traits, by first creating genetically altered cells. In other embodiments, the methods of the present invention can be used to create genetically altered animals useful as laboratory models, such as rodents, including mice, rats, guinea pigs; lagomorphs, such as rabbits; monkeys; apes; dogs; and cats. Methods for producing transgenic animals comprising genetically
15 modified cells are known in the art, and are disclosed, for example, in WO 00/51424, "Genetic Modification of Somatic Cells and Uses Thereof," the disclosure of which is hereby incorporated herein by reference in its entirety.

[0158] Further aspects of the present invention are the non-human animals produced
thereby.

[0159] In other *ex vivo* embodiments of the methods of the present invention, the
20 targeted sequence alterations are made in human ES cells, which are thereafter used, where legally permissible, to generate tissue or, where permitted, a viable embryo.

[0160] In other *ex vivo* embodiments of the methods of the present invention, in which
25 targeted sequence alterations are made in human non-ES cells, such as hematopoietic progenitor or stem cells, such as CD34⁺CD38⁻ hematopoietic stem cells, the sequence-altered cells can be reintroduced into a human subject for *ex vivo* gene therapies.

[0161] In certain particularly useful embodiments of the methods of the present
invention, the first and second oligonucleotides are designed to alter the nucleic acid sequence of an expressed human gene or a plant gene.

[0162] The oligonucleotides used in the methods, compositions and kits of the invention
30 can be introduced into cells or tissues by any technique known to one of skill in the art. Such techniques include, for example: electroporation; carrier-mediated delivery using, e.g., liposomes, aqueous-cored

lipid vesicles, lipid nanospheres or polycations; naked nucleic acid insertion; particle bombardment and calcium phosphate precipitation. In some embodiments, the oligonucleotides are introduced using electroporation, for example using a BTX ECM® 830 Square Wave electroporator. In other embodiments the transfection is performed with a liposomal transfer compound, for example, DOTAP (N-1-(2,3-
5 Dioleoyloxy)propyl-N,N,N-trimethylammonium methylsulfate, Boehringer-Mannheim) or an equivalent, such as LIPOFECTIN®. In other embodiments, the transfection technique uses cationic lipids. In some embodiments, transfection is performed with Lipofectamine™ 2000 (Invitrogen Corporation, Carlsbad, CA).

[0163] The methods of the invention can be used with a wide range of concentrations
10 of oligonucleotides. For example, good results can be achieved with 10 nM/10⁵ cells. A ratio of about 500 ng of oligonucleotide in 3 µg of DOTAP per 10⁵ cells can be used. The transfected cells may be cultured in different media, including, for example, in serum-free media, media supplemented with fetal calf serum, human serum albumin, or human serum. The first and second oligonucleotides are typically used in a 1:1 stoichiometric ratio, but other ratios including, e.g., 1:2, 1:3, 1:4 and 1:5, may be used in the methods,
15 composition and kits of the invention. In some embodiments, the first and second oligonucleotides used in the methods and compositions of the invention are administered simultaneously; in other embodiments the oligonucleotides are adjunctively administered.

[0164] Further embodiments of the invention are compositions and kits comprising a cell, cell-free extract, or cellular repair protein and at least one oligonucleotide which is capable of
20 effecting a desired sequence alteration at a nucleic acid target site, which sequence alteration confers a selectable phenotype. In some embodiments, the compositions and kits also comprise a second oligonucleotide that is capable of effecting a desired sequence alteration, typically a sequence alteration that is frequently desired and/or is not selectable. In some embodiments the compositions or kits comprise a nucleic acid molecule comprising a nucleic acid sequence which is the target for the at least
25 one oligonucleotide which capable of effecting a desired sequence alteration at a nucleic acid target site, which sequence alteration confers a selectable phenotype.

[0165] A cell, cell-free extract, or cellular repair protein for a composition or kit of the invention may be derived from any organism. Compositions and kits of the invention and may comprise any combination of cells, cell-free extracts, or cellular repairs proteins and the cells, cell-free extracts, or
30 cellular repair proteins may be from the same organism or from different organisms. Cellular repair proteins that may be used include, for example, proteins from the RAD52 epistasis group, the mismatch repair group, or the nucleotide excision repair group. In some embodiments, the cell, cell-free extract, or

cellular repair protein is or is from a eukaryotic cell or tissue. In some embodiments, the eukaryotic cell is a fungal cell, e.g. a yeast cell. In other embodiments, the cell is a plant cell, e.g., a maize, rice, wheat, barley, soybean, cotton, potato or tomato cell. Other exemplary plant cells include those described elsewhere herein. In some embodiments, the kits comprise a chemical compound selected from the group consisting of: a trichostatin, a histone deacetylase inhibitor and the lambda beta protein. In some
5 embodiments such kits also include instructions for use.

[0166] Other embodiments of the invention relate to kits comprising a nucleic acid molecule the nucleic acid sequence of which has been altered according to a method of the invention or using a composition or kit of the invention. In some embodiments, the invention relates to kits comprising
10 a cell comprising a nucleic acid molecule the nucleic acid sequence of which has been altered according to the methods of the invention or using a composition or kit of the invention. In some embodiments, the nucleic acid molecule is selected from the group consisting of: mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), plasmids, viruses or other recombinant vectors.

[0167] The purified oligonucleotides compositions may be formulated in accordance with routine procedures as a pharmaceutical composition adapted for bathing cells in culture, for microinjection into cells in culture, and for intravenous administration to human beings or animals. Typically, compositions for cellular administration or for intravenous administration into animals, including humans, are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also
20 include a solubilizing agent and a local anaesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients will be supplied either separately or mixed together in unit dosage form, for example, as a dry, lyophilized powder or water-free concentrate. The composition may be stored in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent in activity units. Where the composition is administered by infusion, it can be dispensed with an infusion
25 bottle containing sterile pharmaceutical grade "water for injection" or saline. Where the composition is to be administered by injection, an ampule of sterile water for injection or saline may be provided so that the ingredients may be mixed prior to administration.

[0168] Pharmaceutical compositions of this invention comprise the oligonucleotides used in the methods of the present invention and pharmaceutically acceptable salts thereof, with any
30 pharmaceutically acceptable ingredient, excipient, carrier, adjuvant or vehicle.

[0169] The oligonucleotides of the invention are preferably administered to the subject in the form of an injectable composition. The composition is preferably administered parenterally,

meaning intravenously, intraarterially, intrathecally, interstitially or intracavitarily. Pharmaceutical compositions of this invention can be administered to mammals including humans in a manner similar to other diagnostic or therapeutic agents. The dosage to be administered, and the mode of administration will depend on a variety of factors including age, weight, sex, condition of the subject and genetic factors, and will ultimately be decided by medical personnel subsequent to experimental determinations of varying dosage as described herein. In general, dosage required for targeted nucleic acid sequence alteration and therapeutic efficacy will range from about 0.001 to 50,000 µg/kg, e.g. between 1 to 250 µg/kg of host cell or body mass or a concentration of between 30 and 60 micromolar.

[0170] For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In one method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim), Lipofectamine™ 2000 (Invitrogen™) or an equivalent such as lipofectin. The amount of the oligonucleotide pair used, for example, is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells or about 1 microgram with 1 microliter Lipofectamine™ 2000 per 1,000,000 cells. For electroporation, between 20 nanograms and 30 micrograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein.

[0171] In order that this invention may be better understood, the following examples are set forth. These examples are for purposes of illustration only, and are not to be construed as limiting the scope of the invention in any manner.

EXAMPLE 1

Yeast Cell Targeting Assay Method for Nucleic Acid Sequence Alteration and Preferred Oligonucleotide Selection

[0172] In this example, we use single-stranded oligonucleotides to measure oligonucleotide-directed nucleic acid sequence alteration using a Mata wild-type yeast strain with an integrated plasmid with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair (Mata+IntHYG(x)eGFP). Modifications to the oligonucleotides and construction of target vectors are disclosed in WO 01/73002, the disclosure of which is hereby incorporated by reference.

[0173] *In vivo* assay systems. We monitor targeted alteration of genetic material in yeast using both episomal and chromosomal targets. To monitor gene alteration of episomal targets, we

employ a yeast system using the plasmids pAURHYG(rep)eGFP, which contains a point mutation in the hygromycin resistance gene, pAURHYG(ins)eGFP, which contains a single-base insertion in the hygromycin resistance gene and pAURHYG(Δ)eGFP which has a single base deletion (shown in Figure 1). We also use the same plasmid containing a functional copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)eGFP, as a control. These plasmids are collectively designated pAURHYG(x)eGFP. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)eGFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, in codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In pAURHYG(ins)eGFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, in codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene. In pAURHYG(Δ)eGFP, hygromycin resistance gene function and green fluorescence from eGFP are restored when a C is inserted at the site of the single nucleotide deletion.

[0174] We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows: (rep) indicates a T137G replacement, (Δ) represents a deletion of G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)eGFP and ligation into pAUR123 (Panvera, CA). We digest 10 μ g pAUR123 vector DNA as well as 10 μ g of each pHyg(x)eGFP construct with KpnI and SalI (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pAUR123 vector at a 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify plasmid DNA using a Qiagen maxiprep kit.

[0175] To monitor oligonucleotide-directed alteration of chromosomal nucleic acid sequence targets, we typically employ a yeast system in which we monitor chromosomal genes or we use integrational plasmids such as those designated pAUR101-HYG(x)eGFP. These plasmids do not replicate in yeast. These plasmids comprise the HYG(x)eGFP fusion proteins used in the pAURHYG(x)eGFP episomal plasmid system (shown in Figure 1) and an aureobasidinA resistance gene. Therefore, like pAURHYG(x)eGFP, these constructs can also be used to monitor all types of gene alterations, i.e. replacements, insertions and deletions. We designate yeast strains into which the

pAUR101-HYG(x)eGFP plasmid integrates as "+IntHYG(x)eGFP." In addition to this construct, we monitor gene alteration of specific yeast genes including, for example, CYC1.

[0176] *Oligonucleotide synthesis and cells.* We synthesize and purify the chimeric, RNA-DNA oligonucleotides with internally duplexed conformation and single-stranded oligonucleotides (including those with the indicated modifications) using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, the oligonucleotides are gel-purified using, for example, procedures such as those described in Gamper et al., *Biochem.* 39, 5808-5816 (2000), or the oligonucleotides are ion-exchange HPLC-purified. We determine the concentration of the oligonucleotides spectrophotometrically (33 or 40 $\mu\text{g/ml}$ per A_{260} unit of single-stranded or hairpin oligonucleotide, respectively). We introduce the oligonucleotides into yeast cells by electroporation as follows: we prepare electrocompetent yeast cells by inoculating 10 ml of YPD media supplemented with 250 $\mu\text{g/ml}$ aureobasidin from a single colony and grow the cultures overnight with shaking at 300 rpm at 30°C. We pellet the cells from the overnight culture by centrifuging at 3000 rpm for 5 minutes, resuspend the cells in 40 ml YPD media (OD_{600} approximately 0.2). We incubate the cells with shaking at 30°C until the OD_{600} is between 0.5 and 1.0 (3-5 hours). We wash the cells by centrifuging at 4°C at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We centrifuge at 4°C at 3000 rpm for 5 minutes and resuspend in 1 ml ice-cold 1M sorbitol and then finally centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the cells in 120 μl 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40 μl of cells with oligonucleotide (typically 5 μg or amounts as indicated) and incubate on ice for 5 minutes. We transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene Pulser apparatus at 1.5 kV, 25 μF , 200 Ω for one five-second pulse. We then immediately resuspend the cells in 3 ml YPD media supplemented with 2M sorbitol and incubate the cultures at 30°C with shaking at 300 rpm for 6 hours. We spread 200 μl of this culture on selective plates containing 300 $\mu\text{g/ml}$ hygromycin and spread 200 μl of a 10^5 dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We count the colonies on the plates and calculate the gene conversion efficiency by determining the number of hygromycin resistance colonies per 10^5 aureobasidinA resistant colonies.

[0177] *Oligonucleotides direct gene alteration.* We use this system to assay the ability of various oligonucleotides (sequences shown in Table 1) to support correction under a variety of conditions. The oligonucleotides are designed so that they can direct correction of the replacement, insertion and deletion mutations in Mata+IntHYG(x)eGFP. The oligonucleotides generally are centered

around the base targeted for alteration. In this example, we test the ability of these oligonucleotides to direct alteration of nucleic acid sequence in Mata+IntHYG(rep)eGFP (see Table 2).

[0178] We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in both the pAURHYG(x)eGFP plasmid and in yeast strains with integrated copies of pAUR101-HYG(x)eGFP. These include, for example, an oligonucleotide that alters two basepairs that are 3 nucleotides apart with the sequence 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG **G**T ACG TCC TGC GGG TAA ATA GCT GCG CCG ATG GTT TCT AC-3' (SEQ ID NO: _); a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT **A**CG TCC TGC GGG TAA **A**CA GCT GCG CCG ATG GTT TCT AC-3' (SEQ ID NO: _); and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT **A**CG TCC TGC GGG TAA ATA GCT GCG CCG **A**CG GTT TCT AC (SEQ ID NO: _). The nucleotides in these oligonucleotides that direct alteration of the target sequence are in boldface. These oligonucleotides are chemically modified to enable them to effect oligonucleotide-directed nucleic acid sequence alteration.

Table 1: Oligonucleotides used in Examples 1 and 2

Name	Size	Sequence	SEQ ID NO:
Hyg3S/74T	74mer	5'-C*T*C* GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT A CG TCC TGC GGG TAA ATA GCT GCG CCG ATG GTT TC *T*A*C-3'	
Hyg3S/74NT	74mer	5'-G*T*A* GAA ACC ATC GGC GCA GCT ATT TAC CCG CAG GAC G TA TCC ACG CCC TCC TAC ATC GAA GCT GAA AGC AC*G *A*G-3'	

Phosphorothioate linkages are indicated as "*" between the bases. The base corresponding to the location of the replacement mutation in the Hyg(rep) target is in bold.

Table 2: Gene alteration in Mata+IntHYG(rep)eGFP

Oligonucleotide assayed	Alteration per 10 ⁵ Aureobasidin ^R colonies ¹	Fold correction (relative to Hyg3S/74T)
Hyg3S/74T	0.22 ± 0.3	1x
Hyg3S/74NT	0.89 ± 1.3	4.0x

¹These numbers represent an average of four experiments with the standard deviation indicated for alteration efficiency.

EXAMPLE 2

Selection for a First Alteration Reduces Screening Required to Identify a Second Alteration in the Same Cell

[0179] In this example we demonstrate that the efficiency of alteration of nucleic acid
5 sequence at a second site is enhanced in a population of nucleic acid molecules that have been
previously selected for alteration at a first target site. We use yeast strains having an integrated copy of
the pAUR101-HYG(rep)eGFP plasmid described in Example 1 that also contain the β S YAC (230 kb YAC
comprising the human β -globin gene). In some experiments, the yeast strains also contain a plasmid that
overexpresses yeast Rad51, designated pYNARad51. We use several oligonucleotides: Hyg3S/74NT,
10 which, as described in Example 1, is capable of directing alteration of the mutated Hyg(x)eGFP target to
confer hygromycin resistance; and β S-386m and β S-378m, each of which is a 71-mer oligonucleotide
with 3 phosphorothioate linkages on each end, which is capable of directing a mutation in the human β -
globin gene. The sequence of β S-386m is 5' – G*C*C* TCA CCA CCA ACT TCA TCC ACG TTC ACC
TTG CCT CAC AGG GCA GTA ACG GCA GAC TTC TCC ACA GG*A *G*T – 3' (SEQ ID NO: _) and the
15 sequence of β S-378m is 5' – T*A*A* CGG CAG ACT TCT CCA CAG GAG TCA GGT GCA CCG TGG
TGT CTG TTT GAG GTT GCT AGT GAA CAC AG*T *T*G – 3' (SEQ ID NO: _). β S-386m and β S-378m
both hybridize to the non-transcribed sequence of the human β -globin gene and direct a nucleic acid
sequence alteration that creates a β -thalassemia mutation: β S-386m converts a TGG codon to a stop
codon (TGA) and β S-378m converts the ATG start codon to ACG.

20 [0180] We introduce the oligonucleotides into the yeast cells by electroporation as
follows: we prepare electrocompetent yeast cells by inoculating a single colony into 10 ml of appropriate
media supplemented with 250 μ g/ml aureobasidin and grow the cultures overnight with shaking at 300
rpm at 30°C. In this Example, we use YPD media unless the cells contain a plasmid to overexpress a
repair protein when we use SC-ade media. We dilute the cells into 40 ml media to an initial OD₆₀₀ of
25 approximately 0.15. We incubate the cells with shaking at 30°C until the OD₆₀₀ is approximately 0.25 and,
in some experiments, we add 100 mM hydroxyurea (HU). We continue to incubate the cells with shaking
at 30°C until the OD₆₀₀ is approximately 0.6. We spin down the cells at 3000 rpm for 5 minutes and
resuspend in 1 ml YPD supplemented with 25 μ l 1M DTT and incubate the culture with shaking at 30°C
for 20 minutes. We wash the cells four times by centrifuging at 4°C at 3000 rpm for 5 minutes and
30 resuspending the cells twice in 25 ml ice-cold distilled water; once in 25 ml ice-cold 1M sorbitol; and once
in 1 ml ice-cold 1M sorbitol. We centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the
cells in 120 μ l 1M sorbitol. We transform the electrocompetent cells with Hyg3S/74NT and either β S-

386m or β S-378m by mixing 40 μ l of cells with 30 μ g oligonucleotide (or 30 μ g of each oligonucleotide) and incubate on ice for 5 minutes. We transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD® Gene Pulser® apparatus at 1.5 kV, 25 μ F, 200 Ω for one approximately five-second pulse. We then resuspend the cells in 3 ml YPD media supplemented with Aureobasidin and allow the cells to recover by incubating them overnight at 30°C with shaking at 300 rpm. In some experiments, we supplement the culture with 50 mg/ml Trichostatin A (TSA) during this recovery phase. We spin down the cells, resuspend in 1 ml YPD and spread 100 μ l of this culture (and/or 100 μ l of 10^1 or 10^2 dilutions) on selective plates containing 300 μ g/ml hygromycin and spread 200 μ l of a 10^5 dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We count the colonies on the plates and calculate the conversion efficiency for the hygromycin target by determining the number of hygromycin resistance colonies per 10^5 aureobasidinA resistant colonies. We pick individual colonies from YPD-hygromycin plates into 96-well plates with 150 μ l YPD/well and allow the cells to grow overnight at 30°C. We screen individual wells for alteration of the β -globin target in the β S YAC as follows: we PCR amplify a 345 bp fragment of the β -globin gene using forward primer PCO2; 5'- TCC TAA GCC AGT GCC AGA AGA -3' (SEQ ID NO:) and reverse primer PCO5; 5'- CTA TTG GTC TCC TTA AAC CTG -3' (SEQ ID NO:) and purify the PCR product. We analyze the sequence at the target nucleotide in the PCR products by SNaPshot™ analysis on an ABI3100 (Applied Biosystems™) using primers corresponding to the different alterations directed by β S-386m and β S-378m as follows: 386RC; 5'- CCC CCC CCC CCC CCC CCA AGT CTG CCG TTA CTG CCC TGT G -3' (SEQ ID NO:) and 378MF; 5'- TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TGC AAC CTC AAA CAG ACA CCA -3' (SEQ ID NO:).

[0181] As shown in Tables 3 and 4, we observe that the alteration efficiency of the β -globin gene is approximately 10-fold higher than for alteration of the hygromycin target. We observe this result with both β S-386m and β S-378m as well as in the presence or absence of additional factors that enhance oligonucleotide-directed nucleic acid sequence alteration such as, e.g., overexpression of Rad51.

[0182] In other experiments, we do the experiments in yeast strains overexpressing other repair protein(s) in place of or in addition to Rad51 and/or yeast strains with one or more mutations in repair proteins. We also do experiments where we add other compounds that enhance oligonucleotide-directed nucleic acid sequence alteration such as histone deacetylase inhibitors and the bacteriophage lambda beta protein.

Table 3: β S-386m Experiment

Yeast Strain and treatment	Oligonucleotide(s)	Hygromycin Alteration Efficiency (/10 ⁵)	β -globin Alteration Efficiency
Mata-intHyg(rep)eGFP/ β YAC (HU + TSA)	Hyg3S/74NT	12.35	NA
Mata-intHyg(rep)eGFP/ β YAC (HU + TSA)	Hyg3S/74NT + β S-386m	30.51	0.0031
Mata-intHyg(rep)eGFP/ β YAC	Hyg3S/74NT	3.22	NA
Mata-intHyg(rep)eGFP/ β YAC	Hyg3S/74NT + β S-386m	5.07	ND

NA = not applicable; ND = not determined

5

Table 4: β S-378m Experiment

Yeast Strain and treatment	Oligonucleotide(s)	Hygromycin Alteration Efficiency (/10 ⁵)	β -globin Alteration Efficiency
Mata-intHyg(rep)eGFP/ β YAC (HU + TSA)	Hyg3S/74NT + β S-378m	44.58	ND
Mata-intHyg(rep)eGFP/ β YAC (HU + TSA)	Hyg3S/74NT	12.79	NA
Mata-intHyg(rep)eGFP/ β YAC (HU + TSA)	KanUD3/71	0.00	NA
Mata-intHyg(rep)eGFP/ β YAC + pYNARad51 (HU + TSA)	Hyg3S/74NT + β S-378m	123.73	0.15
Mata-intHyg(rep)eGFP/ β YAC + pYNARad51 (HU + TSA)	Hyg3S/74NT	96.96	NA
Mata-intHyg(rep)eGFP/ β YAC + pYNARad51 (HU + TSA)	KanUD3/71	0.01	NA

NA = not applicable; ND = not determined; KanUD3/71 is a negative control oligonucleotide

EXAMPLE 3

Selection for a First Alteration Reduces Screening Required to Identify a Second Alteration in Human Blood Cells

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[0183] *Assay system.* We monitor targeted alteration of genetic material in human

blood cells using the chromosomal gene encoding the beta subunit of hemoglobin as the target. We

cointroduce two oligonucleotides with a plasmid comprising a mutant copy of the green fluorescent protein (GFP) gene. The second oligonucleotide is designed to direct an alteration which repairs the mutant GFP

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resulting in fluorescence. The first oligonucleotide is designed to convert the wild-type allele to the sickle

allele. We use first oligonucleotides that correspond in sequence to the wild-type allele at all positions except the single nucleotide position designed to introduce the sickle mutation into the gene. Therefore, these oligonucleotides are identical to the oligonucleotides described in Example 6 and shown in Table 7 except for a single base. For example, we use first oligonucleotides selected from: 5'- C*A*A* CCT CAA
 5 ACA GAC ACC ATG GTG CAC CTG ACT CCT GtG GAG AAG TCT GCC GTT ACT GCC CTG TGG
 GGC AA*G *G*T -3'; SEQ ID NO: _; 5'- A*C*C* TTG CCC CAC AGG GCA GTA ACG GCA GAC TTC
 TCC aCA GGA GTC AGG TGC ACC ATG GTG TCT GTT TGA GG*T *T*G-3'; SEQ ID NO: _; 5'-ACC
 TCA AAC AGA CAC CAT GGT GCA CCT GAC TCC TGt GGA GAA GTC TGC CGT TAC TGC CCT GTG
 GGG CAA GG -3'; SEQ ID NO: _; 5'- G*A*C* ACC ATG GTG CAC CTG ACT CCT GtG GAG AAG TCT
 10 GCC GTT ACT GCC *C*T*G -3'; SEQ ID NO: _; and 5'- A*C*C* TCA AAC AGA CAC CAT GGT GCA
 CCT GAC TCC TGt GGA GAA GTC TGC CGT TAC TGC CCT GTG GGG CA*A *G*G -3'. The bases in
 the oligonucleotides which are mismatched to the wild-type allele are shown in lowercase. The
 oligonucleotides are synthesized with three phosphorothioate linkages on each end (represented with
 asterisks) or with a single LNA base at each end (bold).

15 **[0184]** *Preparation and treatment of cells.* We thaw and electroporate cells as follows.
 We warm QBSF-60 medium (Quality Bio) containing 10% FCS (StemCell Technologies) to 37°C. We
 quickly thaw frozen G-CSF mobilized peripheral blood CD-34⁺ cells (BioWhittaker) in a 37°C water bath,
 wipe the outside of the tube with 70% ethanol and aseptically transfer about 2 ml (approximately 1 x 10⁶
 cells) of cell suspension to a 15 ml or 50 ml conical tube. We rinse the vial in 1 ml of medium and add it
 20 dropwise to the cells, gently swirling the conical tube every few drops. We slowly add medium dropwise
 until the volume is about 5 ml, still gently swirling the conical tube every few drops, and then slowly bring
 the volume up to fill the tube by adding 1-2 ml of medium dropwise, swirling after every addition. We
 centrifuge the cell suspension at 200 x g (1500 rpm) for 15 minutes at room temperature. We use a pipet
 to remove most of the wash to a second tube, leaving a few ml behind to avoid disturbing the cell pellet.
 25 We resuspend the pellet in the remaining medium and transfer to a 15 ml conical tube. We rinse the
 original tube with 5 ml medium and add the wash to the cells dropwise, swirling gently after each addition,
 and recentrifuge at 200 x g for 15 minutes. We pipet off all but 2 ml of the wash and gently resuspend the
 cells in the remaining medium and count them. We rest the cells at 37°C and 5% CO₂ for 1 hour and then
 recount the cells. We add 5 ml QBSF-60 medium without FCS containing the cytokines flt-3, SCF and
 30 TPO at 100 ng/ml final concentration (Stem Cell Technologies), repellet the cells at 200 x g (1500 rpm for
 15 min), and gently remove as much liquid volume as possible without disturbing the pellet. We
 resuspend the cells at about 5 x 10⁵ - 1 x 10⁶ cells/ml and transfer them to 6-well tissue culture treated

dishes. We stimulate the cells for three days with cytokines (QBSF-60 medium without FCS containing the cytokines flt-3, SCF and TPO at 100 ng/ml final concentration) and perform a cell count using trypan blue exclusion staining. We centrifuge the cells at 200 x g (1500 rpm) for 15 minutes. We remove the excess volume by pipet and resuspend the cells in the same medium at 2×10^6 cells/ml.

5 **[0185]** We electroporate the oligonucleotides and the GFP plasmid into the cells under square wave conditions as follows. We add 250 μ l cell suspension, 5 μ g GFP plasmid and 30 μ g each oligonucleotide to a 2 mm gap cuvette and electroporate for one 19 msec pulse at 220 V. We then add 750 μ l Iscove's Medium (Invitrogen™), 10% FCS (StemCell Technologies) and the cytokines flt-3, SCF, TPO at 100 ng/ml final concentration, glutamine and penicillin/streptomycin. Alternatively, we add 250 μ l
10 cell suspension, 250 μ l QBSF-60 medium supplemented with flt-3, SCF and TPO and 30 μ g oligonucleotide to a 4 mm gap cuvette and electroporate for five 19 msec pulse at 220 V with a pulse interval of 1 sec. We then add 500 μ l Iscove's Medium (Invitrogen™), 10% FCS (StemCell Technologies) and the cytokines flt-3, SCF and TPO at 100 ng/ml final concentration. We select for the repair of the mutant GFP protein using by FACS and analyze the sequence of the hemoglobin target by PCR
15 amplification and analysis on the SNaPShot™ device using two oligonucleotides: 5'- TTT TTT TTT TTT TTT GAC ACC ATG GTG CAC CTG ACT CCT G -3'; SEQ ID NO __; and 5'- TTT TTT TTT TTT TTT TTT TTC AGT AAC GGC AGA CTT CTC C -3'; SEQ ID NO __. As we see in other cells, these oligonucleotides direct targeted alteration in human blood cells.

20 **EXAMPLE 4**

Use of HU and TSA in Dual Targeting Experiments

25 **[0186]** The efficiency of targeted alteration can be increased and the cost decreased by using at least two unrelated oligonucleotides simultaneously in dual targeting experiments. In this approach, alteration by a first oligonucleotide confers a selectable phenotype that is selected for. Alterations directed by a second oligonucleotide are then screened for from within this selected population. Because the population identified by selective pressure is enriched for cells that bear an edited base at the non-selective site, the approach is useful as a method, termed gene editing, for rapidly and efficiently introducing a single nucleotide polymorphism of choice into virtually any gene at any
30 desired location using modified single-stranded oligonucleotides.

[0187] The dual targeting strategy is illustrated in FIG. 2A. The LSY678IntHyg(rep) β strain (Table 5) contains a 240 kb human β^S -globin YAC and a cassette containing a chromosomal

hygromycin-resistance gene inactivated by a single base mutation and a functional aureobasidin-resistance gene. See Liu et al., *Nucleic Acids Res.* 31:2742-2750 (2002); Parekh-Olmedo et al., *Chem. Biol.* 9:1073-1084 (2002); and Liu et al., *Mol. Cell Biol.* 22:3852-3863 (2002). FIG. 2B shows the oligonucleotide that is used to direct editing of the chromosomal hygromycin mutant gene. Hyg3S/74NT (SEQ ID NO: __) is a 74-mer that is specific for binding to the nontranscribed strand and contains three terminal phosphorothioate linkages. *Id.* Also shown is the target sequence of the mutant, which contains a TAG stop codon. FIG. 2C illustrates the structure of the β -globin YAC and nucleotides targeted for editing are specified. The two nonselectable changes are directed by different oligonucleotides, β Thal1 (SEQ ID NO: __) and β Thal2 (SEQ ID NO: __), in separate experiments. The YAC contains approximately 230 kb of genomic DNA from human chromosome 11, indicated by the shaded region. The unshaded regions represent the yeast sequences that are on either end of the YAC (not drawn to scale). Yu et al., *Proc. Natl. Acad. Sci. USA* 97:5978-5983 (2000). A portion of the β -globin sequence is shown, beginning with the start codon. β Thal1 directs a change from a G to an A while β Thal2 directs a change from a T to a C. The sequences of the oligonucleotides having nucleic acid sequence alteration activity are shown and are designed to bind to the non-transcribed strand, relative to human transcription of the β -globin locus. Both changes result in single-base substitutions that have been documented to result in β -thalassemia in humans.

[0188] For editing experiments, YAC-containing LSY678IntHyg(rep) β cells (Table 5) are grown in the presence of HU, electroporated with the selectable and nonselectable oligonucleotides, and allowed to recover in the presence of TSA (FIG. 2A). Because the human β -globin gene is likely to be transcriptionally inactive in yeast, HU and TSA are especially important in increasing target accessibility. The results of dual targeting experiments are presented in FIG. 3A. Hygromycin-resistant colonies are observed when the oligonucleotide, Hyg3S/74NT, is used. The ratio of hygromycin-resistant colonies to aureobasidin-resistant colonies is referred to as the correction efficiency (C.E.). The presence of HU and TSA leads to an increase in the C.E. of the hygromycin mutation, here about 4- to 6-fold. In this experiment, hygromycin-resistant colonies are found at roughly 1 per 3000 aureobasidin-resistant colonies. Hygromycin-resistant colonies are then analyzed for second-site editing in the YAC β -globin gene. The β Thal1 oligonucleotide is designed to direct the replacement of a G in TGG codon 16 of exon 1 with an A, giving the stop codon TGA (FIG. 2C). FIG. 3B shows an ABI SNaPshot (middle panels) and direct DNA sequence (bottom panel) of a region of the β -globin gene in a corrected colony from this experiment; in both, the G to A change is evident. Of those colonies that are corrected in the hygromycin

mutation, 1 in 325 also contain the second change in the YAC β -globin sequence. Thus, approximately 10% of the cells with the corrected hygromycin-resistance gene also contain the edited β -globin gene.

[0189] As shown in various experiments above, overexpression of RAD51 consistently increases the frequency of chromosomal gene editing. Accordingly, we introduce an expression plasmid containing the yeast RAD51 gene into LSY678IntHyg(rep) β cells (Table 5). FIG. 4 shows results of dual targeting in this strain and, as expected, expression of RAD51 increases the hygromycin correction efficiency of oligonucleotide Hyg3S/74NT (compare with FIG. 3). For these editing experiments, YAC-containing LSY678IntHyg(rep) β cells (Table 5) are grown in the presence of HU, electroporated with the selectable and nonselectable oligonucleotides, and allowed to recover in the presence of TSA (FIG. 2A). Here too, addition of a second oligonucleotide, β Thal2, increases the correction efficiency further, to roughly 1 hygromycin-resistant colony per 800 aureobasidin-resistant colonies.

[0190] The β Thal2 oligonucleotide is designed to direct the replacement of a T in the initiator ATG codon of exon 1 with a C, giving the non-initiator codon ACG (FIG. 2). FIG. 4B shows an ABI SNaPshot (middle panels) and direct DNA sequence (bottom panel) of the β -globin gene from a corrected Hyg^r colony; the T to C change is evident in both analytical panels. Importantly, of those colonies that are corrected in the hygromycin mutation, 1 in 70 also contain the second single-base change in the YAC β -globin sequence. Thus, the dual targeting approach is again successful; approximately 10% of the cells bearing the corrected hygromycin also contain the edited β -globin gene. In addition, in the presence of high levels of Rad51, gene editing occurs at a higher level, indicating that the presence of HU, TSA, and RAD51 overexpression exhibit synergistic effects on the overall process.

Table 5
Genotype of yeast strains

Strain	Genotype/Description
AB1380	MATa <i>ura3 trp1 ade2-1 can1-100 lys2-1 his5 ψ^+</i>
LSY678	MATa <i>ura3 trp1-1 ade2-1 leu2-3,112 can1 his3-11,15</i>
LSY678IntHyg(rep)	LSY678 with mutant hygromycin gene and functional aureobasidin-resistance gene integrated into the <i>AUR-1</i> locus on chromosome XI
LSY678IntHyg(rep) β	LSY678IntHyg(rep) with 250 kb YAC containing the human β -globin locus
LSY678IntHyg(rep) β + pYNARAD51	The above strain containing an episomal expression plasmid overexpressing <i>RAD51</i>

[0191] Strains. The genotypes of the yeast strains used in these studies are listed in Table 5. Details of the LSY678IntHyg(rep) strain are published in Liu et al., *Mol. Cell Biol.* 22:3852-3863 (2002).

[0192] YAC Manipulations. The β -globin YAC is isolated from a preparative pulsed-field gel as described in Gnirke et al., *Genomics* 15:659-667 (1993). Briefly, concentrated chromosomal DNA from the β S-YAC strain (AB1380 background, see Chang et al., *Proc. Natl. Acad. Sci. USA* 95:14886-14890 (1998)) is prepared and resolved on a 1% low-melt agarose pulsed-field gel at 200V, 14°C, 20-50s, 33 hours. The YAC is isolated, equilibrated with a modified agarase buffer (10mM BisTris-HCl pH6.5, 1mM EDTA, 100mM NaCl), treated with β -agarase I (New England Biolabs), and concentrated to a final volume of ~200 μ l. Thirty μ l of the purified YAC are introduced into competent LSY678IntHyg(rep) cells by spheroplast transformation and selection on agar/sorbitol plates lacking tryptophan. Transformants are restreaked and confirmed by pulsed-field gel electrophoresis, PCR, and sequence analysis for a fragment of the human β -globin gene.

[0193] The pYNARad51 episomal expression plasmid is constructed by replacing the *TRP1* gene of pYNRad51 (see Liu et al., *Nucleic Acids Res.* 31, 2742-2750 (2002)) with the *ADE2* gene. pYNARad51 is introduced into LSY678IntHyg(rep) β by electroporation and selection on agar plates lacking adenine.

[0194] Oligonucleotides. Hyg3S/74NT (SEQ ID NO: __), β Thal1 (SEQ ID NO: __), and β Thal2 (SEQ ID NO: __) are ordered from IDT with HPLC purification. Hyg3S/74NT is a 74mer and both β Thal1 and β Thal2 are 71mers; all three oligonucleotides have three phosphorothioate linkages at the 5' and 3' ends (FIG. 2).

[0195] Dual Targeting. The dual targeting protocol is outlined in FIG. 2A. LSY678IntHyg(rep) β cells are grown overnight in 10 ml YPD media at 30°C. The culture is diluted to OD₆₀₀ ~0.15-0.20 in 40 ml YPD media and grown for one doubling time to OD₆₀₀ ~0.3-0.4. 100mM HU is added to the culture and the cells are grown for one doubling time to OD₆₀₀ ~0.6-0.8. Cells are harvested and resuspended in 1 ml YPD containing 25 μ l 1M DTT and grown for an additional 20 minutes at 30°C. The cells are washed twice with 25 ml cold dH₂O and once with 25 ml cold 1M sorbitol. The cells are resuspended gently in 1 ml cold 1M sorbitol, spun for 5 minutes at 5000 rpm in a microcentrifuge, and resuspended in 120 μ l 1M sorbitol. Forty microliters of cells are electroporated with 30 μ g of each oligonucleotide in a 2 mm gap cuvette using a Bio-Rad Gene Pulser apparatus (Richmond, CA) with 1.5 kV, 25 μ F, 200 Ω , 1 pulse, 5s/pulsed length. The cells are immediately resuspended in 3 ml YPD with 0.8 μ g/ml aureobasidin A and 50 μ g/ml TSA and recovered overnight at 30°C. The cells are spun down and

resuspended in 1 ml fresh YPD. Dilutions are plated on YPD agar plates containing either hygromycin (300 µg/ml) or aureobasidin A (0.5 µg/ml). Correction efficiencies (C.E.s) are determined based on the number of hygromycin-resistant colonies per aureobasidin-resistant colonies.

[0196] Individual colonies are picked from the hygromycin agar plates into 96-well plates (Corning) containing 150 µl YPD and grown overnight at 30°C with shaking. A 345 bp PCR product specific for the human β -globin locus is amplified from each of the 96 wells using the primers PCO2 (5'-TCCTAAGCCAGTGCCAGAAG-3' (SEQ ID NO.: __)) and PCO5 (5'-CTATTGGTCTCCTTAAACCTG-3' (SEQ ID NO.: __)) in order to screen for the β Thal1 or β Thal2 conversion. The PCR reactions are performed by adding 8 pmoles of each primer and 2.5 µl yeast cell culture into pre-aliquoted PCR reaction mixes (Marsh/Abgene). The PCR reactions use an annealing temperature of 45.8°C and an extension time of 1 min for 35 cycles. The PCR reactions are purified using a QiaQuick PCR 96-well purification kit (Qiagen) and eluted in a volume of 80 µl. One microliter of the purified PCR product is used as a template for the ABI SNaPshot reaction. The sequence of the SNaPshot primer used to screen for the β Thal1 conversion is: 5'-CCCCCCCCCCCCCCCCCAAGTCTGCCGTTACTGCCCTGTG-3' (SEQ ID NO: __).

15 The sequence of the SNaPshot primer used to screen for the β Thal2 conversion is: 5'-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCACAGGAGTCAGGTGCACC-3' (SEQ ID NO: __). The SNaPshot reactions are performed using an ABI Prism SNaPshot Multiplex Kit, as specified by the manufacturer, and analyzed on an ABI 3100 Genetic Analyzer.

[0197] *Sequence Analysis.* Any potential converted clones from the SNaPshot reactions are confirmed by sequence analysis. Both strands of the PCR products are sequenced using primers PCO2 and PCO5 by Sanger dideoxy sequencing using an ABI Prism kit, as specified by the manufacturer, on an automated ABI 3100 Genetic Analyzer.

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EXAMPLE 5

Adenosine Deaminase (ADA)

[0198] Adenosine deaminase (ADA, EC 3.5.4.4) catalyses the deamination of adenosine and 2'-deoxyadenosine to inosine or 2'-deoxyinosine respectively. ADA deficiency has been identified as the metabolic basis for 20-30% of cases with recessively inherited severe combined immunodeficiency (SCID). Affected infants are subject to recurrent chronic viral, fungal, protozoal, and bacterial infections and frequently present with persistent diarrhea, failure to thrive and candidiasis. In patients homozygous for ADA deficiency, 2'-deoxyadenosine accumulating during the rapid turnover of cells rich in DNA is converted back to dATP, either by adenosine kinase or deoxycytidine kinase. Many hypotheses have been advanced to explain the specific toxicity to the immune system in ADA deficiency. The apparently selective accumulation of dATP in thymocytes and peripheral blood B cells, with resultant inhibition of ribonucleotide reductase and DNA synthesis is probably the principal mechanism.

[0199] The structural gene for ADA is encoded as a single 32 kb locus containing 12 exons. Studies of the molecular defect in ADA-deficient patients have shown that mRNA is usually detectable in normal or supranormal amounts. Specific base substitution mutations have been detected in the majority of cases with the complete deficiency. A C-to-T base substitution mutation in exon 11 accounts for a high proportion of these, whilst a few patients are homozygous for large deletions encompassing exon I. A common point mutation resulting in a heat-labile ADA has been characterised in some patients with partial ADA deficiency, a disorder with an apparently increased prevalence in the Caribbean.

[0200] As yet no totally effective therapy for ADA deficiency has been reported, except in those few cases where bone marrow from an HLA/MLR compatible sibling donor was available.

[0201] Two therapeutic approaches have provided long-term benefit in specific instances. First, reconstitution using T cell depleted mismatched sibling marrow has been encouraging, particularly in early presenters completely deficient in ADA. Secondly, therapy with polyethylene glycol-modified adenosine deaminase (PEG-ADA) for more than 5 years has produced a sustained increase in lymphocyte numbers and mitogen responses together with evidence of in vivo B cell function. Success has generally been achieved in late presenters with residual ADA activity in mononuclear cells.

[0202] ADA deficiency has been chosen as the candidate disease for gene replacement therapy and the first human experiment commenced in 1990. The clinical consequences of overexpression of ADA activity - one of the potential hazards of gene implant - are known and take the form of an hereditary haemolytic anaemia associated with a tissue-specific increase in ADA activity. The

genetic basis for the latter autosomal dominant disorder seemingly relates to markedly increased levels of structurally normal ADA mRNA.

Table 6

ADA Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency GLN3TERM CAG to TAG	AGAGACCCACCGAGCGGCGGCGGAGGGAGCAGCGCCGGGG CGCACGAGGGCACCATGGCC <u>C</u> AGACGCCCGCCTTCGACAAG CCCAAAGTGAGCGCGCGCGGGGGCTCCGGGGACGGGGGTC	1
	GACCCCGTCCCCGGAGCCCCCGCGCGCGCTCACTTTGGGC TTGTCTGAAGGCGGGCGTCT <u>G</u> GGCCATGGTGCCCTCGTGCGC CCCGGCGCTGCTCCCTCCGCCCGCGCTCGGTGGGTCTCT	2
	CCATGGCC <u>C</u> AGACGCCC	3
	GGCGTCT <u>G</u> GGCCATGG	4
Adenosine deaminase deficiency HIS15ASP CAT to GAT	TATTTGTTCTCTCTCTCCCTTTCTCTCTCTTCCCCCTGCCCC CTTGCAAGTAGAACTG <u>C</u> ATGTCCACCTAGACGGATCCATCAA GCCTGAAACCATCTTATACTATGGCAGGTAAGTCC	5
	GGAATTACCTGCCATAGTATAAGATGGTTTCAGGCTTGATGGA TCCGTCTAGGTGGACAT <u>G</u> CAGTTCTACCTGCAAGGGGGCAG GGGAAGAGAGAGAGAAAGGGAGAGAGAGAAACAAATA	6
	TAGAACTG <u>C</u> ATGTCCAC	7
	GTGGACAT <u>G</u> CAGTTCTA	8
Adenosine deaminase deficiency GLY20ARG GGA to AGA	TCCCTTTCTCTCTCTTCCCCCTGCCCCCTTGCAAGGTAGAAC TGCATGTCCACCTAGAC <u>G</u> GATCCATCAAGCCTGAAACCATCTT ATACTATGGCAGGTAAGTCCATACAGAAGAGCCCT	9
	AGGGCTCTTCTGTATGGACTTACCTGCCATAGTATAAGATGGT TTCAGGCTTGATGGATC <u>C</u> GTCTAGGTGGACATGCAGTTCTAC CTGCAAGGGGGCAGGGGGAAGAGAGAGAGAAAGGGA	10
	ACCTAGAC <u>G</u> GATCCATC	11
	GATGGATC <u>C</u> GTCTAGGT	12
Adenosine deaminase deficiency GLY74CYS GGC to TGC	CCTGGAGCTCCCAAGGGACTTGGGGAAGGTTGTTCCCAACC CCTTTCTTCCCTTCCAGG <u>G</u> GCTGCCGGGAGGCTATCAAAAG GATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGG	13
	CCTCTTTGGCCTTCATCTCTACAAACTCATAGGCGATCCTTTT GATAGCCTCCCGGCAGCC <u>C</u> CTGGGAAGGGAAGAAAGGGGTT GGGAACAACCTTCCCAAGTCCCTTGGGAGCTCCAGG	14

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTATCGCG <u>G</u> GCTGCCGG	15
	CCGGCAGC <u>C</u> CGCGATAG	16
Adenosine Deaminase Deficiency ARG76TRP CGG to TGG	GCTCCCAAGGGACTTGGGGAAGGTTGTTCCCAACCCCTTTCT TCCCTTCCCAGGGGCTGCC <u>G</u> GGGAGGCTATCAAAGGATCGC CTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCGTGG	17
	CCACGCCCTCTTTGGCCTTCATCTCTACAACTCATAGGCGAT CCTTTTGATAGCCTCCC <u>G</u> GCAGCCCCTGGGAAGGGAAGAAA GGGGTTGGGAACAACCTTCCCCAAGTCCCTTGGGAGC	18
	GGGGCTGCC <u>G</u> GGGAGGCT	19
	AGCCTCCC <u>G</u> GCAGCCCC	20
Adenosine Deaminase Deficiency LYS80ARG AAA to AGA	TTGGGGAAGGTTGTTCCCAACCCCTTTCTTCCCTTCCCAGGG GCTGCCGGGAGGCTATCA <u>A</u> AAGGATCGCCTATGAGTTTGTAG AGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAGGT	21
	ACCTCCACATACACCACGCCCTCTTTGGCCTTCATCTCTACAA ACTCATAGGCGATCCTTT <u>T</u> GATAGCCTCCCGGCAGCCCCTGG GAAGGGAAGAAAGGGGTTGGGAACAACCTTCCCCAA	22
	GGCTATCA <u>A</u> AAGGATCG	23
	CGATCCTTTT <u>T</u> GATAGCC	24
Adenosine deaminase deficiency ALA83ASP GCC to GAC	GTTGTTCCCAACCCCTTTCTTCCCTTCCCAGGGGCTGCCGGG AGGCTATCAAAGGATCG <u>C</u> CTATGAGTTTGTAGAGATGAAGG CCAAAGAGGGCGTGGTGTATGTGGAGGTGCGGTACAG	25
	CTGTACCGCACCTCCACATACACCACGCCCTCTTTGGCCTTC ATCTCTACAACTCATAG <u>G</u> CGATCCTTTTGATAGCCTCCCGGC AGCCCCTGGGAAGGGAAGAAAGGGGTTGGGAACAAC	26
	AAGGATCG <u>C</u> CTATGAGT	27
	ACTCATAG <u>G</u> CGATCCTT	28
Adenosine deaminase deficiency TYR97CYS TAT to TGT	AGGCTATCAAAGGATCGCCTATGAGTTTGTAGAGATGAAGG CCAAAGAGGGCGTGGTGT <u>A</u> TGTGGAGGTGCGGTACAGTCCG CACCTGCTGGCCAACCTCAAAGTGAGCCAATCCCCTG	29
	CAGGGGATTGGCTCCACTTTGGAGTTGGCCAGCAGGTGCGG ACTGTACCGCACCTCCACA <u>T</u> ACACCACGCCCTCTTTGGCCTT CATCTCTACAACTCATAGGCGATCCTTTTGATAGCCT	30
	CGTGGTGT <u>A</u> TGTGGAGG	31
	CCTCCACATACACCAG	32

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency ARG101GLN CGG to CAG	GGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCG TGGTGTATGTGGAGGTGCGGTACAGTCCGCACCTGCTGGCC AACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTGA	33
	TCAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCC AGCAGGTGCGGACTGTACCGCACCTCCACATACACCACGCC CTCTTTGGCCTTCATCTCTACAAACTCATAGGCGATCC	34
	GGAGGTGCGGTACAGTC	35
	GACTGTACCGCACCTCC	36
Adenosine deaminase deficiency ARG101LEU CGG to CTG	GGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCG TGGTGTATGTGGAGGTGCGGTACAGTCCGCACCTGCTGGCC AACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTGA	37
	TCAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCC AGCAGGTGCGGACTGTACCGCACCTCCACATACACCACGCC CTCTTTGGCCTTCATCTCTACAAACTCATAGGCGATCC	38
	GGAGGTGCGGTACAGTC	39
	GACTGTACCGCACCTCC	40
Adenosine deaminase deficiency ARG101TRP CGG to TGG	AGGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCG GTGGTGTATGTGGAGGTGCGGTACAGTCCGCACCTGCTGGC CAACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTG	41
	CAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCCA GCAGGTGCGGACTGTACCGCACCTCCACATACACCACGCCCT CTTTGGCCTTCATCTCTACAAACTCATAGGCGATCCT	42
	TGGAGGTGCGGTACAGT	43
	ACTGTACCGCACCTCCA	44
Adenosine deaminase deficiency PRO104LEU CCG to CTG	ATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCGTGGTGTATG TGGAGGTGCGGTACAGTCCGCACCTGCTGGCCAACTCCAAA GTGGAGCCAATCCCCTGGAACCAGGCTGAGTGAGTGAT	45
	ATCACTCACTCAGCCTGGTTCCAGGGGATTGGCTCCACTTTG GAGTTGGCCAGCAGGTGCGGACTGTACCGCACCTCCACATA CACCACGCCCTCTTTGGCCTTCATCTCTACAAACTCAT	46
	GTACAGTCCGCACCTGC	47
	GCAGGTGCGGACTGTAC	48
Adenosine deaminase deficiency LEU106VAL	TTTGTAGAGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAG GTGCGGTACAGTCCGCACCTGCTGGCCAACTCCAAAGTGGA GCCAATCCCCTGGAACCAGGCTGAGTGAGTGATGGGCC	49

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
CTG to GTG	GGCCCATCACTCACTCAGCCTGGTTCCAGGGGATTGGCTCCA CTTTGGAGTTGGCCAGCAGGTGCGGACTGTACCGCACCTCCA CATACACCACGCCCTCTTTGGCCTTCATCTCTACAAA	50
	GTCCGCACCTGCTGGCC	51
	GGCCAGCAGGTGCGGAC	52
Adenosine deaminase deficiency LEU107PRO CTG to CCG	TAGAGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAGGTG CGGTACAGTCCGCACCTGCTGGCCAACTCCAAAGTGGAGCC AATCCCCTGGAACCAGGCTGAGTGAGTGATGGGCCTGGA	53
	TCCAGGCCCATCACTCACTCAGCCTGGTTCCAGGGGATTGGC TCCACTTTGGAGTTGGCCAGCAGGTGCGGACTGTACCGCAC CTCCACATACACCACGCCCTCTTTGGCCTTCATCTCTA	54
	GCACCTGCTGGCCAACT	55
	AGTTGGCCAGCAGGTGC	56
Adenosine deaminase deficiency PRO126GLN CCA to CAA	GCCTTCCTTTTGCCTCAGGCCCATCCCTACTCCTCTCCTCACA CAGAGGGGACCTCACCCAGACGAGGTGGTGGCCCTAGTGG GCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGT	57
	ACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCCTGGCCAC TAGGGCCACCACCTCGTCTGGGGTGAGGTCCCCTCTGTGTG AGGAGAGGAGTAGGGATGGGCCTGAGGCAAAGGAAGGC	58
	CCTCACCCAGACGAGG	59
	CCTCGTCTGGGGTGAGG	60
Adenosine deaminase deficiency VAL129MET GTG to ATG	TTTGCCTCAGGCCCATCCCTACTCCTCTCCTCACACAGAGGG GACCTCACCCAGACGAGGTGGTGGCCCTAGTGGGCCAGGG CCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCC	61
	GGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCC TGGCCCACTAGGGCCACCCTCGTCTGGGGTGAGGTCCCC TCTGTGTGAGGAGAGGAGTAGGGATGGGCCTGAGGCAA	62
	CAGACGAGGTGGTGGCC	63
	GGCCACCACCTCGTCTG	64
Adenosine deaminase deficiency GLY140GLU GGG to GAG	ACAGAGGGGACCTCACCCAGACGAGGTGGTGGCCCTAGTG GGCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCA AGGCCCGGTCCATCCTGTGCTGCATGCGCCACCAGCCCAG	65
	CTGGGCTGGTGGCGCATGCAGCACAGGATGGACCGGGCCTT GACCCCGAAGTCTCGCTCCCCTCCTGCAGGCCCTGGCCCA CTAGGGCCACCACCTCGTCTGGGGTGAGGTCCCCTCTGT	66
	GCAGGAGGGGGAGCGAG	67

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTCGCTCCC <u>C</u> CTCCTGC	68
Adenosine deaminase deficiency ARG142GLN CGA to CAA	GGGACCTCACCCCAGACGAGGTGGTGGCCCTAGTGGGCCAG GGCCTGCAGGAGGGGGAGC <u>G</u> AGACTTCGGGGTCAAGGCC GGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGTA	69
	TACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGACCG GGCCTTGACCCCGAAGTCT <u>C</u> GCTCCCCCTCCTGCAGGCCCT GGCCCACTAGGGCCACCACCTCGTCTGGGGTGAGGTCCC	70
	GGGGGAGC <u>G</u> AGACTTCG	71
	CGAAGTCT <u>C</u> GCTCCCC	72

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency ARG142TERM CGA to TGA	GGGGACCTCACCCCAGACGAGGTGGTGGCCCTAGTGGGCCA GGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCC CGGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGT	73
	ACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGACCGG GCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCCTG GCCACTAGGGCCACCACCTCGTCTGGGGTGAGGTCCCC	74
	AGGGGGAGCGAGACTTC	75
	GAAGTCTCGCTCCCCCT	76
Adenosine deaminase deficiency ARG149GLN CGG to CAG	TGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGGGGGAGCG AGACTTCGGGGTCAAGGCCCCGGTCCATCCTGTGCTGCATGC GCCACCAGCCCAGTGAGTAGGATCACCGCCCTGCCAGGG	77
	CCCTGGGCAGGGCGGTGATCCTACTCACTGGGCTGGTGGCG CATGCAGCACAGGATGGACCGGGCCTTGACCCCGAAGTCTC GCTCCCCCTCCTGCAGGCCCTGGCCCACTAGGGCCACCA	78
	CAAGGCCCCGGTCCATCC	79
	GGATGGACCGGGCCTTG	80
Adenosine deaminase deficiency ARG149TRP CGG to TGG	GTGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGGGGGAGC GAGACTTCGGGGTCAAGGCCCGGTCCATCCTGTGCTGCATG CGCCACCAGCCCAGTGAGTAGGATCACCGCCCTGCCAGG	81
	CCTGGGCAGGGCGGTGATCCTACTCACTGGGCTGGTGGCGC ATGCAGCACAGGATGGACCGGGCCTTGACCCCGAAGTCTCG CTCCCCCTCCTGCAGGCCCTGGCCCACTAGGGCCACCAC	82
	TCAAGGCCCGGTCCATC	83
	GATGGACCGGGCCTTGA	84
Adenosine deaminase deficiency LEU152MET CTG to ATG	CTAGTGGGCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCG GGGTCAAGGCCCGGTCCATCCTGTGCTGCATGCGCCACCAG CCCAGTGAGTAGGATCACCGCCCTGCCAGGGCCGCCCGT	85
	ACGGGCGGCCCTGGGCAGGGCGGTGATCCTACTCACTGGGC TGGTGGCGCATGCAGCACAGGATGGACCGGGCCTTGACCCC GAAGTCTCGTCCCCCTCCTGCAGGCCCTGGCCCACTAG	86
	GGTCCATCCTGTGCTGC	87
	GCAGCACAGGATGGACC	88
Adenosine deaminase deficiency ARG156CYS	GGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCCC GGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGTAG GATCACCGCCCTGCCAGGGCCGCCCGTCTCACCTGGCC	89

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
CGC to TGC	GGCCAGGGTGAGACGGGCGGCCCTGGGCAGGGCGGTGATC CTACTCACTGGGCTGGTGGC <u>G</u> CATGCAGCACAGGATGGACC GGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCC	90
	GCTGCATG <u>C</u> GCCACCAG	91
	CTGGTGGC <u>G</u> CATGCAGC	92
Adenosine deaminase deficiency ARG156HIS CGC to CAC	GCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCCCG GTCCATCCTGTGCTGCATGC <u>G</u> CCACCAGCCCAGTGAGTAGGA TCACCGCCCTGCCAGGGCGCCCGTCTCACCTGGCCC	93
	GGGCCAGGGTGAGACGGGCGGCCCTGGGCAGGGCGGTGAT CCTACTCACTGGGCTGGTGG <u>C</u> GCATGCAGCACAGGATGGAC CGGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGC	94
	CTGCATGC <u>G</u> CCACCAGC	95
	GCTGGTGG <u>C</u> GCATGCAG	96
Adenosine deaminase deficiency VAL177MET GTG to ATG	CTGCCCACAGACTGGTCCCCCAAGGTGGTGGAGCTGTGTAA GAAGTACCAGCAGCAGACC <u>G</u> TGGTAGCCATTGACCTGGCTG GAGATGAGACCATCCCAGGAAGCAGCCTCTTGCCTGGAC	97
	GTCCAGGCAAGAGGCTGCTTCCTGGGATGGTCTCATCTCCAG CCAGGTCAATGGCTACCAC <u>G</u> GTCTGCTGCTGGTACTTCTTAC ACAGCTCCACCACCTTGGGGGACCAGTCTGTGGGCAG	98
	AGCAGACC <u>G</u> TGGTAGCC	99
	GGCTACCAC <u>G</u> GTCTGCT	100
Adenosine deaminase deficiency ALA179ASP GCC to GAC	CAGACTGGTCCCCCAAGGTGGTGGAGCTGTGTAAGAAGTACC AGCAGCAGACCGTGGTAGC <u>C</u> ATTGACCTGGCTGGAGATGAG ACCATCCCAGGAAGCAGCCTCTTGCCTGGACATGTCCA	101
	TGGACATGTCCAGGCAAGAGGCTGCTTCCTGGGATGGTCTCA TCTCCAGCCAGGTCAATG <u>G</u> CTACCACGGTCTGCTGCTGGTAC TTCTTACACAGCTCCACCACCTTGGGGGACCAGTCTG	102
	CGTGGTAGC <u>C</u> ATTGACC	103
	GGTCAATG <u>G</u> CTACCAG	104
Adenosine deaminase deficiency GLN199PRO CAG to CCG	CCATTGACCTGGCTGGAGATGAGACCATCCCAGGAAGCAGC CTCTTGCCTGGACATGTCC <u>A</u> GGCCTACCAGGTGGGTCTCTGTG AGAAGGAATGGAGAGGCTGGCCCTGGGTGAGCTTGTCT	105
	AGACAAGCTCACCCAGGGCCAGCCTCTCCATTCTTCTCACA GGACCCACCTGGTAGGCCT <u>I</u> GGACATGTCCAGGCAAGAGGCT GCTTCTGGGATGGTCTCATCTCCAGCCAGGTCAATGG	106
	ACATGTCC <u>A</u> GGCCTACC	107

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGTAGGCCTGGACATGT	108
Adenosine deaminase deficiency ARG211CYS CGT to TGT	GCTAGGGCACCCATGACCTGGCTCTCCCCCTTCCAGGAGGC TGTGAAGAGCGGCATTACCGTACTGTCCACGCCGGGGAGG TGGGCTCGGCCGAAGTAGTAAAAGAGGTGAGGGCCTGGG	109
	CCCAGGCCCTCACCTCTTTTACTACTTCGGCCGAGCCACCT CCCCGGCGTGGACAGTACGGTGAATGCCGCTCTTCACAGCC TCCTGGAAGGGGGAGAGCCAGGTCATGGGTGCCCTAGC	110
	GCATTACCGTACTGTC	111
	GACAGTACGGTGAATGC	112
Adenosine deaminase deficiency ARG211HIS CGT to CAT	CTAGGGCACCCATGACCTGGCTCTCCCCCTTCCAGGAGGCT GTGAAGAGCGGCATTACCGTACTGTCCACGCCGGGGAGGT GGGCTCGGCCGAAGTAGTAAAAGAGGTGAGGGCCTGGGC	113
	GCCCAGGCCCTCACCTCTTTTACTACTTCGGCCGAGCCACC TCCCCGGCGTGGACAGTACGGTGAATGCCGCTCTTCACAGC CTCCTGGAAGGGGGAGAGCCAGGTCATGGGTGCCCTAG	114
	CATTCACCGTACTGTCC	115
	GGACAGTACGGTGAATG	116
Adenosine deaminase deficiency ALA215THR GCC to ACC	ATGACCTGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGG CATTACCGTACTGTCCACGCCGGGGAGGTGGGCTCGGCCG AAGTAGTAAAAGAGGTGAGGGCCTGGGCTGGCCATGGGG	117
	CCCCATGGCCAGCCAGGCCCTCACCTCTTTTACTACTTCGG CCGAGCCACCTCCCCGGCGTGGACAGTACGGTGAATGCCG CTCTTCACAGCCTCCTGGAAGGGGGAGAGCCAGGTCAT	118
	CTGTCCACGCCGGGGAG	119
	CTCCCCGGCGTGGACAG	120
Adenosine deaminase deficiency GLY216ARG GGG to AGG	ACCTGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGGCATT CACCGTACTGTCCACGCCGGGGAGGTGGGCTCGGCCGAAGT AGTAAAAGAGGTGAGGGCCTGGGCTGGCCATGGGGTCC	121
	GGACCCCATGGCCAGCCAGGCCCTCACCTCTTTTACTACTT CGGCCGAGCCACCTCCCCGGCGTGGACAGTACGGTGAATG CCGCTCTTCACAGCCTCCTGGAAGGGGGAGAGCCAGGT	122
	TCCACGCCGGGGAGGTG	123
	CACCTCCCCGGCGTGA	124

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency GLU217LYS GAG to AAG	TGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGGCATTACAC CGTACTGTCCACGCCGGG <u>G</u> AGGTGGGCTCGGCCGAAGTAGT AAAAGAGGTGAGGGCCTGGGCTGGCCATGGGGTCCCTC	125
	GAGGGACCCCATGGCCAGCCCAGGCCCTCACCTCTTTTACTA CTTCGGCCGAGCCCACCT <u>C</u> CCCGGCGTGGACAGTACGGTGA ATGCCGCTCTTCACAGCCTCCTGGAAGGGGGAGAGCCA	126
	ACGCCGGG <u>G</u> AGGTGGGC	127
	GCCACCT <u>C</u> CCCGGCGT	128
Adenosine deaminase deficiency THR233ILE ACA to ATA	CTGCCTCCTCCCATACTTGGCTCTATTCTGCTTCTCTACAGGC TGTGGACATACTCAAGA <u>C</u> AGAGCGGCTGGGACACGGCTACC ACACCCTGGAAGACCAGGCCCTTTATAACAGGCTGCG	129
	CGCAGCCTGTTATAAAGGGCCTGGTCTTCCAGGGTGTGGTAG CCGTGTCCAGCCGCTCT <u>G</u> TCTTGAGTATGTCCACAGCCTGT AGAGAAGCAGAATAGAGCCAAGTATGGGAGGAGGCAG	130
	ACTCAAGA <u>C</u> AGAGCGGC	131
	GCCGCTCT <u>G</u> TCTTGAGT	132
Adenosine deaminase deficiency ARG253PRO CGG to CCG	CAGAGCGGCTGGGACACGGCTACCACACCCTGGAAGACCAG GCCCTTTATAACAGGCTGC <u>G</u> GCAGGAAAACATGCACTTCGAG GTAAGCGGGCCAGGGAGTGGGGAGGAACCATCCCCGGC	133
	GCCGGGGATGGTTCCTCCCCACTCCCTGGCCCGCTTACCTC GAAGTGCATGTTTTCTGC <u>C</u> GCAGCCTGTTATAAAGGGCCTG GTCTTCCAGGGTGTGGTAGCCGTGTCCCAGCCGCTCTG	134
	CAGGCTGC <u>G</u> GCAGGAAA	135
	TTTCCTGC <u>C</u> GCAGCCTG	136
Adenosine deaminase deficiency GLN254TERM CAG to TAG	GAGCGGCTGGGACACGGCTACCACACCCTGGAAGACCAGGC CCTTTATAACAGGCTGCGG <u>C</u> AGGAAAACATGCACTTCGAGGT AAGCGGGCCAGGGAGTGGGGAGGAACCATCCCCGGCTG	137
	CAGCCGGGGATGGTTCCTCCCCACTCCCTGGCCCGCTTACCT CGAAGTGCATGTTTTCTG <u>C</u> CGCAGCCTGTTATAAAGGGCCT GGTCTTCCAGGGTGTGGTAGCCGTGTCCCAGCCGCTC	138
	GGCTGCGG <u>C</u> AGGAAAAC	139
	GTTTTCTG <u>C</u> CGCAGCC	140
Adenosine deaminase deficiency PRO274LEU	CCACACACCTGCTCTTCCAGATCTGCCCTGGTCCAGCTACC TCACTGGTGCCTGGAAGC <u>C</u> GGACACGGAGCATGCAGTCATT GGTGAGCTCTGTTCCCTGGGCCTGTTCAATTTTGT	141

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
CCG to CTG	AACAAAATTGAACAGGCCCCAGGGGAACAGAGCTCACCGAATG ACTGCATGCTCCGTGTCCGGCTTCCAGGCACCAGTGAGGTAG CTGGACCAGGGGCAGATCTGGAAGAGCAGGTGTGTGG	142
	CTGGAAGCCGGACACGG	143
	CCGTGTCCGGCTTCCAG	144
Adenosine deaminase deficiency SER291LEU TCG to TTG	GGAGGCTGATTCTCTCCTCCTCCCTCTTCTGCAGGCTCAAAA ATGACCAGGCTAACTACTCGCTCAACACAGATGACCCGCTCA TCTTCAAGTCCACCCTGGACACTGATTACCAGATGAC	145
	GTCATCTGGTAATCAGTGTCCAGGGTGGACTTGAAGATGAGC GGGTCATCTGTGTTGAGCGAGTAGTTAGCCTGGTCATTTTTGA GCCTGCAGAAGAGGGAGGAGGAGAGAATCAGCCTCC	146
	TAACTACTCGCTCAACA	147
	TGTTGAGCGAGTAGTTA	148
Adenosine deaminase deficiency PRO297GLN CCG to CAG	CCTCCCTCTTCTGCAGGCTCAAAAATGACCAGGCTAACTACTC GCTCAACACAGATGACCCGGCTCATCTTCAAGTCCACCCTGGA CACTGATTACCAGATGACCAAACGGGACATGGGCTT	149
	AAGCCCATGTCCCGTTTGGTCATCTGGTAATCAGTGTCCAGG GTGGACTTGAAGATGAGCGGGTCATCTGTGTTGAGCGAGTAG TTAGCCTGGTCATTTTTGAGCCTGCAGAAGAGGGAGG	150
	AGATGACCCGGCTCATCT	151
	AGATGAGCGGGTCATCT	152
Adenosine deaminase deficiency LEU304ARG CTG to CGG	AAAATGACCAGGCTAACTACTCGCTCAACACAGATGACCCGC TCATCTTCAAGTCCACCCTGGACACTGATTACCAGATGACCAA ACGGGACATGGGCTTTACTGAAGAGGAGTTTAAAAG	153
	CTTTTAACTCCTCTTCAGTAAAGCCCATGTCCCGTTTGGTCA TCTGGTAATCAGTGTCCAGGGTGGACTTGAAGATGAGCGGGT CATCTGTGTTGAGCGAGTAGTTAGCCTGGTCATTTT	154
	GTCCACCCCTGGACACTG	155
	CAGTGTCCAGGGTGGAC	156
Adenosine deaminase deficiency ALA329VAL C-to-T at base 1081	GCCTTCTTTGTTCTCTGGTTCCATGTTGTCTGCCATTCTGGCC TTTCCAGAACATCAATGCCGGCCAAATCTAGTTTCTCCAGAA GATGAAAAGAGGGAGCTTCTCGACCTGCTCTATAA	157
	TTATAGAGCAGGTCGAGAAGCTCCCTCTTTTCATCTTCTGGGA GGAACTAGATTTGGCCGCATTGATGTTCTGGAAAGGCCAGA ATGGCAGACAACATGGAACCAGAGAACAAGAAGGC	158
	CATCAATGCCGGCCAAAT	159

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATTTGGCC <u>G</u> CATTGATG	160

EXAMPLE 6

P53 Mutations

[0203] The p53 gene codes for a protein that acts as a transcription factor and serves as a key regulator of the cell cycle. Mutation in this gene is probably the most significant genetic change characterizing the transformation of cells from normalcy to malignancy.

[0204] Inactivation of p53 by mutation disrupts the cell cycle which, in turn, sets the stage for tumor formation. Mutations in the p53 gene are among the most commonly diagnosed genetic disorders, occurring in as many as 50% of cancer patients. For some types of cancer, most notably of the breast, lung and colon, p53 mutations are the predominant genetic alternations found thus far. These mutations are associated with genomic instability and thus an increased susceptibility to cancer. Some p53 lesions result in malignancies that are resistant to the most widely used therapeutic regimens and therefore demand more aggressive treatment.

[0205] That p53 is associated with different malignant tumors is illustrated in the Li-Fraumeni autosomal dominant hereditary disorder characterized by familial multiple tumors due to mutation in the p53 gene. Affected individuals can develop one or more tumors, including: brain (12%); soft-tissue sarcoma (12%); breast cancer (25%); adrenal tumors (1%); bone cancer (osteosarcoma) (6%); cancer of the lung, prostate, pancreas, and colon as well as lymphoma and melanoma can also occur.

[0206] Certain of the most frequently mutated codons are codons 175, 248 and 273, however a variety of oligonucleotides are described below in the attached table.

Table 7

p53 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
In 2 families with Li-Fraumeni syndrome, there was a C-to-T mutation at the first nucleotide of	GACTGTACCACCATCCACTACAACCTACATGTGTAAACAGTTCCTGCATGGGCGGCATGAAC <u>C</u> GGAGGCCCATCCTCACCATCATCACACTGGAAGACTCCAGGTCAGGAGCCACTTGCCACC	161
	GGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTCC <u>G</u> GTTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGTC	162

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
codon 248 which changed arginine to tryptophan.	GCATGAAC <u>C</u> GGAGGCC	163
	GGGCCTCC <u>G</u> GTTTCATGC	164
In a family with the Li-Fraumeni syndrome, a G-to-A mutation at the first nucleotide of codon 258 resulting in the substitution of lysine for glutamic acid.	TGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTG <u>G</u> AAGACTCCAGGTCAGGAGCCAC TTGCCACCCTGCACACTGGCCTGCTGTGCCCCAGCCTC	165
	GAGGCTGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGT GGCTCCTGACCTGGAGTCTT <u>C</u> CAGTGTGATGATGGTGAGGAT GGGCCTCCGGTTCATGCCGCCCATGCAGGAAGTGTACA	166
	TCACACTG <u>G</u> AAGACTCC	167
	GGAGTCTT <u>C</u> CAGTGTGA	168
In a family with the Li-Fraumeni syndrome, a G-to-T mutation at the first nucleotide of codon 245 resulting in the substitution of cysteine for glycine.	GTTGGCTCTGACTGTACCACCATCCACTACAACCTACATGTGTA ACAGTTCCTGCATGGGC <u>G</u> GCATGAACCGGAGGCCCATCCTC ACCATCATCACACTGGAAGACTCCAGGTCAGGAGCCA	169
A gly245-to-ser, GGC-to-AGC, mutation was found in a patient in whom osteosarcoma was diagnosed at the age of 18 years.	TGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGGA TGGGCCTCCGGTTCATGCC <u>G</u> CCCCATGCAGGAAGTGTACACA TGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCAAC	170
	GCATGGGC <u>G</u> GCATGAAC	171
	GTTTCATGCC <u>G</u> CCCCATGC	172
In a family with the Li-Fraumeni syndrome, a germline mutation at codon 252: a T-to-C change at the second position resulted in substitution of proline for leucine.	TCCACTACAACCTACATGTGTAACAGTTCCTGCATGGGCGGCA TGAACCGGAGGCCCATCCT <u>T</u> CACCATCATCACACTGGAAGACT CCAGGTCAGGAGCCACTTGCCACCCTGCACACTGGCC	173
	GGCCAGTGTGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTC TTCCAGTGTGATGATGGTG <u>A</u> GGATGGGCCTCCGGTTCATGCC GCCCATGCAGGAAGTGTACACATGTAGTTGTAGTGGA	174
	GCCCATCCT <u>T</u> CACCATCA	175
	TGATGGTG <u>A</u> GGATGGGC	176
Researchers analyzed for mutations in p53 hepatocellular	TACCACCATCCACTACAACCTACATGTGTAACAGTTCCTGCATG GGCGGCATGAACCGGAG <u>G</u> CCCCATCCTCACCATCATCACACT GGAAGACTCCAGGTCAGGAGCCACTTGCCACCCTGCA	177

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
hepatocellular carcinomas from patients in Qidong, an area of high incidence	TGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTGT GATGATGGTGAAGATGGG <u>C</u> CTCCGGTTCATGCCGCCCATGC AGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTA	178
in China, in which both hepatitis B virus and aflatoxin B1 are risk factors. Eight of 16 tumors had a point mutation at the third base position of codon 249. The G-to-T mutation at codon 249 led to a change from arginine to serine (AGG to AGT).	AACCGGAG <u>G</u> CCCATCCT	179
	AGGATGGG <u>C</u> CTCCGGTT	180
In cases of hepatocellular carcinoma in southern Africa, a G-to-T substitution in codon 157 resulting in a change from valine to phenylalanine.	CTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTGATTCCACA CCCCCGCCCGGCACCCG <u>C</u> TCCGCGCCATGGCCATCTACAA GCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCC	181
	GGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGT AGATGGCCATGGCGCGGA <u>C</u> GCGGGTGCCGGGCGGGGGTGT GGAATCAACCCACAGCTGCACAGGGCAGGTCTTGCCAG	182
	GCACCCG <u>C</u> GTCGCGCC	183
	GGCGCGGA <u>C</u> GCGGGTGC	184
In a family with Li-Fraumeni in which noncancerous skin fibroblasts from affected individuals showed an unusual radiation-resistant phenotype, a point mutation in codon 245 of the P53 gene. A change from GGC to GAC predicted substitution of aspartic acid for glycine.	TTGGCTCTGACTGTACCACCATCCACTACAACCTACATGTGTAA CAGTTCCTGCATGGGCG <u>G</u> CATGAACCGGAGGCCCATCCTCA CCATCATCACACTGGAAGACTCCAGGTCAGGAGCCAC	185
	GTGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGG ATGGGCCTCCGGTTCATG <u>C</u> CGCCCATGCAGGAAGTGTACAC ATGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCAA	186
	CATGGGCG <u>G</u> CATGAACC	187
	GGTTCATG <u>C</u> CGCCCATG	188
In 2 of 8 families with Li-Fraumeni syndrome, a mutation	ACTGTACCACCATCCACTACAACCTACATGTGTAAACAGTTCCTG CATGGGCGGCATGAACC <u>G</u> GAGGCCCATCCTCACCATCATCA CACTGGAAGACTCCAGGTCAGGAGCCACTTGCCACCC	189

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
syndrome, a mutation in codon 248: a CCG-to-CAG change resulting in substitution	GGGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTGTGAT GATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGG AACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGT	190
of glutamine for arginine.	CATGAACCCGGAGGCCCA	191
	TGGGCCTCCGGTTCATG	192
In 9 members of an extended family with Li-Fraumeni syndrome, a germline mutation at codon 133 (ATG-to-ACG), resulted in the substitution of threonine for methionine (M133T), and completely cosegregated with the cancer syndrome.	CCCTGACTTTCAACTCTGTCTCCTTCCTCTTCTACAGTACTC CCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACCTG CCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCC	193
	GGCGGGGGTGTGGAATCAACCCACAGCTGCACAGGGCAGGT CTTGCCAGTTGGCAAACATCTTGTTGAGGGCAGGGGAGTA CTGTAGGAAGAGGAAGGAGACAGAGTTGAAAGTCAGGG	194
	CAACAAGATGTTTTGCC	195
	GGCAAACATCTTGTTG	196
In 1 pedigree consistent with the Li-Fraumeni syndrome, a germline G-to-T transversion at codon 272 (valine to leucine) was found.	TCTTGCTTCTCTTTTCCTATCCTGAGTAGTGGTAATCTACTGG GACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGA GAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGA	197
	TCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTCCCAG GACAGGCACAAACACGCACTCAAAGCTGTTCCGTCCCAGTA GATTACCACTACTCAGGATAGGAAAAGAGAAGCAAGA	198
	GCTTTGAGGTGCGTGTT	199
	AACACGCACTCAAAGC	200
A ser241-to-phe mutation due to a TCC-to-TTC change was found in a patient with hepatoblastoma and multiple foci of osteosarcoma.	TTATCTCCTAGGTTGGCTCTGACTGTACCACCATCCACTACAA CTACATGTGTAACAGTTCTGTCATGGGCGGCATGAACCGGAG GCCCATCCTCACCATCATCACACTGGAAGACTCCAG	201
	CTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTCCG GTTTCATGCCGCCCATGCAGGAAGTGTACACATGTAGTTGTA GTGGATGGTGGTACAGTCAGAGCCAACCTAGGAGATAA	202
	TAACAGTTCTGTCATGG	203
	CCATGCAGGAAGTGTGA	204
An AAG-to-TAG change of codon 120, resulting in conversion	CAGAAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTC TTGCATTCTGGGACAGCCAAAGTCTGTGACTTGACGGTCAGT TGCCCTGAGGGGCTGGCTTCATGAGACTTCAATGCC	205

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
resulting in conversion from lysine to a stop codon, was found in a patient with osteosarcoma and adenocarcinoma of the lung at age 18 and brain tumor (glioma) at the age of 27.	GGCATTGAAGTCTCATGGAAGCCAGCCCCTCAGGGCAACTGACCGTGCAAGTCACAGACTTGGCTGTCCCAGAATGCAAGAAGCCAGACGGAAACCGTAGCTGCCCTGGTAGGTTTTCTG	206
	GGACAGCCAAAGTCTGTG	207
	CACAGACTTGGCTGTCC	208
A CGG-to-TGG change at codon 282, resulting in the substitution of tryptophan for arginine, was found in a patient who developed osteosarcoma at the age of 10 years.	GGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCCCCAG	209
	CTGGGGGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATTACC	210
	GGAGAGACCGGCGCACAA	211
	TGTGCGCCGGTCTCTCC	212
In 5 of 6 anaplastic carcinomas of the thyroid and in an anaplastic carcinoma thyroid cell line ARO, a CGT-to-CAT mutation converted arginine-273 to histidine.	GCTTCTCTTTTCTATCCTGAGTAGTGGAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGG	213
	CCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATTACCACTACTCAGGATAGGAAAAGAGAAGC	214
	TGAGGTGCGTGTTTGTG	215
	CACAAACACGCACCTCA	216
A germline GGA-to-GTA mutation resulting in a change of glycine-325 to valine was found in a patient who had non-Hodgkin lymphoma diagnosed at age 17 and colon carcinoma at age 26.	TCCTAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAGAAACCACTGGATGGAGAGAATATTTACCCTTCAGGTACTAAGTCTTGGGACCTCTTATCAAGTGGAAGTTTCCA	217
	TGGAAACTTTCCACTTGATAAGAGGTCCCAAGACTTAGTACCTGAAGGGTGAAATATTCTCCATCCAGTGTTTCTTCTTTGGCTGGGAGAGGAGCTGGTGTTGTTGGGCAGTGCTAGGA	218
	ACTGGATGGAGAATATT	219
	AATATTCTCCATCCAGT	220
CGC-CCC Arg-72 to Pro	AATGGTTCACTGAAGACCCAGGTCCAGATGAAGCTCCCAGAA TGCCAGAGGCTGCTCCCCCGGTGGCCCCTGCACCAGCAGCT CCTACACCGGCGGCCCTGCACCAGCCCCCTCCTGGCC	221

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
association with Lung cancer	GGCCAGGAGGGGGCTGGTGCAGGGGCCCGCGGTGTAGGAG CTGCTGGTGCAGGGGCCACGCGGGGAGCAGCCTCTGGCATT CTGGGAGCTTCATCTGGACCTGGGTCTTCAGTGAACCATT	222
	TGCTCCCCGCGTGGCCC	223
	GGGCCACGCGGGGAGCA	224
CCG-CTG Pro-82 to Leu Breast cancer	AAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCT GCACCAGCAGCTCCTACACCGGGCGGCCCTGCACCAGCCCC CTCCTGGCCCCGTGCATCTTCTGTCCCTTCCCAGAAAAC	225
	GTTTTCTGGGAAGGGACAGAAGATGACAGGGGCCAGGAGGG GGCTGGTGCAGGGGCCCGCGGTGTAGGAGCTGCTGGTGC GGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTT	226
	TCCTACACCGGCGGCC	227
	GGCCGCGCGGTGTAGGA	228
cCAA-TAA Gln-136 to Term Li-Fraumeni syndrome	TTCAACTCTGTCTCCTTCCTCTTCTACAGTACTCCCCTGCCC TCAACAAGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGC AGCTGTGGGTTGATTCCACACCCCCGCCCCGGCACCC	229
	GGGTGCCGGGCGGGGGTGTGGAATCAACCCACAGCTGCACA GGGCAGGTCTTGCCAGTTGGCAAACATCTTGTTGAGGGCA GGGGAGTACTGTAGGAAGAGGAAGGAGACAGAGTTGAA	230
	TGTTTTGCCAACTGGCC	231
	GGCCAGTTGGCAAACA	232
TGC-TAC Cys-141 to Tyr Li-Fraumeni syndrome	TCCTCTTCTACAGTACTCCCCTGCCCTCAACAAGATGTTTTG CCAACTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTGATT CACACCCCCGCCCCGGCACCCGCGTCCGCGCCATGGC	233
	GCCATGGCGCGGACGCGGGTGCCGGGCGGGGGTGTGGAAT CAACCCACAGCTGCACAGGGCAGGTCTTGCCAGTTGGCAA AACATCTTGTTGAGGGCAGGGGAGTACTGTAGGAAGAGGA	234
	CAAGACCTGCCCTGTGC	235
	GCACAGGGCAGGTCTTG	236
aCCC-TCC Pro-151 to Ser Li-Fraumeni syndrome	AACAAGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGCAG CTGTGGGTTGATTCCACACCCCCGCCCCGGCACCCGCGTCCG CGCCATGGCCATCTACAAGCAGTCACAGCACATGACGG	237
	CCGTCATGTGCTGTGACTGCTGTAGATGGCCATGGCGCGGA CGCGGGTGCCGGGCGGGGGTGTGGAATCAACCCACAGCTG CACAGGGCAGGTCTTGCCAGTTGGCAAACATCTTGTT	238
	ATTCCACACCCCCGCCC	239

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGGCGGGG <u>G</u> TGTGGAAT	240
CCG-CTG Pro-152 to Leu Adrenocortical carcinoma	AGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGT GGGTTGATTCCACACCCC <u>C</u> GCCCCGGCACCCGCGTCCGCGCC ATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGT	241
	ACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCG CGGACGCGGGTGCCGGGC <u>G</u> GGGGTGTGGAATCAACCCACA GCTGCACAGGGCAGGTCTTGGCCAGTTGGCAAAACATCT	242
	CACACCCC <u>C</u> GCCCCGGCA	243
	TGCCGGGC <u>G</u> GGGGTGTG	244
GGC-GTC Gly-154 to Val Glioblastoma	TTTGCCAAGTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTG ATTCCACACCCCCGCCCC <u>G</u> CACCCGCGTCCGCGCCATGGCC ATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAG	245
	CTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCC ATGGCGCGGACGCGGGTG <u>C</u> CGGGCGGGGGTGTGGAATCAA CCCACAGCTGCACAGGGCAGGTCTTGGCCAGTTGGCAAA	246
	CCCGCCCG <u>G</u> CACCCGCG	247
	CGCGGGTG <u>C</u> CGGGCGGG	248
CGC-CAC Arg-175 to His Li-Fraumeni syndrome	CCCGCGTCCGCGCCATGGCCATCTACAAGCAGTCACAGCAC ATGACGGAGGTTGTGAGGC <u>G</u> CTGCCCCACCATGAGCGCTG CTCAGATAGCGATGGTGAGCAGCTGGGGCTGGAGAGACG	249
	CGTCTCTCCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAG CGCTCATGGTGGGGGCAG <u>C</u> GCCTCACAACCTCCGTCATGTG CTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGG	250
	TGTGAGGC <u>G</u> CTGCCCCC	251
	GGGGGCAG <u>C</u> GCCTCACA	252
tGAG-AAG Glu-180 to Lys Li-Fraumeni syndrome	ATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTG AGGCGCTGCCCCACCAT <u>G</u> AGCGCTGCTCAGATAGCGATGG TGAGCAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGC	253
	GCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCACCAT CGCTATCTGAGCAGCGCT <u>C</u> ATGGTGGGGGCAGCGCCTCACA ACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCAT	254
	CCCACCAT <u>G</u> AGCGCTGC	255
	GCAGCGCT <u>C</u> ATGGTGGG	256
gCGC-TGC Arg-181 to Cys Breast cancer	GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGG CGTGCCCCACCATGAG <u>C</u> GCTGCTCAGATAGCGATGGTGA GCAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGCCCA	257

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGGGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCAC CATCGCTATCTGAGCAGC <u>G</u> CTCATGGTGGGGGCAGCGCCTC ACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGC	258
	ACCATGAGC <u>G</u> CTGCTCA	259
	TGAGCAGC <u>G</u> CTCATGGT	260
CGC-CAC Arg-81 to His Breast cancer	CCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGC GCTGCCCCCACCATGAGC <u>G</u> CTGCTCAGATAGCGATGGTGAG CAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGCCAG	261
	CTGGGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCA CCATCGCTATCTGAGCAGC <u>G</u> CTCATGGTGGGGGCAGCGCCT CACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGG	262
	CCATGAGC <u>G</u> CTGCTCAG	263
	CTGAGCAGC <u>G</u> CTCATGG	264
CAT-CGT His-193 to Arg Li-Fraumeni syndrome	CCAGGGTCCCCAGGCCTCTGATTCCTCACTGATTGCTCTTAG GTCTGGCCCCTCCTCAGC <u>A</u> TCTTATCCGAGTGGAAGGAAATT TGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCG	265
	CGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTTC CTTCCACTCGGATAAGAT <u>G</u> CTGAGGAGGGGCCAGACCTAAGA GCAATCAGTGAGGAATCAGAGGCCTGGGGACCCTGG	266
	TCCTCAGC <u>A</u> TCTTATCC	267
	GGATAAGAT <u>G</u> CTGAGGA	268
cCGA-TGA Arg-196 to Term Adrenocortical carcinoma	CCCAGGCCTCTGATTCCTCACTGATTGCTCTTAGGTCTGGCC CCTCCTCAGCATCTTATC <u>G</u> GAGTGGAAGGAAATTTGCGTGTG GAGTATTTGGATGACAGAAACACTTTTCGACATAGTG	269
	CACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACG CAAATTTCTTCCACTC <u>G</u> GATAAGATGCTGAGGAGGGGCCAG ACCTAAGAGCAATCAGTGAGGAATCAGAGGCCTGGG	270
	ATCTTATC <u>G</u> GAGTGGAA	271
	TTCCACTC <u>G</u> GATAAGAT	272
cAGA-TGA Arg-209 to Term Li-Fraumeni syndrome	GCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAATTTGCGT GTGGAGTATTTGGATGAC <u>A</u> GAAACACTTTTCGACATAGTGTG GTGGTGCCCTATGAGCCGCCTGAGGTCTGGTTTGCAA	273
	TTGCAAACCAGACCTCAGGCGGCTCATAGGGCACCACCACAC TATGTCGAAAAGTGTTTCT <u>G</u> TGCATCCAAATACTCCACACGCAA ATTTCTTCCACTCGGATAAGATGCTGAGGAGGGGC	274
	TGGATGAC <u>A</u> GAAACACT	275

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGTGTTCCTGTCATCCA	276
tCGA-TGA Arg-213 to Term Li-Fraumeni syndrome	CATCTTATCCGAGTGGAAGGAAATTTGCGTGTGGAGTATTTG GATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT GAGCCGCCTGAGGTCTGTTTGCAACTGGGGTCTCTG	277
	CAGAGACCCCAGTTGCAAACCAGACCTCAGGCGGCTCATAG GGCACCACCACACTATGTCGAAAAGTGTTCGTGCATCCAAAT ACTCCACACGCAAATTCCTTCCACTCGGATAAGATG	278
	ACACTTTTCGACATAGT	279
	ACTATGTGCGAAAAGTGT	280
gCCC-TCC Pro-219 to Ser Adrenocortical carcinoma	GGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTC GACATAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTCTGG TTTGCAACTGGGGTCTCTGGGAGGAGGGGTTAAGGGT	281
	ACCCTTAACCCCTCCTCCCAGAGACCCCAGTTGCAAACCAGA CCTCAGGCGGCTCATAGGGCACCACCACACTATGTGCGAAAAG TGTTTCTGTGCATCCAAATACTCCACACGCAAATTTCC	282
	TGGTGGTGCCCTATGAG	283
	CTCATAGGGCACCACCA	284
TAT-TGT Tyr-220 to Cys Li-Fraumeni syndrome	ATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACA TAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTCTGGTTTGC AACTGGGGTCTCTGGGAGGAGGGGTTAAGGGTGGTT	285
	AACCACCCTTAACCCCTCCTCCCAGAGACCCCAGTTGCAAAC CAGACCTCAGGCGGCTCATAGGGCACCACCACACTATGTGCGA AAAGTGTTCGTGCATCCAAATACTCCACACGCAAAT	286
	GGTGCCCTATGAGCCGC	287
	GCGGCTCATAGGGCACC	288
cTCT-ACT Ser-227 to Thr Rhabdomyosarcoma	CACAGGTCTCCCCAAGGCGCACTGGCCTCATCTTGGGCCTGT GTTATCTCCTAGGTTGGCTCTGACTGTACCACCATCCACTACA ACTACATGTGTAACAGTTCCTGCATGGGCGGCATGA	289
	TCATGCCGCCCATGCAGGAAGTGTACACATGTAGTTGTAGT GGATGGTGGTACAGTCAGAGCCAACCTAGGAGATAACACAG GCCCAAGATGAGGCCAGTGCGCCTTGGGGAGACCTGTG	290
	AGGTTGGCTCTGACTGT	291
	ACAGTCAGAGCCAACCT	292
cCAC-AAC His-233 to Asn Glioma	GCACTGGCCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGC TCTGACTGTACCACCATCCACTACAACCTACATGTGTAACAGTT CCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCA	293

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTG TTACACATGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCA ACCTAGGAGATAACACAGGCCCAAGATGAGGCCAGTGC	294
	CCACCATCCACTACAAC	295
	GTTGTAGTGGATGGTGG	296
cAAC-GAC Asn-235 to Asp Adrenocortical carcinoma	GCCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGCTCTGAC TGTACCACCATCCACTACA A ACTACATGTGTAACAGTTCCTGCA TGGGCGGCATGAACCGGAGGCCCATCCTCACCATCA	297
	TGATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAG GAACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGTCA GAGCCAACCTAGGAGATAACACAGGCCCAAGATGAGGC	298
	TCCACTACA A ACTACATG	299
	CATGTAGTTGTAGTGGA	300
AAC-AGC Asn-235 to Ser Rhabdomyosarcoma	CCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGCTCTGACT GTACCACCATCCACTACA A CTACATGTGTAACAGTTCCTGCAT GGGCGGCATGAACCGGAGGCCCATCCTCACCATCAT	301
	ATGATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCA GAACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGTC AGAGCCAACCTAGGAGATAACACAGGCCCAAGATGAGG	302
	CCACTACA A CTACATGT	303
	ACATGTAGTTGTAGTGGA	304
ATCc-ATG Ile-251 to Met Glioma	CATCCACTACA A CTACATGTGTAACAGTTCCTGCATGGGCGG CATGAACCGGAGGCCCAT C CTCACCATCATCACACTGGAAGA CTCCAGGTCAGGAGCCACTTGCCACCCTGCACACTGG	305
	CCAGTGTGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTCTT CCAGTGTGATGATGGTGA G GATGGGCCTCCGGTTCATGCCG CCCATGCAGGAAGTGTACACATGTAGTTGTAGTGGATG	306
	AGGCCCAT C CTCACCAT	307
	ATGGTGAG G ATGGGCCT	308
ACA-ATA Thr-256 to Ile Glioblastoma	ACATGTGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGG CCCATCCTCACCATCATCA C ACTGGAAGACTCCAGGTCAGGA GCCACTTGCCACCCTGCACACTGGCCTGCTGTGCCCA	309
	TGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGTGGCTCC TGACCTGGAGTCTTCCAGT G TGATGATGGTGAGGATGGGCCT CCGGTTCATGCCGCCCATGCAGGAAGTGTACACATGT	310
	CATCATCA C ACTGGAAG	311

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTTCCAGT <u>G</u> TGATGATG	312
CTG-CAG Leu-257 to Gln Li-Fraumeni syndrome	TGTGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGGCCC ATCCTCACCATCATCACACT <u>G</u> GGAAGACTCCAGGTCAGGAGCC ACTTGCCACCCTGCACACTGGCCTGCTGTGCCCCAGCC	313
	GGCTGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGTGG CTCCTGACCTGGAGTCTTCC <u>A</u> GTGTGATGATGGTGAGGATGG GCCTCCGGTTCATGCCGCCCATGCAGGAAGTGTACACA	314
	CATCACACT <u>G</u> GGAAGACT	315
	AGTCTTCC <u>A</u> GTGTGATG	316
CTG-CCG Leu-265 to Pro Li-Fraumeni syndrome	GACCTGATTTCTTACTGCCTCTTGCTTCTTTTTCTATCCTG AGTAGTGGTAATCTACT <u>T</u> GGGACGGAACAGCTTTGAGGTGCGT GTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGA	317
	TCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCAC CTCAAAGCTGTTCCGTCCC <u>A</u> GTAGATTACCACTACTCAGGATA GGAAAAGAGAAGCAAGAGGCAGTAAGGAAATCAGGTC	318
	TAATCTACT <u>G</u> GGACGGA	319
	TCCGTCCC <u>A</u> GTAGATTA	320
gCGT-TGT Arg-273 to Cys Li-Fraumeni syndrome	TGCTTCTCTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGAC GGAACAGCTTTGAGGTG <u>C</u> GTGTTTGTGCCTGTCCTGGGAGAG ACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAG	321
	CTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCC CAGGACAGGCACAAACAC <u>G</u> CACCTCAAAGCTGTTCCGTCCCA GTAGATTACCACTACTCAGGATAGGAAAAGAGAAGCA	322
	TTGAGGTG <u>C</u> GTGTTTGT	323
	ACAAACAC <u>G</u> CACCTCAA	324
TGT-TAT Cys-275 to Tyr Li-Fraumeni syndrome	CTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGACGGAACA GCTTTGAGGTGCGTGTTT <u>G</u> TGCCTGTCCTGGGAGAGACCGG CGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCC	325
	GGCTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGG TCTCTCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTC CGTCCCAGTAGATTACCACTACTCAGGATAGGAAAAG	326
	GCGTGTTT <u>G</u> TGCCTGTC	327
	GACAGGCACAAACACGC	328
CCT-CTT Pro-278 to Leu Breast cancer	TCCTGAGTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGG TGCGTGTTTGTGCCTGT <u>C</u> TGGGAGAGACCGGCGCACAGAG GAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGA	329

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATTACCACTACTCAGGA	330
	TGCCTGTCC <u>T</u> GGGAGAG	331
	CTCTCCCAGGACAGGCA	332
AGA-AAA Arg-280 to Lys Glioma	GTAGTGGAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGAGGAAGAG AATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCC	333
	GGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCT <u>C</u> TCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATTACCACTAC	334
	TCCTGGGAGAGACCGGC	335
	GCCGGTCT <u>C</u> TCCCAGGA	336
GAA-GCA Glu-286 to Ala Adrenocortical carcinoma	GGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGAGGAAGAGAAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCC	337
	CCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCTCCCTTTCTTGCGGAGATTCTCTTCTCCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCC	338
	AGAGGAAGAGAAATCTCC	339
	GGAGATTCTCTTCCTCT	340
CGA-CCA Arg-306 to Pro Rhabdomyosarcoma	AAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCCCAGGGAGCACTAAGCGAGGTAAGCAAGCAGGACAAGAAGCGGTGGAGGAGACCAAGGGTGCAAGTTATGCCTCAGAT	341
	ATCTGAGGCATAACTGCACCCTTGGTCTCCTCCACCGCTTCTTGTCTGCTTGCTTACCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTT	342
	CACTAAGCGAGGTAAGC	343
	GCTTACCTCGCTTAGTG	344
gCGA-TGA Arg-306 to Term Li-Fraumeni syndrome	GAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCCCAGGGAGCACTAAGCGAGGTAAGCAAGCAGGACAAGAAGCGGTGGAGGAGACCAAGGGTGCAAGTTATGCCTCAGA	345
	TCTGAGGCATAACTGCACCCTTGGTCTCCTCCACCGCTTCTTGTCTGCTTGCTTACCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTT	346
	GCACTAAGCGAGGTAAG	347

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTTACCTC <u>G</u> CTTAGTGC	348
gCGC-TGC Arg-337 to Cys Osteosarcoma	GGTACTGTGAATATACTTACTTCTCCCCCTCCTCTGTTGCTGC AGATCCGTGGGCGTGAG <u>C</u> GCTTCGAGATGTTCCGAGAGCTG AATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGA	349
	TCCCAGCCTGGGCATCCTTGAGTTCCAAGGCCTCATTGAGCT CTCGGAACATCTCGAAGC <u>G</u> CTCACGCCACGGATCTGCAGC AACAGAGGAGGGGGAGAAGTAAGTATATTACAGTACC	350
	GGCGTGAG <u>C</u> GCTTCGAG	351
	CTCGAAGC <u>G</u> CTCACGCC	352
CTG-CCG Leu-344 to Pro Li-Fraumeni syndrome	CTCCCCCTCCTCTGTTGCTGCAGATCCGTGGGCGTGAGCGCT TCGAGATGTTCCGAGAGCT <u>T</u> GAATGAGGCCTTGGAACTCAAGG ATGCCCAGGCTGGGAAGGAGCCAGGGGGGAGCAGGGC	353
	GCCCTGCTCCCCCTGGCTCCTTCCCAGCCTGGGCATCCTTG AGTTCCAAGGCCTCATT <u>C</u> AGCTCTCGGAACATCTCGAAGCGC TCACGCCACGGATCTGCAGCAACAGAGGAGGGGGAG	354
	CCGAGAGCTGAATGAGG	355
	CCTCATT <u>C</u> AGCTCTCGG	356

EXAMPLE 7

beta globin

[0207] Hemoglobin, the major protein in the red blood cell, binds oxygen reversibly and is responsible for the cells' capacity to transport oxygen to the tissues. In adults, the major hemoglobin is hemoglobin A, a tetrameric protein consisting of two identical alpha globin chains and two beta globin chains. Disorders involving hemoglobin are among the most common genetic disorders worldwide, with approximately 5% of the world's population being carriers for clinically important hemoglobin mutations. Approximately 300,000 severely affected homozygotes or compound heterozygotes are born each year.

[0208] Mutation of the glutamic acid at position 7 in beta globin to valine causes sickle cell anemia, the clinical manifestations of which are well known. Mutations that cause absence of beta chain cause beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. For clinical purposes, beta-thalassemia is divided into thalassemia major (transfusion dependent), thalassemia intermedia (of intermediate severity), and thalassemia minor (asymptomatic). Patients with thalassemia major present in the first year of life with severe anemia; they are unable to maintain a hemoglobin level about 5 gm/dl.

[0209] The beta-thalassemias were among the first human genetic diseases to be examined by means of recombinant DNA analysis. Baysal et al., *Hemoglobin* 19(3-4):213-36 (1995) and others provide a compendium of mutations that result in beta-thalassemia.

[0210] Hemoglobin disorders were among the first to be considered for gene therapy.

- 5 Transcriptional silencing of genes transferred into hematopoietic stem cells, however, poses one of the most significant challenges to its success. If the transferred gene is not completely silenced, a progressive decline in gene expression is often observed. Position effect variegation (PEV) and silencing mechanisms may act on a transferred globin gene residing in chromatin outside of the normal globin locus during the important terminal phases of erythroblast development when globin transcripts normally
- 10 accumulate rapidly despite heterochromatinization and shutdown of the rest of the genome. The attached table discloses the correcting oligonucleotide base sequences for the beta globin oligonucleotides of the invention.

Table 8

Beta Globin Mutations and Genome-Correcting Oligos

15

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Sickle Cell Anemia GLU-7-VAL GAG to GTG	TCTGACACAACCTGTGTTCACTAGCAACCTCAAACAGACACCA TGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCC CTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGA	357
	TCACCACCAACTTCATCCACGTTACCTTGCCCCACAGGGCA GTAACGGCAGACTTCTCCTCAGGAGTCAGGTGCACCATGGT GTCTGTTTGAGGTTGCTAGTGAACACAGTTGTGTGTCAGA	358
	GACTCCTGAGGAGAAGT	359
	ACTTCTCCTCAGGAGTC	360
Thalassaemia Beta MET-0-ARG ATG to AGG	CTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCA ACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT	361
	ACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCTA GTGAACACAGTTGTGTGAGAAGCAAATGTAAGCAATAG	362
	AGACACCATGGTGCACC	363
	GGTGCACCATGGTGTCT	364

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia Beta MET-0-ILE ATG to ATA	TATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCAA CCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTG	365
	CACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCT CCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCT AGTGAACACAGTTGTGTGAGAAGCAAATGTAAGCAATA	366
	GACACCATGGTGCACCT	367
	AGGTGCACCATGGTGTCT	368
Thalassaemia Beta MET-0-ILE ATG to ATT	TATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCAA CCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTG	369
	CACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCT CCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCT AGTGAACACAGTTGTGTGAGAAGCAAATGTAAGCAATA	370
	GACACCATGGTGCACCT	371
	AGGTGCACCATGGTGTCT	372
Thalassaemia Beta MET-0-LYS ATG to AAG	CTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCA ACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT	373
	ACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCTA GTGAACACAGTTGTGTGAGAAGCAAATGTAAGCAATAG	374
	AGACACCATGGTGCACCT	375
	GGTGCACCATGGTGTCT	376
Thalassaemia Beta MET-0-THR ATG to ACG	CTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCA ACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT	377
	ACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCTA GTGAACACAGTTGTGTGAGAAGCAAATGTAAGCAATAG	378
	AGACACCATGGTGCACCT	379
	GGTGCACCATGGTGTCT	380
Thalassaemia Beta MET-0-VAL ATG to GTG	TCTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGC AACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAG AAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACG	381

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTCC TCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCTAG TGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATAGA	382
	CAGACACCAATGGTGCAC	383
	GTGCACCATGGTGTCTG	384
Thalassaemia Beta TRP-16-Term TGG to TGA	TCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAAGT CTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAA GTTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTTA	385
	TAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTTC ATCCACGTTACCTTGCCCACAGGGCAGTAACGGCAGACT TCTCCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGA	386
	GCCCTGTGGGGCAAGGT	387
	ACCTTGCCCCACAGGGC	388
Thalassaemia Beta TRP-16-Term TGG to TAG	CTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAAG TCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGA AGTTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTT	389
	AACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTTCA TCCACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTT CTCCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGA	390
	TGCCCTGTGGGGCAAGG	391
	CCTTGCCCCACAGGGCA	392
Thalassaemia Beta LYS-18-Term AAG to TAG	ACAGACACCATGGTGCACCTGACTCCTGAGGAGAAGTCTGC CGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTG GTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTTACAAG	393
	CTTGTAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAA CTTCATCCACGTTACCTTGCCCCACAGGGCAGTAACGGCA GACTTCTCCTCAGGAGTCAGGTGCACCATGGTGTCTGT	394
	TGTGGGGCAAGGTGAAC	395
	GTTACCTTGCCCCACA	396
Thalassaemia Beta ASN-20-SER AAC to AGC	CCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTACT GCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGA GGCCCTGGGCAGGTTGGTATCAAGGTTACAAGACAGGTT	397
	AACCTGTCTTGTAACCTTGATACCAACCTGCCCAGGGCCTCA CCACCAACTTCATCCACGTTACCTTGCCCCACAGGGCAGTA ACGGCAGACTTCTCCTCAGGAGTCAGGTGCACCATGG	398
	CAAGGTGAACGTGGATG	399

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CATCCACG <u>T</u> TACCTTG	400
Thalassaemia Beta GLU-23-ALA GAA to GCA	ACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGG GGCAAGGTGAACGTGGATG <u>A</u> AGTTGGTGGTGAGGCCCTGG GCAGGTTGGTATCAAGGTTACAAGACAGGTTTAAGGAGAC	401
	GTCTCCTTAAACCTGTCTTGTAACCTTGATACCAACCTGCCCA GGGCCTCACCACCAACT <u>T</u> CATCCACGTTACCTTGCCCCACA GGGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGT	402
	CGTGGATG <u>A</u> AGTTGGTG	403
	CACCAACT <u>T</u> CATCCACG	404
Thalassaemia Beta GLU-23-term GAA to TAA	CACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTG GGGCAAGGTGAACGTGGATG <u>G</u> AAGTTGGTGGTGAGGCCCTG GGCAGGTTGGTATCAAGGTTACAAGACAGGTTTAAGGAGA	405
	TCTCCTTAAACCTGTCTTGTAACCTTGATACCAACCTGCCCAG GGCCTCACCACCAACTT <u>C</u> ATCCACGTTACCTTGCCCCACAG GGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGTG	406
	ACGTGGATG <u>G</u> AAGTTGGT	407
	ACCAACTT <u>C</u> ATCCACGT	408
Thalassaemia Beta GLU-27-LYS GAG to AAG	GAGGAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAA CGTGGATGCAGTTGGTGGT <u>G</u> AGGCCCTGGGCAGGTTGGTAT CAAGGTTATAAGAGAGGCTCAAGGAGGCAAATGGAACT	409
	AGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGATAC CAACCTGCCCAGGGCCT <u>C</u> ACCACCAACTGCATCCACGTTCA CTTGCCCCACAGGGCATTGACAGCAGTCTTCTCCTC	410
	TTGGTGGT <u>G</u> AGGCCCTG	411
	CAGGGCCT <u>C</u> ACCACCAA	412
Thalassaemia Beta GLU-27-Term GAG to TAG	GAGGAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAA CGTGGATGCAGTTGGTGGT <u>G</u> AGGCCCTGGGCAGGTTGGTAT CAAGGTTATAAGAGAGGCTCAAGGAGGCAAATGGAACT	413
	AGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGATAC CAACCTGCCCAGGGCCT <u>C</u> ACCACCAACTGCATCCACGTTCA CTTGCCCCACAGGGCATTGACAGCAGTCTTCTCCTC	414
	TTGGTGGT <u>G</u> AGGCCCTG	415
	CAGGGCCT <u>C</u> ACCACCAA	416

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia Beta ALA-28-SER GCC to TCC	GAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAACGT GGATGCAGTTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAA GGTTATAAGAGAGGCTCAAGGAGGCAAATGGAAACTGGG	417
	CCCAGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGA TACCAACCTGCCCAGGGCCTCACCACCAACTGCATCCACGTT CACTTTGCCCCACAGGGCATTGACAGCAGTCTTCTC	418
	GTGGTGAGGCCCTGGGC	419
	GCCCAGGGCCTCACCAC	420
Thalassaemia Beta ARG-31-THR AGG to ACG	CTGTCAATGCCCTGTGGGGCAAAGTGAACGTGGATGCAGTT GGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTTATAAGA GAGGCTCAAGGAGGCAAATGGAACTGGGCATGTGTAGA	421
	TCTACACATGCCCAGTTTCCATTTGCCTCCTTGAGCCTCTCTT ATAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTG CATCCACGTTCACTTTGCCCCACAGGGCATTGACAG	422
	CCTGGGCAGGTTGGTAT	423
	ATACCAACCTGCCCAGG	424
Thalassaemia Beta Leu-33-GLN CTG to CAG	TGGGTTTCTGATAGGCACTGACTCTCTGTCCCTTGGGCTGTT TTCCTACCCTCAGATTACTGGTGGTCTACCCTTGGACCCAGA GGTTCTTTGAGTCCTTTGGGGATCTGTCCTCTCCTGA	425
	TCAGGAGAGGACAGATCCCCAAAGGACTCAAAGAACCTCTG GGTCCAAGGGTAGACCACCAAGTAATCTGAGGGTAGGAAAAC AGCCCAAGGGACAGAGAGTCAGTGCCTATCAGAAACCCA	426
	CAGATTACTGGTGGTCT	427
	AGACCACCAAGTAATCTG	428
Thalassaemia Beta TYR-36-Term TAC to TAA	ATAGGCACTGACTCTCTGTCCCTTGGGCTGTTTTCTACCCT CAGATTACTGGTGGTCTACCTTGGACCCAGAGGTTCTTTGA GTCCTTTGGGGATCTGTCCTCTCCTGATGCTGTTATG	429
	CATAACAGCATCAGGAGAGGACAGATCCCCAAAGGACTCAA AGAACCTCTGGGTCCAAGGGTAGACCACCAAGTAATCTGAGG GTAGGAAAACAGCCCAAGGGACAGAGAGTCAGTGCCTAT	430
	GTGGTCTACCTTGGAC	431
	GTCCAAGGGTAGACCAC	432
Thalassaemia Beta TRP-38-Term TGG to TGA	ACTGACTCTCTGTCCCTTGGGCTGTTTTCTACCCTCAGATTA CTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTT GGGGATCTGTCCTCTCCTGATGCTGTTATGGGCAAC	433

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTTGCCCAT AACAGCATCAGGAGAGGACAGATCCCCAAAGG ACTCAAAGAACCTCTGGGTCCAAGGGTAGACCACCAGTAATC TGAGGGTAGGAAAACAGCCCAAGGGACAGAGAGTCACT	434
	TACCCTTGACCCAGAG	435
	CTCTGGGTCCAAGGGTA	436
Thalassaemia Beta TRP-38-Term TGG to TAG	CACTGACTCTGTCCCTTGGGCTGTTTTCTACCCTCAGAT TACTGGTGGTCTACCCTTGACCCAGAGGTTCTTTGAGTCCT TTGGGGATCTGTCTCTCCTGATGCTGTTATGGGCAA	437
	TTGCCCAT AACAGCATCAGGAGAGGACAGATCCCCAAAGGA CTCAAAGAACCTCTGGGTCCAAGGGTAGACCACCAGTAATCT GAGGGTAGGAAAACAGCCCAAGGGACAGAGAGTCACTG	438
	CTACCCTTGACCCAGA	439
	TCTGGGTCCAAGGGTAG	440
Thalassaemia Beta GLN-40-Term CAG-TAG	ACTCTCTGTCCCTTGGGCTGTTTTCTACCCTCAGATTACTG GTGGTCTACCCTTGACCCAGAGGTTCTTTGAGTCCTTTGGG GATCTGTCTCTCCTGATGCTGTTATGGGCAACCCTA	441
	TAGGGTTGCCCAT AACAGCATCAGGAGAGGACAGATCCCCA AAGGACTCAAAGAACCTCTGGGTCCAAGGGTAGACCACCAG TAATCTGAGGGTAGGAAAACAGCCCAAGGGACAGAGAGT	442
	CTTGACCCAGAGGTTT	443
	GAACCTCTGGGTCCAAG	444
Thalassaemia Beta GLU-44-Term GAG to TAG	TTGGGCTGTTTTCTACCCTCAGATTACTGGTGGTCTACCCT TGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCTGTCTCT CCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTC	445
	GAGCCTTCACCTTAGGGTTGCCCAT AACAGCATCAGGAGAG GACAGATCCCCAAAGGACTCAAAGAACCTCTGGGTCCAAGG GTAGACCACCAGTAATCTGAGGGTAGGAAAACAGCCCAA	446
	GGTCTTTGAGTCCTTT	447
	AAAGGACTCAAAGAACC	448
Thalassaemia Beta LYS-62-Term AAG to TAG	TTCTTTGAGTCCTTTGGGGATCTGTCTCTCCTGATGCTGTTA TGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAGGTGCTA GGTGCTTTAGTGATGGCCTGGCTCACCTGGACAACC	449
	GGTTGTCCAGGTGAGCCAGGCCATCACTAAAGGCACCTAGC ACCTTCTTGCCATGAGCCTTACCTTAGGGTTGCCCATACA GCATCAGGAGAGGACAGATCCCCAAAGGACTCAAAGAA	450
	CTAAGGTGAAGGCTCAT	451

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGAGCCTTCACCTTAG	452
Thalassaemia Beta SER-73-ARG AGT to AGA	TGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGA AGGTGCTAGGTGCCTTTAGTGATGGCCTGGCTCACCTGGAC AACCTCAAGGGCACTTTTTCTCAGCTGAGTGAGCTGCAC	453
	GTGCAGCTCACTCAGCTGAGAAAAAGTGCCCTTGAGGTTGTC CAGGTGAGCCAGGCCATCACTAAAGGCACCTAGCACCTTCT TGCCATGAGCCTTCACCTTAGGGTTGCCATAACAGCA	454
	GCCTTTAGTGATGGCCT	455
	AGGCCATCACTAAAGGC	456
Haemolytic Anaemia GLY-75-VAL GGC to GTC	TTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAGGTG CTAGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTC AAGGGCACTTTTTCTCAGCTGAGTGAGCTGCACTGTGA	457
	TCACAGTGCAGCTCACTCAGCTGAGAAAAAGTGCCCTTGAG GTTGTCCAGGTGAGCCAGGCCATCACTAAAGGCACCTAGCA CCTTCTTGCCATGAGCCTTCACCTTAGGGTTGCCATAA	458
	TAGTGATGGCCTGGCTC	459
	GAGCCAGGCCATCACTA	460
Thalassaemia Beta GLU-91-Term GAG to TAG	GCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGG CACCTTTGCCACACTGAGTGAGCTGCACTGTGACAAGCTGCA CGTGGATCCTGAGAACTTCAGGGTGAGTCTATGGGACC	461
	GGTCCCATAGACTCACCTGAAGTTCTCAGGATCCACGTGCA GCTTGTACAGTGCAGCTCACTCAGTGTGGCAAAGGTGCCC TTGAGGTTGTCCAGGTGAGCCAGGCCATCACTAAAGGC	462
	CACTGAGTGAGCTGCAC	463
	GTGCAGCTCACTCAGTG	464
Thalassaemia Beta VAL-99-MET GTG to ATG	CTGGACAACCTCAAGGGCACTTTTTCTCAGCTGAGTGAGCTG CACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGGT GAGTCCAGGAGATGCTTCACTTTTCTCTTTTACTTTC	465
	GAAAGTAAAAAGAGAAAAGTGAAGCATCTCCTGGACTCACCC TGAAGTTCTCAGGATCCAAGTGCAGCTTGTACAGTGCAGCT CACTCAGCTGAGAAAAAGTGCCCTTGAGGTTGTCCAG	466
	AGCTGCACGTGGATCCT	467
	AGGATCCACGTGCAGCT	468

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia Beta LEU-111-PRO CTG-CCG	CCCTTTTGCTAATCATGTTTCATACCTCTTATCTTCCTCCCACA GCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACT TTGGCAAAGAATTCACCCCACCAGTGCAGGCTGCCTA	469
	TAGGCAGCCTGCACTGGTGGGGTGAATTCTTTGCCAAAGTG ATGGGCCAGCACACAGACCAGCACGTTGCCCAGGAGCTGTG GGAGGAAGATAAGAGGTATGAACATGATTAGCAAAGGG	470
	CAACGTGCTGGTCTGTG	471
	CACAGACCAGCACGTTG	472
Thalassaemia Beta CYS-113-Term TGT to TGA	GCTAATCATGTTTCATACCTCTTATCTTCCTCCCACAGCTCCTG GGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA AGAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAA	473
	TTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCTTTGCC AAAGTGATGGGCCAGCACACAGACCAGCACGTTGCCCAGGA GCTGTGGGAGGAAGATAAGAGGTATGAACATGATTAGC	474
	CTGGTCTGTGTGCTGGC	475
	GCCAGCACACAGACCAG	476
Thalassaemia Beta LEU-115-PRO CTG to CCG	TCATGTTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCAA CGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATT CACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGT	477
	ACCACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCT TTGCCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGCC CAGGAGCTGTGGGAGGAAGATAAGAGGTATGAACATGA	478
	CTGTGTGCTGGCCCATC	479
	GATGGGCCAGCACACAG	480
Thalassaemia Beta ALA-116-ASP GCC to GAC	TGTTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCAACG TGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCA CCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGC	481
	GCCACCACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAA TTCTTTGCCAAAGTGATGGGCCAGCACACAGACCAGCACGTT GCCCAGGAGCTGTGGGAGGAAGATAAGAGGTATGAACA	482
	TGTGCTGGCCCATCACT	483
	AGTGATGGGCCAGCAC	484
Thalassaemia Beta GLU-122-Term GAA to TAA	TTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCT GGCCCATCACTTTGGCAAAGAATTACCCCACCAGTGCAGG CTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCC	485

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGGCATTAGCCACACCAGCCACCACTTTCTGATAGGCAGCC TGCACTGGTGGGGTGAATTCTTTGCCAAAGTGATGGGCCAG CACACAGACCAGCACGTTGCCAGGAGCTGTGGGAGGAA	486
	TTGGCAAAGAATTCACC	487
	GGTGAATTCTTTGCCAA	488
Thalassaemia Beta GLN-128-PRO CAG to CCG	GCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA GAATTCACCCACCAAGTGCAGGCTGCCTATCAGAAAGTGGT GGCTGGTGTGGCTAATGCCCTGGCCACAAGTATCACTA	489
	TAGTGATACTTGTGGGCCAGGGCATTAGCCACACCAGCCAC CACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCTTT GCCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGC	490
	ACCAGTGCAGGCTGCCT	491
	AGGCAGCCTGCACTGGT	492
Thalassaemia Beta GLN-128-Term CAG to TAG	GGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA AGAATTCACCCACCAAGTGCAGGCTGCCTATCAGAAAGTGGT GGCTGGTGTGGCTAATGCCCTGGCCACAAGTATCACT	493
	AGTGATACTTGTGGGCCAGGGCATTAGCCACACCAGCCACC ACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCTTTG CCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGCC	494
	CACCAGTGCAGGCTGCC	495
	GGCAGCCTGCACTGGTG	496
Thalassaemia Beta GLN-132-LYS CAG to AAG	GTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCA CCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGC TAATGCCCTGGCCACAAGTATCACTAAGCTCGCTTTC	497
	GAAAGCGAGCTTAGTGATACTTGTGGGCCAGGGCATTAGCC ACACCAGCCACCACTTTCTGATAGGCAGCCTGCACTGGTGG GGTGAATTCTTTGCCAAAGTGATGGGCCAGCACACAGAC	498
	CTGCCTATCAGAAAGTG	499
	CACTTTCTGATAGGCAG	500

EXAMPLE 8

Retinoblastoma

- [0211] Retinoblastoma (RB) is an embryonic neoplasm of retinal origin. It almost
5 always presents in early childhood and is often bilateral. The risk of osteogenic sarcoma is increased

500-fold in bilateral retinoblastoma patients, the bone malignancy being at sites removed from those exposed to radiation treatment of the eye tumor.

[0212] The retinoblastoma susceptibility gene (pRB; pRb) plays a pivotal role in the regulation of the cell cycle. pRB restrains cell cycle progression by maintaining a checkpoint in late G₁ that controls commitment of cells to enter S phase. The critical role that pRB plays in cell cycle regulation explains its status as archetypal tumor suppressor: loss of pRB function results in an inability to maintain control of the G₁ checkpoint; unchecked progression through the cell cycle is, in turn, a hallmark of neoplasia.

[0213] Blanquet *et al.*, *Hum. Molec. Genet.* 4: 383-388 (1995) performed a mutation survey of the RB1 gene in 232 patients with hereditary or nonhereditary retinoblastoma. They systematically explored all 27 exons and flanking sequences, as well as the promoter. All types of point mutations were represented and found to be unequally distributed along the RB1 gene sequence. In the population studied, exons 3, 8, 18, and 19 were preferentially altered. The attached table discloses the correcting oligonucleotide base sequences for the retinoblastoma oligonucleotides of the invention.

Table 9

pRB Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Retinoblastoma Trp99Term TGG-TAG	AATATTTGATCTTTATTTTTTTGTTCCCAGGGAGGTTATATTCAA AAGAAAAAGGAAGTGTGGGGAATCTGTATCTTTATTGCAGCA GTTGACCTAGATGAGATGTCGTTCACTTTTACTGA	501
	TCAGTAAAAGTGAACGACATCTCATCTAGGTCAACTGCTGCA ATAAAGATACAGATTCCCCACAGTTCCTTTTCTTTTGAATATA ACCTCCCTGGGAACAAAAATAAAGATCAAATATT	502
	GGAAGTGTGGGGAATCT	503
	AGATCCCCACAGTTCC	504
Retinoblastoma Glu137Asp GAA-GAT	ATTTACTTTTTTCTATTCTTTCCTTTGTAGTGTCCATAAATTCTT TAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAAT GCTATGTCAAGACTGTTGAAGAAGTATGATGTA	505
	TACATCATACTTCTTCAACAGTCTTGACATAGCATTATCAACT TTGGTACTGGTATCAATTCTTTTAGTAAGTTAAAGAATTTATG GACACTACAAAGGAAAGAATAGAAAAAGTAAAT	506
	CTAAAAGAAATTGATAC	507

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTATCAATTTCTTTTAG	508
Retinoblastoma Glu137Term GAA-TAA	TGATTTACTTTTTCTATTCTTTCTTTGTAGTGTCCATAAATT CTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGAT AATGCTATGTCAAGACTGTTGAAGAAGTATGATG	509
	CATCATACTTCTTCAACAGTCTTGACATAGCATTATCAACTTT GGTACTGGTATCAATTTCTTTTAGTAAGTTAAAGAATTTATGG ACACTACAAAGGAAAGAATAGAAAAAAGTAAATCA	510
	TACTAAAAGAAATTGAT	511
	ATCAATTTCTTTTAGTA	512
Retinoblastoma Gln176Term C	AAAATGTTAAAAAGTCATAATGTTTTCTTTTCAGGACATGTG AACTTATATATTTGACACAACCCAGCAGTTCGTAAGTAGTTCA CAGAATGTTATTTTCACTTAAAAAAAAGATTTT	513
	AAAATCTTTTTTTTTAAGTGAAAAATAACATTCTGTGAACTACT TACGAACTGCTGGGTTGTGTCAAATATATAAGTTCACATGTCC TGAAAAGAAAAACATTATGACTTTTTAACATTTT	514
	ATTTGACACAACCCAGC	515
	GCTGGGTTGTGTCAAAT	516
Retinoblastoma Ile185Thr ATA-ACA	TGATACATTTTCTGTTTTTTTTCTGCTTTCTATTTGTTTAATA GGATATCTACTGAAAATAATTCTGCATTGGTGCTAAAAGTTTC TTGGATCACATTTTATTAGCTAAAGGTAAGTT	517
	AACTTACCTTTAGCTAATAAAAATGTGATCCAAGAACTTTTA GCACCAATGCAGAATTTATTTTCAGTAGATATCCTATTAAACAA ATAGAAAGCAGAAAAAAACAGGAAAAATGTATCA	518
	TACTGAAATAAATTCTG	519
	CAGAATTTATTTTCAGTA	520
Retinoblastoma Gln207Term CAA-TAA	AAAGATCTGAATCTCTAACTTTCTTTAAAAATGTACATTTTTTT TTCAGGGGAAGTATTCAAATGGAAGATGATCTGGTGATTTTC ATTTTCAGTTAATGCTATGTGTCCTTGACTATTTTA	521
	TAAAATAGTCAAGGACACATAGCATTAACTGAAATGAAATCAC CAGATCATCTTCCATTTGTAATACTTCCCCTGAAAAAAAATG TACATTTTTAAAGAAAGTTAGAGATTCAGATCTTT	522
	AAGTATTACAAATGGAA	523
	TTCCATTTGTAATACTT	524
Retinoblastoma Arg251Term CGA to TGA	GTTCTTATCTAATTTACCACTTTTACAGAAACAGCTGTTATAC CCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAA GGAGTGCACGGATAGCAAAACAACTAGAAAATGATA	525

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TATCATTCTTAGTTGTTTTGCTATCCGTGCACTCCTGTTCTG ACCTCGCCTGGGTGTTCCAGGTGAACCATTAAATGGGTATAAC AGCTGTTTCTGTAAAAGTGGTAAATTAGATAAGAAC	526
	GTTACCTCGAACACCC	527
	GGGTGTTCCAGGTGAAC	528
Retinoblastoma Arg255Term CGA to TGA	TTTACCACTTTTACAGAAACAGCTGTTATACCCATTAAATGGTT CACCTCGAACACCCAGGCGAGGTGAGAACAGGAGTGACCGG ATAGCAAAACAACCTAGAAAATGATACAAGAATTATTG	529
	CAATAATTCTTGTATCATTTTTCTAGTTGTTTTGCTATCCGTGCA CTCCTGTTCTGACCTCGCCTGGGTGTTGAGGTGAACCATTAA ATGGGTATAACAGCTGTTTCTGTAAAAGTGGTAAA	530
	CACCCAGGCGAGGTGAG	531
	CTGACCTCGCCTGGGTG	532
Retinoblastoma Gln266Te	ATTAATGGTTCACCTCGAACACCCAGGCGAGGTGAGAACAG GAGTGCACGGATAGCAAAACAACCTAGAAAATGATACAAGAAT TATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAG	533
	CTATATTACATTCATGTTCTTTACAGAGAACTTCAATAATTCTT GTATCATTTTTCTAGTTGTTTTGCTATCCGTGCACTCCTGTTCT GACCTCGCCTGGGTGTTGAGGTGAACCATTAAAT	534
	TAGCAAAACAACCTAGAA	535
	TTCTAGTTGTTTTGCTA	536
Retinoblastoma Arg320Term CGA to TGA	TGACATGTAAAGGATAATTGTCAGTGACTTTTTCTTTCAAGG TTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT AAAGATCTAGATGCAAGATTATTTTTGGATCATG	537
	CATGATCCAAAAATAATCTTGCATCTAGATCTTTATTTTAAAGA TAAATTTCTTCGTATCGTTTAGAAAGATTTTCAACCTTGAAAG AAAAAAGTCACTGACAATTATCCTTTACATGTCA	538
	TTTCTAAACGATACGAA	539
	TTCGTATCGTTTAGAAA	540
Retinoblastoma Gln354Term CAG to TAG	ACAAATTGTAAATTTTCAGTATGTGAATGACTTCACTTATTGTT ATTTAGTTTTGAAACAAGAGAACACCACGAAAAAGTAACCTT GATGAAGAGGTGAATGTAATTCCTCCACACACTC	541
	GAGTGTGTGGAGGAATTACATTACCTCTTCATCAAGGTTAC TTTTTCGTGGTGTTCTCTGTGTTTCAAACTAAATAACAATAA GTGAAGTCATTCACATACTGAAAATTTACAATTTGT	542
	TTGAAACAAGAGAACAA	543

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGTTCTCT <u>G</u> TGTTTCAA	544
Retinoblastoma Arg358Gly CGA to GGA	TTTTCAGTATGTGAATGACTTCACTTATTGTTATTTAGTTTTGA AACACAGAGAACACCAC <u>G</u> AAAAAGTAACCTTGATGAAGAGGT GAATGTAATTCCTCCACACACTCCAGTTAGGTATG	545
	CATACCTAACTGGAGTGTGTGGAGGAATTACATTCACCTCTT CATCAAGGTTACTTTTT <u>C</u> GTGGTGTTCTCTGTGTTTCAAACT AAATAACAATAAGTGAAGTCATTCACATACTGAAAA	546
	GAACACCAC <u>G</u> AAAAAGT	547
	ACTTTTT <u>C</u> GTGGTGTT	548
Retinoblastoma Ar	TTTTCAGTATGTGAATGACTTCACTTATTGTTATTTAGTTTTGA AACACAGAGAACACCAC <u>G</u> AAAAAGTAACCTTGATGAAGAGGT GAATGTAATTCCTCCACACACTCCAGTTAGGTATG	549
	CATACCTAACTGGAGTGTGTGGAGGAATTACATTCACCTCTT CATCAAGGTTACTTTTT <u>C</u> GTGGTGTTCTCTGTGTTTCAAACT AAATAACAATAAGTGAAGTCATTCACATACTGAAAA	550
	GAACACCAC <u>G</u> AAAAAGT	551
	ACTTTTT <u>C</u> GTGGTGTT	552
Retinoblastoma Ser397Term TCA to TAA	CTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA GCAAGTGATCAACCTT <u>C</u> AGAAAATCTGATTTCTATTTTAACG TAAGCCATATATGAAACATTATTTATTGTAATAT	553
	ATATTACAATAAATAATGTTTCATATATGGCTTACGTTAAAATA GGAAATCAGATTTTCT <u>G</u> AAGGTTGATCACTTGCTGAATTTAAA ATCATCATTAAATTGTTGGATAGTGTTTCATAACAG	554
	TCAACCTT <u>C</u> AGAAAATC	555
	GATTTTCT <u>G</u> AAGGTTGA	556
Retinoblastoma Arg445Term CGA to TGA	TTTCATAATTGTGATTTTCTAAAATAGCAGGCTCTTATTTTTCT TTTTGTTTGTGTTAG <u>C</u> GATACAACTTGAGTTGCTTGAT TACCGAGTAATGGAATCCATGCTTAAATCAGTAA	557
	TACTGATTTAAGCATGGATTCCATTACTCGGTAATACAAGCG AACTCCAAGTTTGTATC <u>G</u> CTACAAACAAACAAAAAGAAAAATA AGAGCCTGCTATTTTAGAAAATCACAATTATGAAA	558
	GTTTGTAG <u>C</u> GATACAAA	559
	TTTGTATC <u>G</u> CTACAAAC	560
Retinoblastoma Arg455Term CGA to TGA	GCTCTTATTTTTCTTTTTGTTTGTGTTGTAGCGATACAACTTGG AGTTGCTTGATTAAC <u>G</u> GAGTAATGGAATCCATGCTTAAATCA GTAAGTTAAAAACAATATAAAAAAATTCAGCCG	561

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGGCTGAAATTTTTTATATTGTTTTAACTTACTGATTTAAGC ATGGATTCCATTACTCGGTAATACAAGCGAACTCCAAGTTTGT ATCGCTACAAACAAACAAAAAGAAAAATAAGAGC	562
	TGTATTACCGAGTAATG	563
	CATTACTCGGTAATACA	564
Retinoblastoma Arg552Term CGA to TGA	ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAA ATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT CCCTTGCATGGCTCTCAGTAAGTAGCTAAATAATTG	565
	CAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGATTCCAT GATTGATGTTACATCGTTCTAAATGTTTTATCATTCTCTTG TCAAGTTGCCTTCTGCTTTGATAAACTTTTCGAT	566
	ATTTAGAACGATGTGAA	567
	TTCACATCGTTCTAAAT	568
Retinoblastoma Cys553Term TGT to TGA	AAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGAT AAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT GCATGGCTCTCAGTAAGTAGCTAAATAATTGAAGAA	569
	TTCTTCAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGAT TCCATGATTGATGTTACATCGTTCTAAATGTTTTATCATTTT TCTTGCAAGTTGCCTTCTGCTTTGATAAACTT	570
	GAACGATGTGAACATCG	571
	CGATGTTACATCGTTC	572
Retinoblastoma Glu554Term GAA to TAA	AGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT GCATGGCTCTCAGTAAGTAGCTAAATAATTGAAGAAA	573
	TTTCTTCAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGA TTCCATGATTGATGTTACATCGTTCTAAATGTTTTATCATTT CTTTGTCAAGTTGCCTTCTGCTTTGATAAACT	574
	AACGATGTGAACATCGA	575
	TCGATGTTACATCGTT	576
Retinoblastoma Ser567Leu TCA to TTA	TACCTGGGAAAATTATGCTTACTAATGTGGTTTTAATTTATC ATGTTTCATATAGGATTACCTTTATTTGATCTTATTAACAAT CAAAGGACCGAGAAGGACCAACTGATCACCTTGA	577
	TCAAGGTGATCAGTTGGTCCTTCTCGGTCCTTTGATTGTTTAA TAAGATCAAATAAAGGTGAATCCTATATGAAACATGATGAAAT TAAACCACATTAGTAAGCATAATTTCCAGGTA	578
	ATAGGATTACCTTTAT	579

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATAAAGGTGAATCCTAT	580
Retinoblastoma Gln575Term CAA to TAA	AATGTGGTTTTAATTTTCATCATGTTTCATATAGGATTCACCTTT ATTTGATCTTATTAACAATCAAAGGACCGAGAAGGACCAACT GATCACCTTGAATCTGCTTGCCTCTTAATCTTC	581
	GAAGATTAAGAGGACAAGCAGATTCAAGGTGATCAGTTGGTC CTTCTCGGTCCTTTGATTGTTTAATAAGATCAAATAAAGGTGA ATCCTATATGAAACATGATGAAATTAACCACATT	582
	TTATTAAACAATCAAAG	583
	CTTTGATTGTTTAATAA	584
Retinoblastoma Arg579Term CGA to TGA	ATTTTCATCATGTTTCATATAGGATTCACCTTTATTTGATCTTAT TAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGA ATCTGCTTGCCTCTTAATCTTCTCTCCAGAATA	585
	TATTCTGGAGAGGAAGATTAAGAGGACAAGCAGATTCAAGGT GATCAGTTGGTCCTTCTCGGTCCTTTGATTGTTTAATAAGATC AAATAAAGGTGAATCCTATATGAAACATGATGAAAT	586
	CAAAGGACCGAGAAGGA	587
	TCCTTCTCGGTCCTTG	588
Retinoblastoma Glu580Term GAA to TAA	TCATCATGTTTCATATAGGATTCACCTTTATTTGATCTTATTAA ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC TGCTTGCCTCTTAATCTTCTCTCCAGAATAATC	589
	GATTATTCTGGAGAGGAAGATTAAGAGGACAAGCAGATTCAA GGTGATCAGTTGGTCCTTCTCGGTCCTTTGATTGTTTAATAAG ATCAAATAAAGGTGAATCCTATATGAAACATGATGA	590
	AGGACCGAGAAGGACCA	591
	TGGTCCTTCTCGGTCCT	592
Retinoblastoma Ser634Term TCA to TGA	AGAAAAAGGTTCAACTACGCGTGTAATTCTACTGCAAATG CAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGG	593
	CCTTTTTTATAAACAGTGAAAGAGAGGTAGATTTCATGGCT TCTGGGTCTGGAAGGCTGAGGTTGCTTGTGTCTCTGCATTG CAGTAGAATTTACACGCGTAGTTGAACCTTTTTTCT	594
	AGCAACCTCAGCCTTCC	595
	GGAAGGCTGAGGTTGCT	596
Retinoblastoma Ala635P	AAAAAAGGTTCAACTACGCGTGTAATTCTACTGCAAATGCA GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATT GAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGGTT	597

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AACCTTTTTTATAAAACAGTGAAAGAGAGGTAGATTTCAATGG CTTCTGGGTCTGGAAGGCTGAGGTTGCTTGTGTCTCTGCATT TGCAGTAGAATTTACACGCGTAGTTGAACCTTTTTT	598
	CAACCTCAGCCTTCCAG	599
	CTGGAAGGCTGAGGTTG	600
Retinoblastoma Gln639Term CAG to TAG	ACTACGCGTGTAATTCTACTGCAAATGCAGAGACACAAGCA ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCT CTTCACTGTTTTATAAAAAAGGTTAGTAGATGATTA	601
	TAATCATCTACTAACCTTTTTTATAAAACAGTGAAAGAGAGGT AGATTTCAATGGCTTCTGGGTCTGGAAGGCTGAGGTTGCTTG TGTCTCTGCATTTGCAGTAGAATTTACACGCGTAGT	602
	TCCAGACCCAGAAGCCA	603
	TGGCTTCTGGGTCTGGA	604
Retinoblastoma L	TTGTAATTCAAAATGAACAGTAAAAATGACTAATTTTTCTTATT CCCACAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTT TGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGA	605
	TCTAATTCTGGGTGCTCAGACAGAAGGCGTTCACAAAGTGTA TTTAGCCGGAGATAGGCTAGCCGATACACTGTGGGAATAAG AAAAATTAGTCATTTTTACTGTTTCAATTTGAATTACAA	606
	GTATCGGCTAGCCTATC	607
	GATAGGCTAGCCGATAC	608
Retinoblastoma Arg661Trp CGG to TGG	AATGAACAGTAAAAATGACTAATTTTTCTTATTCCCACAGTGT ATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCC TTCTGTCTGAGCACCCAGAATTAGAACATATCATCT	609
	AGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGGCGTT CACAAAGTGATTTAGCCGGAGATAGGCTAGCCGATACACTG TGGGAATAAGAAAAATTAGTCATTTTTACTGTTTCAAT	610
	CCTATCTCCGGCTAAAT	611
	ATTTAGCCGGAGATAGG	612
Retinoblastoma Leu662Pro CTA to CCA	AACAGTAAAAATGACTAATTTTTCTTATTCCCACAGTGTATCG GCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCT GTCTGAGCACCCAGAATTAGAACATATCATCTGGAC	613
	GTCCAGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGG CGTTCACAAAGTGATTTAGCCGGAGATAGGCTAGCCGATAC ACTGTGGGAATAAGAAAAATTAGTCATTTTTACTGTT	614
	TCTCCGGCTAAATACAC	615

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTGTATTTAGCCGGAGA	616
Retinoblastoma Glu675Term GAA to TAA	TATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC CTTCTGTCTGAGCACCCAGAAATTAGAACATATCATCTGGACC CTTTCCAGCACACCCTGCAGAATGAGTATGAACTCA	617
	TGAGTTCATACTCATTCTGCAGGGTGTGCTGGAAAAGGGTCC AGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGGCGTT CACAAAGTGATTTAGCCGGAGATAGGCTAGCCGATA	618
	AGCACCCAGAAATTAGAA	619
	TTCTAATTCTGGGTGCT	620
Retinoblastoma Gln685Pro CAG to CCG	TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATA TCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATG AACTCATGAGAGACAGGCATTTGGACCAAGTAAGAAA	621
	TTTCTTACTTGGTCCAAATGCCTGTCTCTCATGAGTTCATACT CATTCTGCAGGGTGTGCTGGAAAAGGGTCCAGATGATATGTT CTAATTCTGGGTGCTCAGACAGAAGGCGTTCACAAA	622
	CCTTTTCCAGCACACCC	623
	GGGTGTGCTGGAAAAGG	624
Retinoblastoma Cys706Tyr TGT to TAT	AAAACCATGTAATAAAATTCTGACTACTTTTACATCAATTTATT TACTAGATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA AGAATATAGACCTTAAATTCAAATCATTGTAAC	625
	GTTACAATGATTTTGAATTTAAGGTCTATATTCTTCACTTTGCA TATGCCATACATGGAACACATCATAATCTAGTAAATAAATTGA TGTAAGTAGTCAGAATTTTATTACATGGTTTT	626
	TATGATGTGTTCCATGT	627
	ACATGGAACACATCATA	628
Retinoblastoma Cys712Arg TGC to CGC	TTCTGACTACTTTTACATCAATTTATTTACTAGATTATGATGTG TTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA TTCAAATCATTGTAACAGCATAACAAGGATCTTC	629
	GAAGATCCTTGTATGCTGTTACAATGATTTTGAATTTAAGGTC TATATTCTTCACTTTGCATATGCCATACATGGAACACATCATA ATCTAGTAAATAAATTGATGTAAAAGTAGTCAGAA	630
	ATGGCATATGCAAAGTG	631
	CACTTTGCATATGCCAT	632
Retinoblastom TAC to TAA	GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAA ATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTTCA GAGGTAGGTAATTTCCATAGTAAGTTTTTTTGATA	633

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TATCAAAAAA ACTT ACTATGGAAAATTACCTACCTCCTGAACAGCATGAGGAAGATCCTT G TATGCTGTTACAATGATTTTGAATTAAAGGTCTATATTCTTCACTTTGCATATGCCATAC	634
	ACAGCATAC A AAGGATCT	635
	AGATCCTT G TATGCTGT	636
Retinoblastoma Glu748Term GAG to TAG	TTTTTTTTTTTTTTTACTGTTCTTCCTCAGACATTCAAACGTGT TTTGATCAAAGAAGAG G AGTATGATTCTATTATAGTATTCTAT AACTCGGTCTTCATGCAGAGACTGAAAACAAATA	637
	TATTTGTTTTTCAGTCTCTGCATGAAGACCGAGTTATAGAATAC TATAATAGAATCATACT C CTCTTCTTTGATCAAAACACGTTTG AATGTCTGAGGAAGAACAGTAAAAAAAAAAAAAAAAA	638
	AAGAAGAG G AGTATGAT	639
	ATCATACT C CTCTTCTT	640
Retinoblastoma Gln762Term CAG to TAG	GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCT ATAACTCGGTCTTCATG C AGAGACTGAAAACAAATATTTTGCA GTATGCTTCCACCAGGGTAGGTCAAAGTATCCTT	641
	AAGGATACTTTTGACCTACCCTGGTGAAGCATACTGCAAAA TATTTGTTTTTCAGTCTCT G CATGAAGACCGAGTTATAGAATAC TATAATAGAATCATACTCCTCTTCTTTGATCAAAAC	642
	TCTTCATG C AGAGACTG	643
	CAGTCTCT G CATGAAGA	644
Retinoblastoma Arg787Term CGA-TGA	TAATCTACTTTTTTGTTTTGCTCTAGCCCCCTACCTTGTCCAC CAATACCTCACATTCCT C GAAGCCCTTACAAGTTTCCTAGTTC ACCCTTACGGATTCTTGAGGGGAACATCTATATT	645
	AAATATAGATGTTCCCTCCAGGAATCCGTAAGGGTGAAGTAG GAAACTTGTAAGGGCTTC G AGGAATGTGAGGTATTGGTGACA AGGTAGGGGGCTAGAGCAAAAACAAAAAAGTAGATTA	646
	ACATTCCT C GAAGCCCT	647
	AGGGCTTC G AGGAATGT	648

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Retinoblastoma Ser816Term TCA to TGA	CCTTACGGATTCTCTGGAGGGAACATCTATATTTACCCCCTGA AGAGTCCATATAAAATTTGAGAAGGTCTGCCAACACCAACAA AAATGACTCCAAGATCAAGGTGTGTGTTTTCTCTTA	649
	TAAAGAGAAAACACACACCTTGATCTTGGAGTCATTTTTGTTG GTGTTGGCAGACCTTCTGAAATTTTATATGGACTCTTCAGGG GTGAAATATAGATGTTCCCTCCAGGAATCCGTAAGG	650
	TAAAATTTGAGAAGGTC	651
	GACCTTCTGAAATTTTA	652

EXAMPLE 9

BRCA1 and BRCA2

[0214] Breast cancer is the second major cause of cancer death in American women, with an estimated 44,190 lives lost (290 men and 43,900 women) in the US in 1997. While ovarian cancer accounts for fewer deaths than breast cancer, it still represents 4% of all female cancers. In 1994, two breast cancer susceptibility genes were identified: BRCA1 on chromosome 17 and BRCA2 on chromosome 13. When a woman carries a mutation in either BRCA1 or BRCA2, she is at increased risk of being diagnosed with breast or ovarian cancer at some point in her life.

[0215] Ford *et al.*, *Am. J. Hum. Genet.* 62: 676-689 (1998) assessed the contribution of BRCA1 and BRCA2 to inherited breast cancer by linkage and mutation analysis in 237 families, each with at least 4 cases of breast cancer. Families were included without regard to the occurrence of ovarian or other cancers. Overall, disease was linked to BRCA1 in an estimated 52% of families, to BRCA2 in 32% of families, and to neither gene in 16%, suggesting other predisposition genes. The majority (81%) of the breast-ovarian cancer families were due to BRCA1, with most others (14%) due to BRCA2. Conversely, the majority (76%) of families with both male and female breast cancer were due to BRCA2. The largest proportion (67%) of families due to other genes were families with 4 or 5 cases of female breast cancer only.

[0216] More than 75% of the reported mutations in the BRCA1 gene result in truncated proteins. Couch *et al.*, *Hum. Mutat.* 8: 8-18, 1996. (1996) reported a total of 254 BRCA1 mutations, 132 (52%) of which were unique. A total of 221 (87%) of all mutations or 107 (81%) of the unique mutations are small deletions, insertions, nonsense point mutations, splice variants, and regulatory mutations that result in truncation or absence of the BRCA1 protein. A total of 11 disease-associated missense

mutations (5 unique) and 21 variants (19 unique) as yet unclassified as missense mutations or polymorphisms had been detected. Thirty-five independent benign polymorphisms had been described. The most common mutations were 185delAG and 5382insC, which accounted for 30 (11.7%) and 26 (10.1%), respectively, of all the mutations.

5 **[0217]** Most BRCA2 mutations are predicted to result in a truncated protein product. The smallest known cancer-associated deletion removes from the C terminus only 224 of the 3,418 residues constituting BRCA2, suggesting that these terminal amino acids are critical for BRCA2 function. Studies (Spain *et al.*, Proc. Natl. Acad. Sci. 96:13920-13925 (1999)) suggest that such truncations eliminate or interfere with 2 nuclear localization signals that reside within the final 156 residues of BRCA2, 10 suggesting that the vast majority of BRCA2 mutants are nonfunctional because they are not translocated into the nucleus.

[0218] The attached table discloses the correcting oligonucleotide base sequences for the BRCA1 and BRCA2 oligonucleotides of the invention.

Table 10

15 **BRCA1 Mutations and Genome-Correcting Oligos**

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Met-1-Ile ATG to ATT	CTGCGCTCAGGAGGCCTTCACCCTCTGCTCTGGGTAAAGTT CATTGGAACAGAAAGAAATGGATTTATCTGCTCTTCGCGTTG AAGAAGTACAAAATGTCATTAATGCTATGCAGAAAATC	653
	GATTTTCTGCATAGCATTAAATGACATTTTGTACTTCTTCAACG CGAAGAGCAGATAAATCCATTTCTTTCTGTTCCAATGAACTTT ACCCAGAGCAGAGGGTGAAGGCCTCCTGAGCGCAG	654
	AAAGAAATGGATTTATC	655
	GATAAATCCATTTCTTT	656
Breast Cancer Val-11-Ala GTA to GCA	CTGGGTAAAGTTCATTGGAACAGAAAGAAATGGATTTATCTG CTCTTCGCGTTGAAGAAGTACAAAATGTCATTAATGCTATGCA GAAAATCTTAGAGTGTCCCATCTGTCTGGAGTTGAT	657
	ATCAACTCCAGACAGATGGGACACTCTAAGATTTTCTGCATA GCATTAATGACATTTTGTACTTCTTCAACGCGAAGAGCAGATA AATCCATTTCTTTCTGTTCCAATGAACTTTACCCAG	658
	TGAAGAAGTACAAAATG	659
	CATTTTGTACTTCTTCA	660

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Ile-21-Val ATC to GTC	ATGGATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCA TTAATGCTATGCAGAAAATCTTAGAGTGTCCCATCTGTCTGG AGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC	661
	GGTCACACTTTTGTGGAGACAGGTTCCCTTGATCAACTCCAGAC AGATGGGACACTCTAAGATTTTCTGCATAGCATTAAATGACATT TTGTACTTCTTCAACGCGAAGAGCAGATAAATCCAT	662
	TGCAGAAAATCTTAGAG	663
	CTCTAAGATTTTCTGCA	664
Breast Cancer Leu-22-Ser TTA to TCA	ATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCATTAA TGCTATGCAGAAAATCTTAGAGTGTCCCATCTGTCTGGAGTT GATCAAGGAACCTGTCTCCACAAAGTGTGACCACAT	665
	ATGTGGTCACACTTTTGTGGAGACAGGTTCCCTTGATCAACTCC AGACAGATGGGACACTCTAAGATTTTCTGCATAGCATTAAATG ACATTTTGTACTTCTTCAACGCGAAGAGCAGATAAAT	666
	GAAAATCTTAGAGTGTC	667
	GACACTCTAAGATTTTC	668
Breast Cancer Cys-39-Tyr TGT to TAT	AGAAAATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGG AACCTGTCTCCACAAAGTGTGACCACATATTTTGCAAATTTTG CATGCTGAACTTCTCAACCAGAAGAAAGGGCCTTC	669
	GAAGGCCCTTTCTTCTGGTTGAGAAGTTTCAGCATGCAAAT TTGCAAATATGTGGTCAACTTTGTGGAGACAGGTTCCCTTG ATCAACTCCAGACAGATGGGACACTCTAAGATTTTCT	670
	CACAAAGTGTGACCACA	671
	TGTGGTCAACTTTGTG	672
Breast Cancer Cys-61-Gly TGT to GGT	CACATATTTTGCAAATTTTGCATGCTGAACTTCTCAACCAGA AGAAAGGGCCTTCACAGTGTCTTTATGTAAGAATGATATAA CCAAAAGGAGCCTACAAGAAAGTACGAGATTTAGTC	673
	GACTAAATCTCGTACTTTCTTGTAGGCTCCTTTTGGTTATATC ATTCTTACATAAAGGACACTGTGAAGGCCCTTTCTTCTGGTT GAGAAGTTTCAGCATGCAAATTTGCAAATATGTG	674
	CTTCACAGTGTCTTTA	675
	TAAAGGACACTGTGAAG	676
Breast Cancer Leu-63-Stop TTA to TAA	TTTGCAAATTTTGCATGCTGAACTTCTCAACCAGAAGAAAGG GCCTTCACAGTGTCTTTATGTAAGAATGATATAACCAAAGG AGCCTACAAGAAAGTACGAGATTTAGTCAACTGT	677

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTTTGG TTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTTCTT CTGGTTGAGAAGTTTCAGCATGCAAATTTGCAA	678
	GTGTCCTTTATGTAAGA	679
	TCTTACATAAAGGACAC	680
Breast Cancer Cys-64-Arg TGT to CGT	TGCAAATTTTGCATGCTGAACTTCTCAACCAGAAGAAAGGG CCTTCACAGTGTCTTTATGTAAGAATGATATAACCAAAGGA GCCTACAAGAAAGTACGAGATTTAGTCAACTTGTTG	681
Breast Cancer Cys-64-Gly TGT to GGT	CAACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTTT GGTTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTTC TTCTGGTTGAGAAGTTTCAGCATGCAAATTTGCA	682
	GTCCTTTATGTAAGAAT	683
	ATTCTTACATAAAGGAC	684
Breast Cancer Cys-64-Tyr TGT to TAT	GCAAATTTTGCATGCTGAACTTCTCAACCAGAAGAAAGGGC CTTCACAGTGTCTTTATGTAAGAATGATATAACCAAAGGAG CCTACAAGAAAGTACGAGATTTAGTCAACTTGTTGA	685
	TCAACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTT TGTTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTT CTTCTGGTTGAGAAGTTTCAGCATGCAAATTTGC	686
	TCCTTTATGTAAGAATG	687
	CATTCTTACATAAAGGA	688
Breast Cancer Gln-74-Stop CAA to TAA	CAGAAGAAAGGGCCTTCACAGTGTCTTTATGTAAGAATGAT ATAACCAAAGGAGCCTACAAGAAAGTACGAGATTTAGTCAA CTTGTTGAAGAGCTATTGAAATCATTGTGCTTTTC	689
	GAAAAGCACAAATGATTTCAATAGCTCTTCAACAAGTTGACT AAATCTCGTACTTTCTTGTAAGGCTCCTTTTGTTATATCATTCT TACATAAAGGACACTGTGAAGGCCCTTTCTTCTG	690
	GGAGCCTACAAGAAAGT	691
	ACTTTCTTGTAAGGCTCC	692
Breast Cancer Tyr-105-Cys TAT to TGT	AGCTATTGAAAATCATTGTGCTTTTCAGCTTGACACAGGTTT GGAGTATGCAAACAGCTATAATTTTGCAAAAAGGAAAATAA CTCTCCTGAACATCTAAAAGATGAAGTTTCTATCAT	693
	ATGATAGAACTTCATCTTTTAGATGTTTCAAGGAGAGTTATTTT CCTTTTTTGCAAATTATAGCTGTTTGCATACTCCAAACCTGT GTCAAGCTGAAAAGCACAAATGATTTTCAATAGCT	694
	AAACAGCTATAATTTTG	695

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAAAATTATAGCTGTTT	696
Breast Cancer Asn-158-Tyr AAC to TAC	CTACAGAGTGAACCCGAAAATCCTTCCTTGCAGGAAACCAGT CTCAGTGTCCAACCTCTCTAACCTTGGAAGTGTGAGAACTCTG AGGACAAAGCAGCGGATACAACCTCAAAAGACGTCTG	697
	CAGACGTCTTTTGAGGTTGTATCCGCTGCTTTGTCCTCAGAG TTCTCACAGTTCCAAGGTAGAGAGTTGGACACTGAGACTGG TTTCTGCAAGGAAGGATTTTCGGGTTCACTCTGTAG	698
	AACCTCTCTAACCTTGGA	699
	TCCAAGGTAGAGAGTT	700
Breast Cancer Gln-169-Stop CAG to TAG	GAAACCAGTCTCAGTGTCCAACCTCTAACCTTGGAAGTGTG AGAAGTCTGAGGACAAAGCAGCGGATACAACCTCAAAAGAC GTCTGTCTACATTGAATTGGGATCTGATTCTTCTGAAG	701
	CTTCAGAAGAATCAGATCCCAATTCAATGTAGACAGACGTCT TTTGAGGTTGTATCCGCTGCTTTGTCCTCAGAGTTCTCACAG TTCCAAGGTTAGAGAGTTGGACACTGAGACTGGTTTC	702
	GGACAAAGCAGCGGATA	703
	TATCCGCTGCTTTGTCC	704
Breast Cancer Trp-353-Stop TGG to TAG	CTCCCAGCACAGAAAAAAGGTAGATCTGAATGCTGATCCCC TGTGTGAGAGAAAAGAATGGAATAAGCAGAACTGCCATGCT CAGAGAATCCTAGAGATACTGAAGATGTTCTTGGAT	705
	ATCCAAGGAACATCTTCAGTATCTCTAGGATTCTCTGAGCAT GGCAGTTTCTGCTTATTCCATTCTTTTCTCTCACACAGGGGAT CAGCATTGAGATCTACCTTTTTTCTGTGCTGGGAG	706
	AAAAGAATGGAATAAGC	707
	GCTTATTCCATTCTTTT	708
Breast Cancer Ile-379-Met ATT to ATG	ATGCTCAGAGAATCCTAGAGATACTGAAGATGTTCTTGGAT AACACTAAATAGCAGCATTCAGAAAGTTAATGAGTGGTTTTCC AGAAGTGATGAACTGTTAGGTTCTGATGACTCACAT	709
	ATGTGAGTCATCAGAACCTAACAGTTCATCACTTCTGGAAAA CCACTCATTAACCTTTCTGAATGCTGCTATTTAGTGTATCCAA GGAACATCTTCAGTATCTCTAGGATTCTCTGAGCAT	710
	AGCAGCATTCAGAAAGT	711
	ACTTTCTGAATGCTGCT	712
Breast Cancer Glu-421-Gly GAA to GGA	GGGAGTCTGAATCAAATGCCAAAGTAGCTGATGTATTGGACG TTCTAAATGAGGTAGATGAATATTCTGGTTCTTCAGAGAAAAT AGACTTACTGGCCAGTGATCCTCATGAGGCTTTAAT	713

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATTAAAGCCTCATGAGGATCACTGGCCAGTAAGTCTATTTTCTCTGAAGAACCAGAATATTCATCTACCTCATTTAGAACGTCCAA TACATCAGCTACTTTGGCATTGATTGAGACTCCC	714
	GGTAGATGAATATTCTG	715
	CAGAATATTCATCTACC	716
Breast Cancer Phe-461-Leu TTT to CTT	ATATGTAAAAGTGAAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAATTTGGGAAAACCTATCGGAAGAAG GCAAGCCTCCCCAACTTAAGCCATGTAAGTGAAGATC	717
	GATTTTCAGTTACATGGCTTAAGTTGGGGAGGCTTGCCTTCTTCCGATAGGTTTTCCCAAATATTTTGTCTTCAATATTACTCTCT ACTGATTTGGAGTGAAGTCTTTCACTTTTACATAT	718
	ACAAAATATTTGGGAAA	719
	TTTCCCAAATATTTTGT	720
Breast Cancer Tyr-465-Leu TAT to GAT	GAAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATATTTGGGAAAACCTATCGGAAGAAGGCAAGCCTCCCC AACTTAAGCCATGTAAGTGAAGTCTAATTATAGGAG	721
	CTCCTATAATTAGATTTTCAGTTACATGGCTTAAGTTGGGGAGGCTTGCCTTCTTCCGATAGGTTTTCCCAAATATTTTGTCTTCA ATATTACTCTCTACTGATTTGGAGTGAAGTCTTTC	722
	GGAAAACCTATCGGAAG	723
	CTTCCGATAGGTTTTCC	724
Breast Cancer Gly-484-Stop GGA to TGA	ACCTATCGGAAGAAGGCAAGCCTCCCCAACTTAAGCCATGTA ACTGAAAATCTAATTATAGGAGCATTGTGTTACTGAGCCACAGATAATACAAGAGCGTCCCCTCACAAATAAATTAAAGC	725
	GCTTTAATTTATTTGTGAGGGGACGCTCTTGATTATCTGTGGCTCAGTAACAAATGCTCCTATAATTAGATTTTCAGTTACATGG CTTAAGTTGGGGAGGCTTGCCTTCTTCCGATAGGT	726
	TAATTATAGGAGCATT	727
	AAATGCTCCTATAATTA	728
Breast Cancer Arg-507-Ile AGA to ATA	TACTGAGCCACAGATAATACAAGAGCGTCCCCTCACAAATA AATTAAAGCGTAAAGGAGACCTACATCAGGCCTTCATCCTG AGGATTTTATCAAGAAAGCAGATTTGGCAGTTCAAAA	729
	TTTTGAAGTGCCTAAATCTGCTTTCTTGATAAAATCCTCAGGAT GAAGGCCTGATGTAGGTCTCCTTTTACGCTTTAATTTATTTGT GAGGGGACGCTCTTGATTATCTGTGGCTCAGTAA	730
	TAAAAGGAGACCTACAT	731

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGTAGGT <u>C</u> TCCTTTTA	732
Breast Cancer Ser-510-Stop TCA to TGA	CACAGATAATACAAGAGCGTCCCCTCACAAATAAATTAAAGC GTAAAAGGAGACCTACAT <u>C</u> AGGCCTTCATCCTGAGGATTTTA TCAAGAAAGCAGATTTGGCAGTTCAAAGACTCCTGA	733
	TCAGGAGTCTTTTGAAGTGCCAAATCTGCTTTCTTGATAAAAT CCTCAGGATGAAGGCCT <u>G</u> ATGTAGGTCTCCTTTTACGCTTTA ATTTATTTGTGAGGGGACGCTCTTGATTATCTGTG	734
	ACCTACAT <u>C</u> AGGCCTTC	735
	GAAGGCCT <u>G</u> ATGTAGGT	736
Breast Cancer Gln-526-Stop CAA to TAA	AGGAGACCTACATCAGGCCTTCATCCTGAGGATTTTATCAAG AAAGCAGATTTGGCAGTT <u>C</u> AAAAGACTCCTGAAATGATAAAT CAGGGAACCTAACCAACGGAGCAGAATGGTCAAGTGA	737
	TCACTTGACCATTCTGCTCCGTTTGGTTAGTTCCCTGATTTAT CATTTCAGGAGTCTTTT <u>G</u> AAGTGCCAAATCTGCTTTCTTGATA AAATCCTCAGGATGAAGGCCTGATGTAGGTCTCCT	738
	TGGCAGTT <u>C</u> AAAAGACT	739
	AGTCTTTT <u>G</u> AAGTGCCA	740
Breast Cancer Gln-541-Stop CAG to TAG	AGGAGACCTACATCAGGCCTTCATCCTGAGGATTTTATCAAG AAAGCAGATTTGGCAGTT <u>C</u> AAAAGACTCCTGAAATGATAAAT CAGGGAACCTAACCAACGGAGCAGAATGGTCAAGTGA	741
	TCACTTGACCATTCTGCTCCGTTTGGTTAGTTCCCTGATTTAT CATTTCAGGAGTCTTTT <u>G</u> AAGTGCCAAATCTGCTTTCTTGATA AAATCCTCAGGATGAAGGCCTGATGTAGGTCTCCT	742
	AAACGGAG <u>C</u> AGAATGGT	743
	ACCATTCT <u>G</u> CTCCGTTT	744
Breast Cancer Gly-552-Val GGT to GTT	TAAATCAGGGAACCTAACCAACGGAGCAGAATGGTCAAGTGA TGAATATTACTAATAGT <u>G</u> TCATGAGAATAAAACAAAAGGTGA TTCTATTGAGAATGAGAAAAATCCTAACCCAATAGA	745
	TCTATTGGGTTAGGATTTTCTCATTCTGAATAGAATCACCTT TTGTTTTATTCTCATG <u>A</u> CCACTATTAGTAATATTCATCACTTGA CCATTCTGCTCCGTTTGGTTAGTTCCCTGATTTA	746
	TAATAGT <u>G</u> TCATGAGA	747
	TCTCATG <u>A</u> CCACTATTA	748
Breast Cancer Gln-563-Stop CAG to TAG	GGTCAAGTGATGAATATTACTAATAGTGGTCATGAGAATAAAA CAAAGGTGATTCTATT <u>C</u> AGAATGAGAAAAATCCTAACCCAAT AGAATCACTCGAAAAAGAATCTGCTTTCAAACGA	749

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCGTTTTGAAAGCAGATTCTTTTTCGAGTGATTCTATTGGGTT AGGATTTTTCTCATTCTGAATAGAATCACCTTTTGTATTCT CATGACCACTATTAGTAATATTCACCTTGACC	750
	ATTCTATTGAGAATGAG	751
	CTCATTCTGAATAGAAT	752
Ovarian Cancer Lys-607-Stop AAA to TAA	ATAAGCAGCAGTATAAGCAATATGGAAGCTCGAATTAAATATCC ACAATTCAAAAGCACCTAAAAAGAATAGGCTGAGGAGGAAGT CTTCTACCAGGCATATTCATGCGCTTGAAGTAGTAG	753
	CTACTAGTTCAAGCGCATGAATATGCCTGGTAGAAGACTTCC TCCTCAGCCTATTCTTTTAGGTGCTTTTGAATTGTGGATATT TAATTCGAGTTCCATATTGCTTATACTGCTGCTTAT	754
	AAGCACCTAAAAAGAAT	755
	ATTCTTTTAGGTGCTT	756
Breast Cancer Leu-639-Stop TTG to TAG	ATATTCATGCGCTTGAAGTAGTAGTCAGTAGAAATCTAAGCC CACCTAATTGTACTGAATTGCAAATTGATAGTTGTTCTAGCAG TGAAGAGATAAAGAAAAAAGTACAACCAAATGCC	757
	GGCATTGGTTGTACTTTTTTTCTTTATCTCTTCACTGCTAGA ACAAGTATCAATTTGCAATTTCAGTACAATTAGGTGGGCTTAGA TTTCTACTGACTACTAGTTCAAGCGCATGAATAT	758
	TACTGAATTGCAAATTG	759
	CAATTTGCAATTTCAGTA	760
Breast Cancer Asp-693-Asn GAC to AAC	GAACCTGCAACTGGAGCCAAGAAGAGTAACAAGCCAAATGA ACAGACAAGTAAAAGACATGACAGCGATACTTTCCAGAGCT GAAGTTAACAAATGCACCTGGTTCTTTACTAAGTGTT	761
	AACACTTAGTAAAAGAACCAGGTGCATTTGTAACTTCAGCTC TGGGAAAGTATCGCTGTATGTCTTTTACTTGTCTGTTCAATTT GGCTTGTTACTCTTCTTGGCTCCAGTTGCAGGTTT	762
	AAAGACATGACAGCGAT	763
	ATCGCTGTATGTCTTT	764
Ovarian Cancer Glu-720-Stop GAA to TAA	CTGAAGTTAACAAATGCACCTGGTTCTTTTACTAAGTGTTCAA ATACCAGTGAAGTTAAAGAAATTTGTCAATCCTAGCCTTCCAAG AGAAGAAAAAGAAGAGAACTAGAAACAGTTAAAG	765
	CTTTAACTGTTTCTAGTTTCTTCTTTTCTTCTCTTGAAGG CTAGGATTGACAAATTTCTTTAAGTTCACTGGTATTTGAACACT TAGTAAAAGAACCAGGTGCATTTGTAACTTCAG	766
	AACTTAAAGAATTTGTC	767

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GACAAATTCTTTAAGTT	768
Breast Cancer Glu-755-Stop GAA to TAA	CTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAA GATCTCATGTAAAGTGGAGAAAGGGTTTTGCAAACGAAAGA TCTGTAGAGAGTAGCAGTATTTTCATTGGTACCTGGTA	769
	TACCAGGTACCAATGAAATACTGCTACTCTCTACAGATCTTTC AGTTTGCAAACCCCTTTCTCCACTTAACATGAGATCTTTGGGG TCTTCAGCATTATTAGACACTTTAACTGTTTCTAG	770
	TAAGTGGAGAAAGGGTT	771
	AACCCTTTCTCCACTTA	772
Breast Cancer Ser-770-Stop TCA to TAA	TCATGTTAAGTGGAGAAAGGGTTTTGCAAACGAAAGATCTG TAGAGAGTAGCAGTATTTTCATTGGTACCTGGTACTGATTATG GCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCAC	773
	GTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTGCCATAA TCAGTACCAGGTACCAATGAAATACTGCTACTCTCTACAGAT CTTTCAGTTTGCAAACCCCTTTCTCCACTTAACATGA	774
	CAGTATTTTCATTGGTAC	775
	GTACCAATGAAATACTG	776
Breast Cancer Val-772-Ala GTA to GCA	TAAGTGGAGAAAGGGTTTTGCAAACGAAAGATCTGTAGAGA GTAGCAGTATTTTCATTGGTACCTGGTACTGATTATGGCACTC AGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGG	777
	CCTAGAGTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTG CCATAATCAGTACCAGGTACCAATGAAATACTGCTACTCTCTA CAGATCTTTCAGTTTGCAAACCCCTTTCTCCACTTA	778
	TTCATTGGTACCTGGTA	779
	TACCAGGTACCAATGAA	780
Breast Cancer Gln-780-Stop CAG to TAG	ACTGAAAGATCTGTAGAGAGTAGCAGTATTTTCATTGGTACCT GGTACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAA GTTAGCACTCTAGGGAAGGCAAAAACAGAACCAAATA	781
	TATTTGGTTCTGTTTTTGCCTTCCCTAGAGTGCTAACTTCCAG TAACGAGATACTTTCCTGAGTGCCATAATCAGTACCAGGTAC CAATGAAATACTGCTACTCTCTACAGATCTTTCAGT	782
	ATGGCACTCAGGAAAGT	783
	ACTTTCCTGAGTGCCAT	784
Breast Cancer Glu-797-Stop GAA to TAA	TATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACT CTAGGGAAGGCAAAAACAGAACCAATAAATGTGTGAGTCAG TGTGCAGCATTTGAAAACCCCAAGGGACTAATTCATG	785

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CATGAATTAGTCCCTTGGGGTTTTCAAATGCTGCACACTGAC TCACACATTTATTTGGTTCTGTTTTTGCCTTCCCTAGAGTGCT AACTTCCAGTAACGAGATACTTTCCTGAGTGCCATA	786
	CAAAAACAGAACCAAAT	787
	ATTTGGTTCTGTTTTTG	788
Breast Cancer Lys-820-Glu AAA to GAA	AAATGTGTGAGTCAGTGTGCAGCATTTGAAAACCCCAAGGGA CTAATTCATGGTTGTTCCAAAGATAATAGAAATGACACAGAAG GCTTTAAGTATCCATTGGGACATGAAGTTAACCACA	789
	TGTGGTTAACTTCATGTCCCAATGGATACTTAAAGCCTTCTGT GTCATTTCTATTATCTTTGGAACAACCATGAATTAGTCCCTTG GGGTTTTCAAATGCTGCACACTGACTCACACATTT	790
	GTTGTTCCAAAGATAAT	791
	ATTATCTTTGGAACAAC	792
Breast Cancer Thr-826-Lys ACA to AAA	CAGCATTTGAAAACCCCAAGGGACTAATTCATGGTTGTTCCA AAGATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGG GACATGAAGTTAACCACAGTCGGGAAACAAGCATAGA	793
	TCTATGCTTGTTTTCCCGACTGTGGTTAACTTCATGTCCCAATG GATACTTAAAGCCTTCTGTGTCAATTTCTATTATCTTTGGAACA ACCATGAATTAGTCCCTTGGGGTTTTCAAATGCTG	794
	AAATGACACAGAGGCT	795
	AGCCTTCTGTGTCAATTT	796
Breast Cancer Arg-841-Trp CGG to TGG	GATAATAGAAATGACACAGAAGGCTTTAAGTATCCATTGGGA CATGAAGTTAACCACAGTCGGGAAACAAGCATAGAAATGGAA GAAAGTGAAGTTGATGCTCAGTATTTGCAGAATACAT	797
	ATGTATTCTGCAAATACTGAGCATCAAGTTCACCTTTCTTCCAT TTCTATGCTTGTTTTCCCAGCTGTGGTTAACTTCATGTCCCAAT GGATACTTAAAGCCTTCTGTGTCAATTTCTATTATC	798
	ACCACAGTCGGGAAACA	799
	TGTTTCCCAGCTGTGGT	800
Breast Cancer Pro-871-Leu CCG to CTG	AACCTTGATGCTCAGTATTTGCAGAATACATTCAAGGTTTCAA GCGCCAGTCATTTGCTCCGTTTTCAAATCCAGGAAATGCAGA AGAGGAATGTGCAACATTCTCTGCCCACTCTGGGTC	801
	GACCCAGAGTGGGCAGAGAATGTTGCACATTCCTCTTCTGCA TTTCCTGGATTTGAAAACGGAGCAAATGACTGGCGCTTTGAA ACCTTGAATGTATTCTGCAAATACTGAGCATCAAGTT	802
	ATTTGCTCCGTTTTCAA	803

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTGAAAAC <u>G</u> GAGCAAAT	804
Breast Cancer Leu-892-Ser TTA to TCA	TTTCAAATCCAGGAAATGCAGAAGAGGAATGTGCAACATTCT CTGCCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCA CTTTTGAATGTGAACAAAAGGAAGAAAATCAAGGAAA	805
	TTTCCTTGATTTTCTTCCTTTTGTTCACATTCAAAAGTGACTTT TGGACTTTGTTTCTTTAAGGACCCAGAGTGGGCAGAGAATGT TGCACATTCTCTTCTGCATTTCCTGGATTTGAAA	806
	TGGGTCCTTAAAGAAAC	807
	GTTTCTTTAAGGACCCA	808
Breast Cancer Glu-908-Stop GAA to TAA	CACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACTTTT GAATGTGAACAAAAGGAAGAAATCAAGGAAAGAATGAGTCT AATATCAAGCCTGTACAGACAGTTAATATCACTGCAG	809
	CTGCAGTGATATTAAGTGTCTGTACAGGCTTGATATTAGACTC ATTCTTTCTTGATTTTCTTCCTTTTGTTCACATTCAAAAGTGA CTTTTGGACTTTGTTTCTTTAAGGACCCAGAGTG	810
	AAAAGGAAGAAATCAA	811
	TTGATTTTCTTCCTTTT	812
Breast Cancer Gly-960-Asp GGC to GAC	ATAATGCCAAATGTAGTATCAAAGGAGGCTCTAGGTTTTGTCT ATCATCTCAGTTCAGAGGCAACGAACTGGACTCATTACTCC AAATAAACATGGACTTTTACAAAACCCATATCGTAT	813
	ATACGATATGGGTTTTGTAAAGTCCATGTTTATTTGGAGTAA TGAGTCCAGTTTCGTTGCCTCTGAACTGAGATGATAGACAAA ACCTAGAGCCTCCTTTGATACTACATTGGCATTAT	814
	G TTCAGAGGCAACGAAA	815
	TTTCGTTGCCTCTGAAC	816
Breast Cancer Met-1008-Ile ATG to ATA	ATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGGAAAAC TTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAAT GAGAACATTCCAAGTACAGTGAGCACAATTAGCCGT	817
	ACGGCTAATTGTGCTCACTGTACTTGGAATGTTCTCATTTCCC ATTTCTCTTTCAGGTGACATTGAATGTTCTCAAAGTTTTCT CTAGCAGATTTTCTTACATTAGTTTAAACAAAT	818
	CATTCAATGTCACCTGA	819
	TCAGGTGACATTGAATG	820
Breast Cancer Thr-1025-Ile ACA to ATA	ACTTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAA ATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATA ACATTAGAGAAAATGTTTTTAAAGAAGCCAGCTCAAG	821

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTTGAGCTGGCTTCTTTAAAAACATTTTCTCTAATGTTATTAC GGCTAATTGTGCTCACT <u>G</u> TACTTGGAATGTTCTCATTTCCCAT TTCTCTTTCAGGTGACATTGAATGTTCTCCTCAAAGT	822
	TCCAAGTAC <u>A</u> GAGTGAAGCA	823
	TGCTCACT <u>G</u> TACTTGGA	824
Breast Cancer Glu-1038-Gly GAA to GGA	ACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTA GAGAAAATGTTTTTAAAG <u>A</u> AGCCAGCTCAAGCAATATTAATGA AGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTAT	825
	ATACTGGAGCCCACTTCATTAGTACTGGAACCTACTTCATTAA TATTGCTTGAGCTGGCT <u>T</u> CTTTAAAAACATTTTCTCTAATGTTA TTACGGCTAATTGTGCTCACTGTACTTGGAATGT	826
	TTTTAAAG <u>A</u> AGCCAGCT	827
	AGCTGGCT <u>T</u> CTTTAAAA	828
Breast Cancer Ser-1040-Asn AGC to AAC	CAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAA ATGTTTTTAAAGAAGCCAG <u>G</u> CTCAAGCAATATTAATGAAGTAGG TTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA	829
	TCATTAATACTGGAGCCCACTTCATTAGTACTGGAACCTACTT CATTAAATATTGCTTGAG <u>C</u> TGGCTTCTTTAAAAACATTTTCTCTA ATGTTATTACGGCTAATTGTGCTCACTGTACTTG	830
	AGAAGCCAG <u>G</u> CTCAAGCA	831
	TGCTTGAG <u>C</u> TGGCTTCT	832
Breast Cancer Val-1047-Ala GTA to GCA	GCCGTAATAACATTAGAGAAAATGTTTTTAAAGAAGCCAGCTC AAGCAATATTAATGAAGT <u>A</u> GAGTTCCAGTACTAATGAAGTGGG CTCCAGTATTAATGAAATAGGTTCCAGTGATGAAAA	833
	TTTTCATCACTGGAACCTATTTTATTAATACTGGAGCCCACTT CATTAGTACTGGAACCT <u>A</u> CTTCATTAATATTGCTTGAGCTGGC TTCTTTAAAAACATTTTCTCTAATGTTATTACGGC	834
	TAATGAAGT <u>A</u> GAGTTCCA	835
	TGGAACCT <u>A</u> CTTCATTA	836
Breast Cancer Leu-1080-Stop TTG to TAG	AAATAGGTTCCAGTGATGAAAACATTCAAGCAGAACTAGGTA GAAACAGAGGGCCAAAAT <u>T</u> GAATGCTATGCTTAGATTAGGGG TTTTGCAACCTGAGGTCTATAAACAAAGTCTTCCTGG	837
	CCAGGAAGACTTTGTTTATAGACCTCAGGTTGCAAAACCCCT AATCTAAGCATAGCATTCA <u>A</u> ATTTTGGCCCTCTGTTTCTACCTA GTTCTGCTTGAATGTTTTCATCACTGGAACCTATTT	838
	GCCAAAAT <u>T</u> GAATGCTA	839

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAGCATTCAATTTTGGC	840
Breast Cancer Leu-1086-Stop TTA to TGA	AAAACATTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAAT TGAATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCT ATAAACAAAGTCTTCCTGGAAGTAATTGTAAGCATCC	841
	GGATGCTTACAATTACTTCCAGGAAGACTTTGTTTATAGACCT CAGGTTGCAAAACCCCTAATCTAAGCATAGCATTCAATTTTG GCCCTCTGTTTCTACCTAGTTCTGCTTGAATGTTTT	842
	GCTTAGATTAGGGGTTT	843
	AAACCCCTAATCTAAGC	844
Breast Cancer Ser-1130-Stop TCA to TGA	AGCAAGAATATGAAGAAGTAGTTCAGACTGTTAATACAGATTT CTCTCCATATCTGATTTGAGATAACTTAGAACAGCCTATGGGA AGTAGTCATGCATCTCAGGTTTGTCTGAGACACC	845
	GGTGTCTCAGAACAAACCTGAGATGCATGACTACTTCCCATA GGCTGTTCTAAGTTATCTGAAATCAGATATGGAGAGAAATCT GTATTAACAGTCTGAACTACTTCTTCATATTCTTGCT	846
	TCTGATTTGAGATAACT	847
	AGTTATCTGAAATCAGA	848
Breast Cancer Lys-1183-Arg AAA to AGA	CTAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTT TAGCAAAAGCGTCCAGAAAGGAGAGCTTAGCAGGAGTCCTA GCCCTTTCACCCATACACATTTGGCTCAGGGTTACCG	849
	CGGTAACCCTGAGCCAAATGTGTATGGGTGAAAGGGCTAGG ACTCCTGCTAAGCTCTCCTTCTGACGCTTTTGCTAAAAACA GCAGAACTTTCCTTAATGTCAATTTTCAGCAAACTAG	850
	CGTCCAGAAAGGAGAGC	851
	GCTCTCCTTCTGACG	852
Breast Cancer Gln-1200-Stop CAG to TAG	AGCGTCCAGAAAGGAGAGCTTAGCAGGAGTCCTAGCCCTTT CACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGG	853
	CCTCACTAGATAAGTTCTCTTCTGAGGACTCTAATTTCTTGCC CCCTCTTCGGTAACCCTGAGCCAAATGTGTATGGGTGAAAGG GCTAGGACTCCTGCTAAGCTCTCCTTTCTGACGCT	854
	ATTTGGCTCAGGGTTAC	855
	GTAACCCTGAGCCAAAT	856
Breast Cancer Arg-1203-Stop CGA to TGA	AAAGGAGAGCTTAGCAGGAGTCCTAGCCCTTTCACCCATACA CATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGAAATTAGA GTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGC	857

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCTCTTCATCCTCACTAGATAAGTTCTCTTCTGAGGACTCTAA TTTCTTGGCCCCCTCTTCGGTAACCCTGAGCCAAATGTGTATG GGTGAAAGGGCTAGGACTCCTGCTAAGCTCTCCTTT	858
	AGGGTTACCGAAGAGGG	859
	CCCTCTTCGGTAACCCT	860
Breast Cancer Glu-1214-Stop GAG to TAG	ACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAA GAAATTAGAGTCCTCAGAAGAGAAGCTTATCTAGTGAGGATGA AGAGCTTCCCTGCTTCCAACACTTGTTATTTGGTAAAG	861
	CTTTACCAAATAACAAGTGTTGGAAGCAGGGAAGCTCTTCAT CCTCACTAGATAAGTTCTCTTCTGAGGACTCTAATTTCTTGGC CCCTCTTCGGTAACCCTGAGCCAAATGTGTATGGGT	862
	CCTCAGAAAGAGAAGCTTA	863
	TAAGTTCTCTTCTGAGG	864
Breast Cancer Glu-1219-Asp GAG to GAC	TCAGGGTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAG AAGAGAAGCTTATCTAGTGAGGATGAAGAGCTTCCCTGCTTCC AACACTTGTTATTTGGTAAAGTAAACAATATACCTTCT	865
	AGAAGGTATATTGTTTACTTTACCAAATAACAAGTGTTGGAAG CAGGGAAGCTCTTCATCCTCACTAGATAAGTTCTCTTCTGAG GACTCTAATTTCTTGGCCCCCTCTTCGGTAACCCTGA	866
	TCTAGTGAGGATGAAGA	867
	TCTTCATCCTCACTAGA	868
Breast Cancer Glu-1221-Stop GAA to TAA	GGTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAGAAGA GAAGCTTATCTAGTGAGGATGAAGAGCTTCCCTGCTTCCAACA CTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT	869
	ACTGAGAAGGTATATTGTTTACTTTACCAAATAACAAGTGTTG GAAGCAGGGAAGCTCTTCATCCTCACTAGATAAGTTCTCTTC TGAGGACTCTAATTTCTTGGCCCCCTCTTCGGTAACC	870
	GTGAGGATGAAGAGCTT	871
	AAGCTCTTCATCCTCAC	872
Breast Cancer Glu-1250-Stop GAG to TAG	TTATTTGGTAAAGTAAACAATATACCTTCTCAGTCTACTAGGC ATAGCACC GTTGCTACCGAGTGTCTGTCTAAGAACACAGAGG AGAATTTATTATCATTGAAGAATAGCTTAAATGACT	873
	AGTCATTTAAGCTATTCTTCAATGATAATAAATTCTCCTCTGTG TTCTTAGACAGACACTCGGTAGCAACGGTGCTATGCCTAGTA GACTGAGAAGGTATATTGTTTACTTTACCAAATAA	874
	TTGCTACCGAGTGTCTG	875

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAGACACT <u>C</u> GGTAGCAA	876
Breast Cancer Ser-1262-Stop TCA to TAA	CTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACA CAGAGGAGAATTTATTAT <u>C</u> ATTGAAGAATAGCTTAAATGACTG CAGTAACCAGGTAATATTGGCAAAGGCATCTCAGGA	877
	TCCTGAGATGCCTTTGCCAATATTACCTGGTTACTGCAGTCAT TTAAGCTATTCTTCAAT <u>G</u> ATAATAAATTCTCCTCTGTGTTCTTA GACAGACACTCGGTAGCAACGGTGCTATGCCTAG	878
	TTTATTAT <u>C</u> ATTGAAGA	879
	TCTTCAAT <u>G</u> ATAATAAA	880
Breast Cancer Gln-1281-Stop CAG to TAG	TTATCATTGAAGAATAGCTTAAATGACTGCAGTAACCAGGTAA TATTGGCAAAGGCATCT <u>C</u> AGGAACATCACCTTAGTGAGGAAA CAAATGTTCTGCTAGCTTGTTTTCTTCACAGTGCA	881
	TGCACTGTGAAGAAAACAAGCTAGCAGAACATTTTGTTCCT CACTAAGGTGATGTTCTT <u>G</u> AGATGCCTTTGCCAATATTACCT GGTACTGCAGTCATTTAAGCTATTCTTCAATGATAA	882
	AGGCATCT <u>C</u> AGGAACAT	883
	ATGTTCTT <u>G</u> AGATGCCT	884
Breast Cancer Gln-1313-Stop CAG to TAG	GCTAGCTTGTTTTCTTCACAGTGCAGTGAATTGGAAGACTTG ACTGCAAATACAAACACCC <u>C</u> AGGATCCTTTCTTGATTGGTTCTT CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAG	885
	CTCCCTGGCTTTTCAGACTGATGCCTCATTTGTTTGAAGAAC CAATCAAGAAAGGATCCTT <u>G</u> GGTGTTTGTATTTGCAGTCAAGT CTTCCAATTCAGTGCAGTGTGAAGAAAACAAGCTAGC	886
	CAAACACCC <u>C</u> AGGATCCT	887
	AGGATCCTT <u>G</u> GGTGTTTG	888
Breast Cancer Ile-1318-Val ATT to GTT	TCACAGTGCAGTGAATTGGAAGACTTGACTGCAAATACAAAC ACCCAGGATCCTTTCTTG <u>A</u> TTGGTTCTTCCAAACAAATGAGG CATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACA	889
	TGTCAGTGCAGTGAATTGGAAGACTTGACTGCAAATACAAAC TTTGTGTTGAAGAACCAAT <u>T</u> CAAGAAAGGATCCTGGGTGTTTG TATTTGCAGTCAAGTCTTCCAATTCAGTGCAGTGTGA	890
	CTTTCTTG <u>A</u> TTGGTTCT	891
	AGAACCAAT <u>T</u> CAAGAAAG	892
Breast Cancer Gln-1323-Stop CAA to TAA	TTGGAAGACTTGACTGCAAATACAAACACCCAGGATCCTTTC TTGATTGGTTCTTCCAAAC <u>C</u> AAATGAGGCATCAGTCTGAAAGC CAGGGAGTTGGTCTGAGTGACAAGGAATTGGTTTCAG	893

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTGAAACCAATTCCTTGTCACTCAGACCAACTCCCTGGCTTT CAGACTGATGCCTCATTTGTTTGAAGAACCAATCAAGAAAG GATCCTGGGTGTTTGTATTTGCAGTCAAGTCTTCCAA	894
	CTTCCAAACAAATGAGG	895
	CCTCATTTGTTTGAAG	896
Breast Cancer Arg-1347-Gly AGA to GGA	CAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACAAGGAATT GGTTTCAGATGATGAAGAAAGAGGAACGGGCTTGAAGAAA ATAATCAAGAAGAGCAAAGCATGGATTCAAACCTTAGGTA	897
	TACCTAAGTTTGAATCCATGCTTTGCTCTTCTTGATTATTTTCT TCCAAGCCCGTTCCTCTTTCTTCATCATCTGAAACCAATTCCT TGCACTCAGACCAACTCCCTGGCTTTCAGACTG	898
	ATGAAGAAAGAGGAACG	899
	CGTTCCTCTTTCTTCAT	900
Breast Cancer Gln-1395-Stop CAG to TAG	GAAACAAGCGTCTCTGAAGACTGCTCAGGGCTATCCTCTCAG AGTGACATTTTAAACCACTCAGGTAAAAAGCGTGTGTGTGTGT GCACATGCGTGTGTGTGGTGTCTTTGCATTTCAGTAG	901
	CTACTGAATGCAAAGGACACCACACACACGCATGTGCACACA CACACACGCTTTTTACCTGAGTGGTTAAATGTCACTCTGAG AGGATAGCCCTGAGCAGTCTTCAGAGACGCTTGTTTC	902
	TAACCACTCAGGTAAAA	903
	TTTTACCTGAGTGGTTA	904
Breast Cancer Gln-1408-Stop CAG to TAG	TGGTGCCATTTATCGTTTTTGAAGCAGAGGGATACCATGCAA CATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAA GCTGTGTTAGAACAGCATGGGAGCCAGCCTTCTAACA	905
	TGTTAGAAGGCTGGCTCCCATGCTGTTCTAACACAGCTTCTA GTTTCAGCCATTTCTGCTGGAGCTTTATCAGGTTATGTTGCAT GGTATCCCTCTGCTTCAAAAACGATAAATGGCACCA	906
	TAAAGCTCCAGCAGGAA	907
	TTCCTGCTGGAGCTTTA	908
Breast Cancer Arg-1443-Gly CGA to GGA Arg-1443-Stop CGA to TGA	AGCCAGCCTTCTAACAGCTACCCTTCCATCATAAGTGACTCT TCTGCCCTTGAGGACCTGCGAAATCCAGAACAAAGCACATCA GAAAAAGGTGTGTATTGTTGGCCAAACACTGATATCT	909
	AGATATCAGTGTTTGGCCAACAATACACACCTTTTTCTGATGT GCTTTGTTCTGGATTTCGAGGTCTCAAGGGCAGAAGAGTC ACTTATGATGGAAGGGTAGCTGTTAGAAGGCTGGCT	910
	AGGACCTGCGAAATCCA	911

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGGATTTC <u>G</u> CAGGTCCT	912
Breast Cancer Ser-1512-Ile AGT to ATT	CAGAATAGAACTACCCATCTCAAGAGGAGCTCATTAAGGTT GTTGATGTGGAGGAGCAAC <u>A</u> CAGCTGGAAGAGTCTGGGCCACA CGATTTGACGGAAACATCTTACTTGCCAAGGCAAGATC	913
	GATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAAATCGTGTG GCCCAGACTCTTCCAGCT <u>G</u> TTGCTCCTCCACATCAACAACCT TAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTG	914
	AGGAGCAAC <u>A</u> CAGCTGGAA	915
	TTCCAGCT <u>G</u> TTGCTCCT	916
Breast Cancer Gln-1538-Stop CAG to TAG	ATCTTTCTAGGTCATCCCCTTCTAAATGCCCATCATTAGATGA TAGGTGGTACATGCACAGTTGCTCTGGGAGTCTTCAGAATAG AAACTACCCATCTCAAGAGGAGCTCATTAAGGTTGT	917
	ACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCT GAAGACTCCCAGAGCAAC <u>T</u> GTGCATGTACCACCTATCATCTA ATGATGGGCATTTAGAAGGGGATGACCTAGAAAGAT	918
	CATGCACAGTTGCTCTG	919
	CAGAGCAAC <u>T</u> GTGCATG	920
Breast Cancer Glu-1541-Stop GAG to TAG	CAGAATAGAACTACCCATCTCAAGAGGAGCTCATTAAGGTT GTTGATGTGGAGGAGCAAC <u>A</u> CAGCTGGAAGAGTCTGGGCCACA CGATTTGACGGAAACATCTTACTTGCCAAGGCAAGATC	921
	GATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAAATCGTGTG GCCCAGACTCTTCCAGCT <u>G</u> TTGCTCCTCCACATCAACAACCT TAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTG	922
	AGGAGCAAC <u>A</u> CAGCTGGAA	923
	TTCCAGCT <u>G</u> TTGCTCCT	924
Breast Cancer Thr-1561-Ile ACC to ATC	AACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTG GAGGAGCAACAGCTGGAAG <u>A</u> GTCTGGGCCACACGATTTGAC GGAAACATCTTACTTGCCAAGGCAAGATCTAGGTAATA	925
	TATTACCTAGATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAA ATCGTGTGGCCAGACT <u>C</u> TTCCAGCTGTTGCTCCTCCACATC AACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTT	926
	AGCTGGAAGAGTCTGGG	927
	CCCAGACT <u>C</u> TTCCAGCT	928
Breast Cancer Tyr-1563-Stop TAC to TAG	TTTGTAATTCAACATTCATCGTTGTGTAAATTAACTTCTCCCA TTCCTTTCAGAGGGAAC <u>C</u> CCCTTACCTGGAATCTGGAATCAGC CTCTTCTCTGATGACCCTGAATCTGATCCTTCTGA	929

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCAGAAGGATCAGATTCAGGGTCATCAGAGAAGAGGCTGATT CCAGATTCCAGGTAAGGG <u>G</u> TTCCCTCTGAAAGGAATGGGAG AAGTTTAATTTACACAACGATGAATGTTGAATTACAAA	930
	AGAGGGAACCCCTTACC	931
	GGTAAGGG <u>G</u> TTCCCTCT	932
Breast Cancer Leu-1564-Pro CTG to CCG	CAACATTCATCGTTGTGTAAATTAACTTCTCCCATTCCTTTC AGAGGGAACCCCTTACC <u>T</u> GGAATCTGGAATCAGCCTCTTCTC TGATGACCCTGAATCTGATCCTTCTGAAGACAGAGC	933
	GCTCTGTCTTCAGAAGGATCAGATTCAGGGTCATCAGAGAAG AGGCTGATTCCAGATTCC <u>A</u> GGTAAGGGGTTCCCTCTGAAAG GAATGGGAGAAGTTTAATTTACACAACGATGAATGTTG	934
	CCCTTACC <u>T</u> GGAATCTG	935
	CAGATTCC <u>A</u> GGTAAGGG	936
Breast Cancer Gln-1604-Stop CAA to TAA	GCCCCAGAGTCAGCTCGTGTGGCAACATACCATCTTCAACC TCTGCATTGAAAGTTCCCC <u>C</u> AATTGAAAGTTGCAGAATCTGCC CAGAGTCCAGCTGCTGCTCATACTACTGATACTGCTG	937
	CAGCAGTATCAGTAGTATGAGCAGCAGCTGGACTCTGGGCA GATTCTGCAACTTTCAATT <u>G</u> GGGAACCTTTCAATGCAGAGGTT GAAGATGGTATGTTGCCAACACGAGCTGACTCTGGGGC	938
	AAGTTCCCC <u>C</u> AATTGAAA	939
	TTTCAATT <u>G</u> GGGAACCTT	940
Breast Cancer Lys-1606-Glu AAA to GAA	GAGTCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCA TTGAAAGTTCCCCAATTG <u>A</u> AAGTTGCAGAATCTGCCAGAGT CCAGCTGCTGCTCATACTACTGATACTGCTGGGTATA	941
	TATACCCAGCAGTATCAGTAGTATGAGCAGCAGCTGGACTCT GGGCAGATTCTGCAACTTT <u>I</u> CAATTGGGGAACCTTTCAATGCAG AGGTTGAAGATGGTATGTTGCCAACACGAGCTGACTC	942
	CCCAATTG <u>A</u> AAGTTGCA	943
	TGCAACTTT <u>I</u> CAATTGGG	944
Breast Cancer Met-1628-Thr ATG to ACG	CAGAATCTGCCAGAGTCCAGCTGCTGCTCATACTACTGATA CTGCTGGGTATAATGCAAT <u>T</u> GGAAGAAAGTGTGAGCAGGGAG AAGCCAGAATTGACAGCTTCAACAGAAAGGGTCAACAA	945
	TTGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCC TGCTCACACTTTCTTCC <u>A</u> TTGCATTATACCCAGCAGTATCAGT AGTATGAGCAGCAGCTGGACTCTGGGCAGATTCTG	946

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAATGCAATGGAAGAAA	947
	TTTCTTCCATTGCATTA	948
Breast Cancer Met-1628-Val ATG to GTG	GCAGAATCTGCCCAGAGTCCAGCTGCTGCTCATACTACTGAT ACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGA GAAGCCAGAATTGACAGCTTCAACAGAAAGGGTCAACA	949
	TGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCT GCTCACACTTTCTTCCATTGCATTATACCCAGCAGTATCAGTA GTATGAGCAGCAGCTGGACTCTGGGCAGATTCTGC	950
	ATAATGCAATGGAAGAA	951
	TTCTTCCATTGCATTAT	952
Breast Cancer Pro-1637-Leu CCA to CTA	CTCATACTACTGATACTGCTGGGTATAATGCAATGGAAGAAA GTGTGAGCAGGGAGAAGCCAGAATTGACAGCTTCAACAGAA AGGGTCAACAAAAGAATGTCCATGGTGGTGTCTGGCCT	953
	AGGCCAGACACCACCATGGACATTCTTTTGTGACCCTTTCT GTTGAAGCTGTCAATTCTGGCTTCTCCCTGCTCACACTTTCTT CCATTGCATTATACCCAGCAGTATCAGTAGTATGAG	954
	GGAGAAGCCAGAATTGA	955
	TCAATTCTGGCTTCTCC	956
Breast Cancer Met-1652-Ile ATG to ATA	GAGCAGGGAGAAGCCAGAATTGACAGCTTCAACAGAAAGGG TCAACAAAAGAATGTCCATGGTGGTGTCTGGCCTGACCCCAG AAGAATTTGTGAGTGTATCCATATGTATCTCCCTAATG	957
	CATTAGGGAGATACATATGGATACACTCACAAATTCTTCTGG GGTCAGGCCAGACACCACCATGGACATTCTTTTGTGACCCT TTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCTGCTC	958
	ATGTCCATGGTGGTGTG	959
	GACACCACCATGGACAT	960
Breast Cancer Glu-1694-Stop GAG to TAG	CACTTCCTGATTTTGTGTTTCAACTTCTAATCCTTTGAGTGTGTTT TCATTCTGCAGATGCTGAGTTTGTGTGTGAACGGACACTGAA ATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAG	961
	CTACCCATTTTCTCCCGCAATTCTAGAAAATATTTTCAGTGT CCGTTACACACAAACTCAGCATCTGCAGAATGAAAAACACT CAAAGGATTAGAAGTTGAAAACAAAATCAGGAAGTG	962
	CAGATGCTGAGTTTGTG	963
	CACAACTCAGCATCTG	964

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Gly-1706-Glu GGA to GAA	GTGTTTTTCATTCTGCAGATGCTGAGTTTGTGTGTGAACGGA CACTGAAATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAG TTAGCTATTTCTGTAAGTATAATACTATTTCTCCCCT	965
	AGGGGAGAAATAGTATTATACTTACAGAAATAGCTAACTACC CATTTTCCTCCCGCAATTCTAGAAAATATTTTCAGTGTCCGTT CACACACAAACTCAGCATCTGCAGAATGAAAAACAC	966
	TTTTCTAGGAATTGCGG	967
	CCGCAATTCTAGAAAA	968
Breast Cancer Ala-1708-Glu GCG to GAG	TTCATTCTGCAGATGCTGAGTTTGTGTGTGAACGGACACTGA AATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAGTTAGCT ATTTCTGTAAGTATAATACTATTTCTCCCCTCCTCCC	969
	GGGAGGAGGGGAGAAATAGTATTATACTTACAGAAATAGCTA ACTACCCATTTTCCTCCC <u>G</u> CAATTCCTAGAAAATATTTTCAGTG TCCGTTACACACAAACTCAGCATCTGCAGAATGAA	970
	AGGAATTGCGGGAGGAA	971
	TTCCTCCC <u>G</u> CAATTCCT	972
Breast Cancer Val-1713-Ala GTA to GCA	CTGAGTTTGTGTGTGAACGGACACTGAAATATTTTCTAGGAAT TGCGGGAGGAAAATGGGTAGTTAGCTATTTCTGTAAGTATAA TACTATTTCTCCCCTCCTCCCTTAACACCTCAGAA	973
	TTCTGAGGTGTTAAAGGGAGGAGGGGAGAAATAGTATTATAC TTACAGAAATAGCTAACTACCCATTTTCCTCCCGCAATTCCTA GAAAATATTTTCAGTGTCCGTTACACACAAACTCAG	974
	AAAATGGGTAGTTAGCT	975
	AGCTAACTACCCATTTT	976
Breast Cancer Trp-1718-Stop TGG to TAG	AACGGACACTGAAATATTTTCTAGGAATTGCGGGAGGAAAAT GGGTAGTTAGCTATTTCTGTAAGTATAATACTATTTCTCCCCT CCTCCCTTAACACCTCAGAATTGCATTTTACACC	977
	GGTGTA AAAATGCAATTCTGAGGTGTTAAAGGGAGGAGGGG AGAAATAGTATTATACTTACAGAAATAGCTAACTACCCATTTT CCTCCCGCAATTCCTAGAAAATATTTTCAGTGTCCGTT	978
	CTATTTCTGTAAGTATA	979
	TATACTTACAGAAATAG	980
Breast Cancer Glu-1725-Stop GAA to TAA	TTCTGCTGTATGTAACTGTCTTTTCTATGATCTCTTTAGGGG TGACCCAGTCTATTAAAGAAAGAAAAATGCTGAATGAGGTAA GTACTTGATGTTACAACTAACCAGAGATATTCATT	981

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AATGAATATCTCTGGTTAGTTTGTAACATCAAGTACTTACCTC ATTGAGCATTCTTTCTTTCTTTAATAGACTGGGTACCCCTAAA GAGATCATAGAAAAGACAGGTTACATACAGCAGAA	982
	CTATTAAAGAAAGAAAA	983
	TTTTCTTTCTTTAATAG	984
Breast Cancer Lys-1727-Stop AAA to TAA	TGTATGTAACCTGTCTTTTCTATGATCTCTTTAGGGGTGACCC AGTCTATTAAAGAAAGAA A AAATGCTGAATGAGGTAAGTACTT GATGTTACAACTAACCAGAGATATTCATTGAGTCA	985
	TGACTGAATGAATATCTCTGGTTAGTTTGTAACATCAAGTACT TACCTCATTGAGCATTCTTTCTTTCTTTAATAGACTGGGTACCC CCTAAAGAGATCATAGAAAAGACAGGTTACATACA	986
	AAGAAAGAA A AAATGCTG	987
	CAGCATTCTTTCTTTCTT	988
Breast Cancer Pro-1749-Arg CCA to CGA	TCTTTCAGCATGATTTTGAAGTCAGAGGAGATGTGGTCAATG GAAGAAACCACCAAGGTCCAAAGCGAGCAAGAGAATCCCAG GACAGAAAGGTAAAGCTCCCTCCCTCAAGTTGACAAAA	989
	TTTTGTCAACTTGAGGGAGGGAGCTTTACCTTTCTGTCCTGG GATTCTCTTGCTCGCTTTGGACCTTGGTGGTTTCTTCCATTGA CCACATCTCCTCTGACTTCAAATCATGCTGAAAGA	990
	CCAAGGTCCAAAGCGAG	991
	CTCGCTTTGGACCTTGG	992
Breast Cancer Arg-1751-Stop CGA to TGA	CAGCATGATTTTGAAGTCAGAGGAGATGTGGTCAATGGAAGA AACCACCAAGGTCCAAAGCGAGCAAGAGAATCCCAGGACAG AAAGGTAAAGCTCCCTCCCTCAAGTTGACAAAAATCTC	993
	GAGATTTTGTCAACTTGAGGGAGGGAGCTTTACCTTTCTGT CCTGGGATTCTCTTGCTCGCTTTGGACCTTGGTGGTTTCTTC CATTGACCACATCTCCTCTGACTTCAAATCATGCTG	994
	GTCCAAAGCGAGCAAGA	995
	TCTTGCTCGCTTTGGAC	996
Breast Cancer Gln-1756-Stop CAG to TAG	GTCAGAGGAGATGTGGTCAATGGAAGAAACCACCAAGGTCC AAAGCGAGCAAGAGAATCCAGGACAGAAAGGTAAAGCTCC CTCCCTCAAGTTGACAAAAATCTCACCCACCACTCTGT	997
	ACAGAGTGGTGGGGTGAGATTTTGTCAACTTGAGGGAGGG AGCTTTACCTTTCTGTCCTGGGATTCTCTTGCTCGCTTTGGAC CTTGGTGGTTTCTTCCATTGACCACATCTCCTCTGAC	998
	GAGAATCCAGGACAGA	999

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCTGTCCTGGGATTCTC	1000
Breast Cancer Met-1775-Arg ATG to AGG	CTCTCTTCTTCCAGATCTTCAGGGGGCTAGAAATCTGTTGCT ATGGGCCCTTCACCAACATGCCCCACAGGTAAGAGCCTGGGA GAACCCCAGAGTTCCAGCACCAGCCTTTGTCTTACATA	1001
	TATGTAAGACAAAGGCTGGTGCTGGAACCTCTGGGGTTCTCCC AGGCTCTTACCTGTGGGCATGTTGGTGAAGGGCCCATAGCA ACAGATTTCTAGCCCCCTGAAGATCTGGAAGAAGAGAG	1002
	CACCAACATGCCCCACAG	1003
	CTGTGGGCATGTTGGTG	1004
Breast Cancer Trp-1782-Stop TGG to TGA	AGTATGCAGATTACTGCAGTGATTTTACATCTAAATGTCCATT TTAGATCAACTGGAATGGATGGTACAGCTGTGTGGTGCTTCT GTGGTGAAGGAGCTTTCATCATTACCCTTGGCACA	1005
	TGTGCCAAGGGTGAATGATGAAAGCTCCTTCACCACAGAAGC ACCACACAGCTGTACCATCCATTCCAGTTGATCTAAAATGGA CATTTAGATGTAAATCACTGCAGTAATCTGCATACT	1006
	CTGGAATGGATGGTACA	1007
	TGTACCATCCATTCCAG	1008
Breast Cancer Gln-1785-His CAG to CAT	ATTACTGCAGTGATTTTACATCTAAATGTCCATTTTATAGTCAA CTGGAATGGATGGTACAGCTGTGTGGTGCTTCTGTGGTGAA GGAGCTTTCATCATTACCCTTGGCACAGTAAGTATT	1009
	AATACTTACTGTGCCAAGGGTGAATGATGAAAGCTCCTTCAC CACAGAAGCACACACAGCTGTACCATCCATTCCAGTTGATC TAAAATGGACATTTAGATGTAAATCACTGCAGTAAT	1010
	ATGGTACAGCTGTGTGG	1011
	CCACACAGCTGTACCAT	1012
Breast Cancer Glu-1794-Asp GAG to GAT	GTCCATTTTATAGTCAACTGGAATGGATGGTACAGCTGTGTGG TGCTTCTGTGGTGAAGGAGCTTTCATCATTACCCTTGGCAC AGTAAGTATTGGGTGCCCTGTCAGAGAGGGAGGACAC	1013
	GTGTCCTCCCTCTCTGACAGGGCACCCAATACTTACTGTGCC AAGGGTGAATGATGAAAGCTCCTTCACCACAGAAGCACCA CAGCTGTACCATCCATTCCAGTTGATCTAAAATGGAC	1014
	GTGAAGGAGCTTTCATC	1015
	GATGAAAGCTCCTTCAC	1016
Breast Cancer Arg-1835-Stop CGA to TGA	CTCTGCTTGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGT GAGGCACCTGTGGTGACCCGAGAGTGGGTGTTGGACAGTGT AGCACTCTACCAGTGCCAGGAGCTGGACACCTACCTGA	1017

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGTGCTACA CTGTCCAACACCCACTCTC <u>G</u> GGTCACCACAGGTGCCTCACA CATCTGCCCAATTGCTGGAGACAGAGAACAACAAGCAGAG	1018
	TGGTGACCC <u>G</u> AGAGTGG	1019
	CCACTCTC <u>G</u> GGTCACCA	1020
Breast Cancer Trp-1837-Arg TGG to CGG	TTGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGTGAGGCA CCTGTGGTGACCCGAGAGT <u>G</u> GGTGTTGGACAGTGTAGCACT CTACCAGTGCCAGGAGCTGGACACCTACCTGATACCCC	1021
	GGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGT GCTACACTGTCCAACACCC <u>A</u> CTCTCGGGTCACCACAGGTGC CTCACACATCTGCCCAATTGCTGGAGACAGAGAACAACA	1022
	CCCGAGAGT <u>G</u> GGTGTTG	1023
	CAACACCC <u>A</u> CTCTCGGG	1024
Breast Cancer Trp-1837-Stop TGG to TAG	TGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGTGAGGCAC CTGTGGTGACCCGAGAGT <u>G</u> GGTGTTGGACAGTGTAGCACTC TACCAGTGCCAGGAGCTGGACACCTACCTGATACCCCA	1025
	TGGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAG TGCTACACTGTCCAACACCC <u>A</u> CTCTCGGGTCACCACAGGTG CCTCACACATCTGCCCAATTGCTGGAGACAGAGAACAACA	1026
	CCGAGAGT <u>G</u> GGTGTTGG	1027
	CCAACACCC <u>A</u> CTCTCGG	1028

Table 10

BRCA2 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast cancer PHE32LEU TTT to CTT	GTAAACTAAGGTGGGATTTTTTTTTTAAATAGATTTAGGAC CAATAAGTCTTAATTGGT <u>T</u> TTGAAGAACTTTCTTCAGAAGCTCC ACCCTATAATTCTGAACCTGCAGAAGAATCTGAAC	1029
	G TTCAGATTCTTCTGCAGGTT CAGAATTATAGGGTGGAGCTT CTGAAGAAAGTTCTTCAA <u>A</u> CCAATTAAGACTTATTGGTCCTAA ATCTATTTAAAAAAAATCCCACCTTAGTTTTAAC	1030
	TTAATTGGT <u>T</u> TTGAAGAA	1031
	TTCTTCAA <u>A</u> CCAATTAA	1032

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast cancer TYR42CYS TAT to TGT	TAGATTTAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTC TTCAGAAGCTCCACCCTATAATTCTGAACCTGCAGAAGAATC TGAACATAAAAACAACAATTACGAACCAAACCTATT	1033
	AATAGGTTTGGTTCGTAATTGTTGTTTTATGTTTCAGATTCTTC TGCAGGTTTCAGAATTATAGGGTGGAGCTTCTGAAGAAAGTTC TTCAAACCAATTAAGACTTATTGGTCCTAAATCTA	1034
	TCCACCCTATAATTCTG	1035
	CAGAATTATAGGGTGG	1036
Breast cancer LYS53ARG AAA to AGA	AAGAACTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGC AGAAGAATCTGAACATAAAAACAACAATTACGAACCAAACCTA TTTAAACTCCACAAAGGAAACCATCTTATAATCA	1037
	TGATTATAAGATGGTTTCCTTTGTGGAGTTTTAAATAGGTTTG GTTTCGTAATTGTTGTTTTATGTTTCAGATTCTTCTGCAGGTTTC AGAATTATAGGGTGGAGCTTCTGAAGAAAGTTCTT	1038
	TGAACATAAAAACAACA	1039
	TGTTGTTTTATGTTCA	1040
Breast cancer Phe81Leu TTC to CTC	CTATTTAAACTCCACAAAGGAAACCATCTTATAATCAGCTGG CTTCAACTCCAATAATATTCAAAGAGCAAGGGCTGACTCTGC CGCTGTACCAATCTCCTGTAAAAGAATTAGATAAAT	1041
	ATTTATCTAATTCTTTTACAGGAGATTGGTACAGCGGCAGAGT CAGCCCTTGCTCTTTGAATATTATTGGAGTTGAAGCCAGCTG ATTATAAGATGGTTTCCTTTGTGGAGTTTTAAATAG	1042
	CAATAATATTCAAAGAG	1043
	CTCTTTGAATATTATTG	1044
Breast cancer TRP194TERM TGG to TAG	GTCAGACACCAAAACATATTTCTGAAAGTCTAGGAGCTGAGG TGGATCCTGATATGTCTTGGTCAAGTTCTTTAGCTACACCACC CACCTTAGTTCTACTGTGCTCATAGGTAATAATAG	1045
	CTATTATTACCTATGAGCACAGTAGAACTAAGGGTGGGTGGT GTAGCTAAAGAACTTGACCAAGACATATCAGGATCCACCTCA GCTCCTAGACTTTCAGAAATATGTTTTGGTGTCTGAC	1046
	TATGTCTTGGTCAAGTT	1047
	AACTTGACCAAGACATA	1048
Breast cancer PRO201ARG CCA to CGA	CTGAAAGTCTAGGAGCTGAGGTGGATCCTGATATGTCTTGGT CAAGTTCTTTAGCTACACCACCCACCCTTAGTTCTACTGTGCT CATAGGTAATAATAGCAAATGTGTATTTACAAGAAA	1049

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTTCTTGTAATACACATTTGCTATTATTACCTATGAGCACAGT AGAACTAAGGGTGGGTGGTGTAGCTAAAGAACTTGACCAAG ACATATCAGGATCCACCTCAGCTCCTAGACTTTTCAG	1050
	AGCTACACCACCCACCC	1051
	GGGTGGGTGGTGTAGCT	1052
Breast cancer Pro222Ser CCT to TCT	ACAATACACATAAATTTTTATCTTACAGTCAGAAATGAAGAAG CATCTGAACTGTATTTCTCATGATACTACTGCTGTAAGTAA ATATGACATTGATTAGACTGTTGAAATTGCTAACA	1053
	TGTTAGCAATTTCAACAGTCTAATCAATGTCATATTTACTTACA GCAGTAGTATCATGAGGAAATACAGTTTCAGATGCTTCTTCAT TTCTGACTGTAAGATAAAAAATTTATGTGTATTGT	1054
	CTGTATTTCTCATGAT	1055
	ATCATGAGGAAATACAG	1056
Breast cancer Leu-414-Term TTG to TAG	AATGGTCTCAACTAACCCCTTCAGGTCTAAATGGAGCCCAGA TGGAGAAAATACCCCTATGTCATATTTCTTCATGTGACCAAAA TATTCAGAAAAAGACCTATTAGACACAGAGAACAA	1057
	TTGTTCTCTGTGTCTAATAGGTCTTTTTCTGAAATATTTTGGTC ACATGAAGAAATATGCAATAGGGGTATTTTCTCCATCTGGGC TCCATTTAGACCTGAAAGGGTTAGTTGAGACCATT	1058
	ACCCCTATTGTCATATTT	1059
	AAATATGCAATAGGGGT	1060
Breast cancer, male Cys554Trp TGT to TGG	AGCCTCTGAAAGTGGACTGGAAATACATACTGTTTGCTCACA GAAGGAGGACTCCTTATGTCCAAATTTAATTGATAATGGAAG CTGGCCAGCCACCACCACACAGAATTCTGTAGCTTTG	1061
	CAAAGCTACAGAATTCTGTGTGGTGGTGGCTGGCCAGCTTC CATTATCAATTAAATTTGGACATAAGGAGTCCTCCTTCTGTGA GCAAACAGTATGTATTTCCAGTCCACTTTCAGAGGCT	1062
	TCCTTATGTCCAAATTT	1063
	AAATTTGGACATAAGGA	1064
Breast cancer Lys944Term AAA to TAA	AACTCTACCATGGTTTTATATGGAGACACAGGTGATAAACAA GCAACCCAAGTGTCAATTAAAAAGATTTGGTTTATGTTCTTG CAGAGGAGAACAAAAATAGTGTAAGCAGCATATAA	1065
	TTATATGCTGCTTTACACTATTTTTGTTCTCCTCTGCAAGAAC ATAAACCAAATCTTTTTTAATTGACACTTGGGTTGCTTGTAT CACCTGTGTCTCCATATAAAACCATGGTAGAGTT	1066
	TGTCAATTAAAAAGAT	1067

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATCTTTTTT <u>A</u> AATTGACA	1068
Breast cancer, male Glu1320Term GAA to TAA	ATGACTACTGGCACTTTTGTGAAGAAATTACTGAAAATTACA AGAGAAATACTGAAAAT <u>G</u> AAGATAACAAATATACTGCTGCCA GTAGAAATTCTCATAACTTAGAATTTGATGGCAGTG	1069
	CACTGCCATCAAATTCTAAGTTATGAGAATTTCTACTGGCAGC AGTATATTTGTTATCTT <u>C</u> ATTTTCAGTATTTCTCTTGTAATTTTC AGTAATTTCTTCAACAAAAGTGCCAGTAGTCAT	1070
	CTGAAAAT <u>G</u> AAGATAAC	1071
	GTTATCTT <u>C</u> ATTTTCAG	1072
Breast cancer Glu1876Term GAA to TAA	CATGAAACAATTAaaaaaAGTGAAAGACATATTTACAGACAGTT TCAGTAAAGTAATTAAG <u>G</u> AAAAACAACGAGAATAAATCAAAAAT TTGCCAAACGAAAATTATGGCAGGTTGTTACGAGG	1073
	CCTCGTAACAACCTGCCATAATTTTCGTTTGGCAAATTTTGA TTTATTCTCGTTGTTTT <u>C</u> CTTAATTACTTTACTGAAACTGTCTG TAAATATGTCTTTCACTTTTTTAATTGTTTCATG	1074
	TAATTAAG <u>G</u> AAAAACAAC	1075
	GTTGTTTT <u>C</u> CTTAATTA	1076
Breast cancer Ser1882Term TCA to TAA	TGAAAGACATATTTACAGACAGTTTCAGTAAAGTAATTAAGGA AAACAACGAGAATAAAT <u>C</u> AAAAATTTGCCAAACGAAAATTATG GCAGGTTGTTACGAGGCATTGGATGATTCAGAGGA	1077
	TCCTCTGAATCATCCAATGCCTCGTAACAACCTGCCATAATTT TCGTTTGGCAAATTTTT <u>G</u> ATTTATTCTCGTTGTTTTCCCTAATT ACTTTACTGAAACTGTCTGTAAATATGTCTTTCA	1078
	GAATAAAT <u>C</u> AAAAATTT	1079
	AAATTTTT <u>G</u> ATTTATTC	1080
Breast cancer Glu1953Term GAA to TAA	AACCAAAATATGTCTGGATTGGAGAAAGTTTCTAAATATCAC CTTGTGATGTTAGTTTG <u>G</u> AAACTTCAGATATATGTAAATGTAG TATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAA	1081
	TTGCAGATGAGACTGACTTATGAAGCTTCCCTATACTACATTT ACATATATCTGAAGTTT <u>C</u> CAAACCTAACATCACAAGGTGATATT TTAGAACTTTCTCCAATCCAGACATATTTTGTT	1082
	TTAGTTTG <u>G</u> AAACTTCA	1083
	TGAAGTTT <u>C</u> CAAACCTAA	1084
Breast cancer Ser1970Term TCA to TAA	TTAGTTTGGAACCTTCAGATATATGTAAATGTAGTATAGGGAA GCTTCATAAGTCAGTCT <u>C</u> ATCTGCAAACTTGTGGGATTTTT AGCACAGCAAGTGGAAAATCTGTCCAGGTATCAGA	1085

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCTGATACCTGGACAGATTTTCCACTTGCTGTGCTAAAAATCC CACAAGTATTTGCAGATGAGACTGACTTATGAAGCTTCCCTAT ACTACATTTACATATATCTGAAGTTTCCAACTAA	1086
	GTCAGTCTCATCTGCAA	1087
	TTGCAGATGAGACTGAC	1088
Breast cancer Gln1987Term CAG	AAGTCAGTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAG CAAGTGGAAAATCTGTCCAGGTATCAGATGCTTCATTACAAA ACGCAAGACAAGTGTTTTCTGAAATAGAAGATAGTA	1089
	TACTATCTTCTATTTTCAGAAAACACTTGTCTTGCGTTTTGTAA GAAGCATCTGATACCTGACAGATTTTCCACTTGCTGTGCTA AAAATCCCACAAGTATTTGCAGATGAGACTGACTT	1090
	AATCTGTCCAGGTATCA	1091
	TGATACCTGGACAGATT	1092
Breast cancer Ala2466Val GCA to GTA	AAAATAAGATTAATGACAATGAGATTCATCAGTTTAACAAAA CAACTCCAATCAAGCAGCAGCTGTAACTTTCACAAAGTGTGA AGAAGAACCTTTAGGTATTGTATGACAATTTGTGTG	1093
	CACACAAATTGTCATACAATACCTAAAGGTTCTTCTTCACACT TTGTGAAAGTTACAGCTGCTGCTTGATTGGAGTTGTTTTTGT AACTGATGAATCTCATTGTCATTAATCTTATTTT	1094
	TCAAGCAGCAGCTGTAA	1095
	TTACAGCTGCTGCTTGA	1096
Breast cancer Arg2	AGGCAACGCGTCTTTCCACAGCCAGGCAGTCTGTATCTTGCA AAAACATCCACTCTGCCTCGAATCTCTCTGAAAGCAGCAGTA GGAGGCCAAGTCCCCTCTGCGTGTCTCATAAACAGG	1097
	CCTGTTTATGAGGACACGCAGAGGGGACTTGGCCTCCTACT GCTGCTTTCAGAGAGATTCCAGGCAGAGTGGATGTTTTTGCA AGATACAGACTGCCTGGCTGTGGAAAGACGCGTTGCCT	1098
	CTCTGCCTCGAATCTCT	1099
	AGAGATTCCAGGCAGAG	1100
Breast cancer Gln2714Term CAA to TAA	ATTCATTGAGCGCAAATATATCTGAACTTCTAGCAATAAAA CTAGTAGTGCAGATACCCAAAAAGTGGCCATTATTGAACTTA CAGATGGGTGGTATGCTGTTAAGGCCCAGTTAGATC	1101
	GATCTAACTGGGCCTTAACAGCATACCAACCATCTGTAAGTT CAATAATGGCCACTTTTTGGGTATCTGCACTACTAGTTTTATT GCTAGAAGTTTCAGATATATTTGCGCTCAATGAAAT	1102
	CAGATACCCAAAAAGTG	1103

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CACTTTTTGGGTATCTG	1104
Breast cancer Leu2776Term TTA to TGA	CAGAACTGGTGGGCTCTCCTGATGCCTGTACACCTCTTGAAG CCCCAGAATCTCTTATGTTAAAGGTAAATTAATTTGCACTCTT GGTAAAAATCAGTCATTGATTGATTAAATTCTAGA	1105
	TCTAGAATTTAACTGAATCAATGACTGATTTTTACCAAGAGTG CAAATTAATTTACCTTTAACATAAGAGATTCTGGGGCTTCAAG AGGTGTACAGGCATCAGGAGAGCCCACCAGTTCTG	1106
	TCTTATGTTAAAGATTT	1107
	AAATCTTTAACATAAGA	1108
Breast cancer Gln2893Term CAG to TAG	CCTTTTGTTTTCTTAGAAAAACACAACAAACCATATTTACCATC ACGTGCACTAACAAGACAGCAAGTTCGTGCTTTGCAAGATGG TGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAG	1109
	CTGCTGCATTCTTCACTGCTTCATAAAGCTCTGCACCATCTTG CAAAGCACGAACTTGCTGTCTTGTTAGTGCACGTGATGGTAA ATATGGTTTTGTTGTGTTTTCTAAGAAAACAAAAGG	1110
	TAACAAGACAGCAAGTT	1111
	AACTTGCTGTCTTGTTA	1112
Breast cancer Ala2951Thr GCC to ACC	AATCACAGGCAAATGTTGAATGATAAGAAACAAGCTCAGATC CAGTTGGAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAG GAACAAGGTTTATCAAGGGATGTCACAACCGTGTGGA	1113
	TCCACACGGTTGTGACATCCCTTGATAAACCTTGTTCCTTTTG TTCAGCAGATTCCATGGCCTTCCTAATTTCCAAGTGGATCTGA GCTTGTTTCTTATCATTCAACATTTGCCTGTGATT	1114
	TTAGGAAGGCCATGGAA	1115
	TTCCATGGCCTTCCTAA	1116
Breast cancer Met3118Th	ACAATTTACTGGCAATAAAGTTTTGGATAGACCTTAATGAGGA CATTATTAAGCCTCATATGTTAATTGCTGCAAGCAACCTCCAG TGCGGACCAGAATCCAAATCAGGCCTTCTTACTTT	1117
	AAAGTAAGAAGGCCTGATTTGGATTCTGGTCGCCACTGGAG GTTGCTTGCAGCAATTAACATATGAGGCTTAATAATGTCCTCA TTAAGGTCTATCCAAAACCTTTATTGCCAGTAAATTGT	1118
	GCCTCATATGTTAATTG	1119
	CAATTAACATATGAGGC	1120
Breast cancer Thr3401Met ACG to ATG	GACTGAAACGACGTTGTACTACATCTCTGATCAAAGAACAGG AGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAATAAG CAGGACACAATTACAATAAAAAATATATCTAAGCATT	1121

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AATGCTTAGATATATTTTTTAGTTGTAATTGTGTCCTGCTTATT TTTCTCACATTCTTCCGACTGGCCTGGGAAGTCTCCTGTTCT TTGATCAGAGATGTAGTACAACGTCGTTTCAGTC	1122
	GGCCAGTACGGAAGAAT	1123
	ATTCTTCCGACTGGCC	1124
Breast cancer Ile3412Val ATT to GTT	AAAGAACAGGAGAGTTCCCAGGCCAGTACGGAAGAATGTGA GAAAAATAAGCAGGACACAATTACAATAAAAAATATATCTAA GCATTTGCAAAGGCGACAATAAATTATTGACGCTTAA	1125
	TTAAGCGTCAATAATTTATTGTCGCCTTTGCAAATGCTTAGAT ATATTTTTTAGTTGTAATTGTGTCCTGCTTATTTTCTCACATT CTTCCGACTGGCCTGGGAAGTCTCCTGTTCTTT	1126
	AGGACACAATTACAAGT	1127
	AGTTGTAATTGTGTCCT	1128

EXAMPLE 10

Cystic Fibrosis - CFTR

[0219] Cystic fibrosis is a lethal disease affecting approximately one in 2,500 live Caucasian births and is the most common autosomal recessive disease in Caucasians. Patients with this disease have reduced chloride ion permeability in the secretory and absorptive cells of organs with epithelial cell linings, including the airways, pancreas, intestine, sweat glands and male genital tract. This, in turn, reduces the transport of water across the epithelia. The lungs and the GI tract are the predominant organ systems affected in this disease and the pathology is characterized by blocking of the respiratory and GI tracts with viscous mucus. The chloride impermeability in affected tissues is due to mutations in a specific chloride channel, the cystic fibrosis transmembrane conductance regulator protein (CFTR), which prevents normal passage of chloride ions through the cell membrane (Welsh et al., Neuron, 8:821-829 (1992)). Damage to the lungs due to mucus blockage, frequent bacterial infections and inflammation is the primary cause of morbidity and mortality in CF patients and, although maintenance therapy has improved the quality of patients' lives, the median age at death is still only around 30 years. There is no effective treatment for the disease, and therapeutic research is focused on gene therapy using exogenous transgenes in viral vectors and/or activating the defective or other chloride channels in the cell membrane to normalize chloride permeability (Tizzano et al., J. Pediat., 120:337-349 (1992)). However, the death of a teenage patient treated with an adenovirus vector carrying an exogenous CFTR gene in clinical trials in the late 1990's has impacted this area of research.

[0220] The oligonucleotides of the invention for correction of the CFTR gene are attached as a table.

Table 12

CFTR Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Ala46Asp GCT to GAT	AAGGATACAGACAGCGCCTGGAATTGTCAGACATATACCAA TCCCTTCTGTTGATTCTGCTGACAATCTATCTGAAAAATTGGA AAGGTATGTTTCATGTACATTGTTAGTTGAAGAGAG	1129
	CTCTCTTCAACTAAACAATGTACATGAACATACCTTTCCAATT TTTCAGATAGATTGTCAAGCAGAATCAACAGAAGGGATTGGT ATATGTCTGACAATTCCAGGCGCTGTCTGTATCCTT	1130
	TGATTCTGCTGACAATC	1131
	GATTGTCAAGCAGAATCA	1132
Cystic fibrosis Ser50Tyr TCT to TAT	AGCGCCTGGAATTGTCAGACATATACCAAATCCCTTCTGTTG ATTCTGCTGACAATCTATCTGAAAAATTGGAAAGGTATGTTCA TGTACATTGTTTAGTTGAAGAGAGAAATTCATATTA	1133
	TAATATGAATTTCTCTCTTCAACTAAACAATGTACATGAACATA CCTTTCCAATTTTTCAAGATAGATTGTCAGCAGAATCAACAGAA GGGATTTGGTATATGTCTGACAATTCCAGGCGCT	1134
	CAATCTATCTGAAAAAT	1135
	ATTTTTCAGATAGATTG	1136
Congenital absence of vas deferens Glu56Lys GAA-AAA	AGGACAACATAAAATATTTGCACATGCAACTTATTGGTCCCACT TTTTATTCTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAA GAAAAATCCTAAACTCATTAATGCCCTTCGGCGAT	1137
	ATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTTCTTTGAAG CCAGCTCTCTATCCCATTTCTCTGCAAAAGAATAAAAAGTGGG ACCAATAAGTTGCATGTGCAAATATTTTAGTTGTCCT	1138
	TTTGCAGAGAATGGGAT	1139
	ATCCCATTTCTCTGCAAA	1140
Cystic fibrosis Trp57Gly TGG to GGG	AGGACAACATAAAATATTTGCACATGCAACTTATTGGTCCCACT TTTTATTCTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAA GAAAAATCCTAAACTCATTAATGCCCTTCGGCGAT	1141
	ATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTTCTTTGAAG CCAGCTCTCTATCCCATTTCTCTGCAAAAGAATAAAAAGTGGG ACCAATAAGTTGCATGTGCAAATATTTTAGTTGTCCT	1142
	TTTGCAGAGAATGGGAT	1143

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATCCCATT <u>C</u> TCTGCAAA	1144
Cystic fibrosis Trp57Term TGG to TGA	AACTAAAATATTTGCACATGCAACTTATTGGTCCCACCTTTTTAT TCTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAA ATCCTAAACTCATTAAATGCCCTTCGGCGATGTTTT	1145
	AAAACATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTTCTTT GAAGCCAGCTCTCTATCCATTCTCTGCAAAAAGAATAAAAAAG TGGGACCAATAAGTTGCATGTGCAAATATTTTAGTT	1146
	AGAGAATGGGATAGAGA	1147
	TCTCTATCCATTCTCT	1148
Congenital absence of vas deferens Asp58Asn GAT to AAT	ACTAAAATATTTGCACATGCAACTTATTGGTCCCACCTTTTTATT CTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAA TCCTAAACTCATTAAATGCCCTTCGGCGATGTTTT	1149
	AAAAACATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTTCTT TGAAGCCAGCTCTCTATCCATTCTCTGCAAAAAGAATAAAAA GTGGGACCAATAAGTTGCATGTGCAAATATTTTAGT	1150
	GAGAATGGGATAGAGAG	1151
	CTCTCTATCCATTCTC	1152
Cystic fibrosis Glu60Term GAG to TAG	ATATTTGCACATGCAACTTATTGGTCCCACCTTTTTATTCTTTTG CAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAA ACTCATTAAATGCCCTTCGGCGATGTTTTTTCTGGA	1153
	TCCAGAAAAACATCGCCGAAGGGCATTAAATGAGTTTAGGAT TTTTCTTTGAAGCCAGCTCTCTATCCATTCTCTGCAAAAGAA TAAAAGTGGGACCAATAAGTTGCATGTGCAAATAT	1154
	GGGATAGAGAGCTGGCT	1155
	AGCCAGCTCTCTATCCC	1156
Cystic fibrosis	GGTCCCACCTTTTTATTCTTTTGCAGAGAATGGGATAGAGAGC TGGCTTCAAAGAAAAATCCTAAACTCATTAAATGCCCTTCGGC GATGTTTTTTCTGGAGATTTATGTTCTATGGAATCTT	1157
	AAGATTCCATAGAACATAAATCTCCAGAAAAACATCGCCGA AGGGCATTAAATGAGTTTAGGATTTTTCTTTGAAGCCAGCTCTC TATCCATTCTCTGCAAAAGAATAAAAAGTGGGACC	1158
	GAAAAATCCTAAACTCA	1159
	TGAGTTTAGGATTTTTTC	1160
Cystic fibrosis Arg74Trp CGG to TGG	TGCAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCT AAACTCATTAAATGCCCTTCGGCGATGTTTTTTCTGGAGATTTA TGTTCTATGGAATCTTTTTATATTTAGGGGTAAGGA	1161

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAAATCT CCAGAAAAAACATCGCCGAGGGGCATTAATGAGTTTAGGATT TTTCTTTGAAGCCAGCTCTCTATCCCATTCTCTGCA	1162
	ATGCCCTTCGGCGATGT	1163
	ACATCGCCGAGGGGCAT	1164
Congenital absence of vas deferens ARG75GLN CGA	GAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAAC TCATTAATGCCCTTCGGCGATGTTTTCTGGAGATTTATGTT CTATGGAATCTTTTATATTTAGGGGTAAGGATCTC	1165
	GAGATCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAA ATCTCCAGAAAAAACATCGCCGAGGGGCATTAATGAGTTTAG GATTTTTCTTTGAAGCCAGCTCTCTATCCCATTCTC	1166
	CCTTCGGCGATGTTTT	1167
	AAAAACATCGCCGAAGG	1168
Cystic fibrosis Arg75Leu CGA to CTA	GAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAAC TCATTAATGCCCTTCGGCGATGTTTTCTGGAGATTTATGTT CTATGGAATCTTTTATATTTAGGGGTAAGGATCTC	1169
	GAGATCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAA ATCTCCAGAAAAAACATCGCCGAGGGGCATTAATGAGTTTAG GATTTTTCTTTGAAGCCAGCTCTCTATCCCATTCTC	1170
	CCTTCGGCGATGTTTT	1171
	AAAAACATCGCCGAAGG	1172
Cystic fibrosis Arg75Term CGA to TGA	AGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAA CTCATTAATGCCCTTCGGCGATGTTTTCTGGAGATTTATGT TCTATGGAATCTTTTATATTTAGGGGTAAGGATCT	1173
	AGATCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAAA TCTCCAGAAAAAACATCGCCGAGGGGCATTAATGAGTTTAGG ATTTTTCTTTGAAGCCAGCTCTCTATCCCATTCTCT	1174
	CCCTTCGGCGATGTTTT	1175
	AAACATCGCCGAAGG	1176
Cystic fibrosis Gly85Glu GGA to GAA	AAAATCCTAAACTCATTAATGCCCTTCGGCGATGTTTTCTG GAGATTTATGTTCTATGGAATCTTTTATATTTAGGGGTAAGG ATCTCATTTGTACATTCATTATGTATCACATAACT	1177
	AGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCC CTAAATATAAAAAAGATTCCATAGAACATAAATCTCCAGAAAA ACATCGCCGAGGGGCATTAATGAGTTTAGGATTTT	1178
	GTTCTATGGAATCTTT	1179

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AAAAGATTCCATAGAAC	1180
Cystic fibrosis G	AAAATCCTAAACTCATTAAATGCCCTTCGGCGATGTTTTCTG GAGATTTATGTTCTATGGAATCTTTTATATTTAGGGGTAAGG ATCTCATTTGTACATTCATTATGTATCACATAACT	1181
	AGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCC CTAAATATAAAAAGATTCCATAGAACATAAATCTCCAGAAAA ACATCGCCGAAGGGCATTAAATGAGTTTAGGATTTT	1182
	GTTCTATGGAATCTTTT	1183
	AAAAGATTCCATAGAAC	1184
Cystic fibrosis Leu88S	AACTCATTAAATGCCCTTCGGCGATGTTTTCTGGAGATTTAT GTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTCATTT GTACATTCATTATGTATCACATAACTATATGCATT	1185
	AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGA TCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCT CCAGAAAAACATCGCCGAAGGGCATTAAATGAGTT	1186
	AATCTTTTATATTTAG	1187
	CTAAATATAAAAAGATT	1188
Cystic fibrosis Phe87Leu TTT to CTT	CCTAAACTCATTAAATGCCCTTCGGCGATGTTTTCTGGAGAT TTATGTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTC ATTTGTACATTCATTATGTATCACATAACTATATG	1189
	CATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCT TACCCCTAAATATAAAAAGATTCCATAGAACATAAATCTCCAG AAAAACATCGCCGAAGGGCATTAAATGAGTTTAGG	1190
	ATGGAATCTTTTATAT	1191
	ATATAAAAAGATTCCAT	1192
Cystic fibrosis Leu88Term TTA to TGA	AACTCATTAAATGCCCTTCGGCGATGTTTTCTGGAGATTTAT GTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTCATTT GTACATTCATTATGTATCACATAACTATATGCATT	1193
	AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGA TCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCT CCAGAAAAACATCGCCGAAGGGCATTAAATGAGTT	1194
	AATCTTTTATATTTAG	1195
	CTAAATATAAAAAGATT	1196
Cystic fibrosis Leu88Term TTA to TAA	AACTCATTAAATGCCCTTCGGCGATGTTTTCTGGAGATTTAT GTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTCATTT GTACATTCATTATGTATCACATAACTATATGCATT	1197

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCTCCAGAAAAACATCGCCGAAGGGCATTAAATGAGTT	1198
	AATCTTTTTATATTTAG	1199
	CTAAATATAAAAAGATT	1200
Cystic fibrosis Gly91Ar	AATGCCCTTCGGCGATGTTTTCTGGAGATTTATGTTCTATGGAATCTTTTTATATTTAGGGGTAAGGATCTCATTTGTACATTCATTATGTATCACATAACTATATGCATTTTTGTGAT	1201
	ATCACAAAAATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAAATCTCCAGAAAAACATCGCCGAAGGGCATT	1202
	TATATTTAGGGGTAAGG	1203
	CCTTACCCCTAAATATA	1204
Cystic fibrosis Gln98A	AATAAATGAAATTTAATTTCTCTGTTTTCCCTTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATA GCTTCCTATGACCCGGATAACAAGGAGGAACGCTC	1205
	GAGCGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAAAGGGGAAAAACAGAGAAATTAATTTTCATTTATT	1206
	AGCAGTACAGCCTCTCT	1207
	AGAGAGGCTGTACTGCT	1208
Cystic fibrosis Gln98Term CAG-TAG	AAATAAATGAAATTTAATTTCTCTGTTTTCCCTTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGCT	1209
	AGCGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAAAGGGGAAAAACAGAGAAATTAATTTTCATTTATT	1210
	AAGCAGTACAGCCTCTC	1211
	GAGAGGCTGTACTGCTT	1212
Cystic fibrosis Ser108Ph	CCCTTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCATAGGCTTATG	1213
	CATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCCTCCTTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAAAGGG	1214
	CATAGCTTCCTATGACC	1215

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGTCATAGGAAGCTATG	1216
Cystic fibrosis Tyr109Cys TAT to TGT	TTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGG GAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAAC GCTCTATCGCGATTTATCTAGGCATAGGCTTATGCCT	1217
	AGGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCC TCCTTGTTATCCGGGTCAAGGAAGCTATGATTCTTCCCAGT AAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAA	1218
	AGCTTCCTATGACCCGG	1219
	CCGGGTCATAGGAAGCT	1220
Cystic fibrosis Asp110Hi	TTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGA AGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGC TCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTC	1221
	GAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTT CCTCCTTGTTATCCGGGTCAAGGAAGCTATGATTCTTCCCA GTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAA	1222
	CTTCCTATGACCCGGAT	1223
	ATCCGGGTCAAGGAAG	1224
Congenital absence of vas deferens Pro111Leu CCG to CTG	AGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAA TCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGCTCTA TCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTT	1225
	AAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAG CGTTCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTT CCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCT	1226
	CTATGACCCGGATAACA	1227
	TGTTATCCGGGTCATAG	1228
Cystic fibrosis A	GTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGAC CCGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGC ATAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGC	1229
	GCAGTGTCTCACATAAAGAGAAGGCATAAGCCTATGCCTA GATAAATCGCGATAGAGCGTTCTCCTTGTTATCCGGGTCAT AGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTAC	1230
	AGGAGGAACGCTCTATC	1231
	GATAGAGCGTTCTCCT	1232
Cystic fibrosis Arg117H	TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC CGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCA TAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT	1233

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGCAGTGTCTCACAATAAAGAGAAGGCATAAGCCTATGCCT AGATAAATCGCGATAGAGCGTTCCTCCTTGTATCCGGGTCA TAGGAAGCTATGATTCTTCCAGTAAGAGAGGCTGTA	1234
	GGAGGAACGCTCTATCG	1235
	CGATAGAGCGTTCCTCC	1236
Cystic fibrosis Arg117L	TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC CGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCA TAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT	1237
	AGCAGTGTCTCACAATAAAGAGAAGGCATAAGCCTATGCCT AGATAAATCGCGATAGAGCGTTCCTCCTTGTATCCGGGTCA TAGGAAGCTATGATTCTTCCAGTAAGAGAGGCTGTA	1238
	GGAGGAACGCTCTATCG	1239
	CGATAGAGCGTTCCTCC	1240
Cystic fibrosis Arg117P	TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC CGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCA TAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT	1241
	AGCAGTGTCTCACAATAAAGAGAAGGCATAAGCCTATGCCT AGATAAATCGCGATAGAGCGTTCCTCCTTGTATCCGGGTCA TAGGAAGCTATGATTCTTCCAGTAAGAGAGGCTGTA	1242
	GGAGGAACGCTCTATCG	1243
	CGATAGAGCGTTCCTCC	1244
Cystic fibrosis	CTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAAC AAGGAGGAACGCTCTATCGCGATTTATCTAGGCATAGGCTTA TGCCTTCTCTTTATTGTGAGGACACTGCTCCTACACC	1245
	GGTGTAGGAGCAGTGTCTCACAATAAAGAGAAGGCATAAG CCTATGCCTAGATAAATCGCGATAGAGCGTTCCTCCTTGTTA TCCGGGTCATAGGAAGCTATGATTCTTCCAGTAAGAG	1246
	GCTCTATCGCGATTTAT	1247
	ATAAATCGCGATAGAGC	1248
Cystic fibrosis Tyr122Te	GGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGG AACGCTCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTCT CTTTATTGTGAGGACACTGCTCCTACACCCAGCCATT	1249
	AATGGCTGGGTGTAGGAGCAGTGTCTCACAATAAAGAGAA GGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCCT CCTTGTATCCGGGTCATAGGAAGCTATGATTCTTCCC	1250
	GCGATTTATCTAGGCAT	1251

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGCCTAGATAAATCGC	1252
Cystic fibrosis	TAGCTTCCTATGACCCGGATAACAAGGAGGAACGCTCTATCG CGATTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGTGAG GACACTGCTCCTACACCCAGCCATTTTTGGCCTTCA	1253
	TGAAGGCCAAAAATGGCTGGGTGTAGGAGCAGTGTCTCAC AATAAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGAT AGAGCGTTCCTCCTTGTATCCGGGTCATAGGAAGCTA	1254
	AGGCATAGGCTTATGCC	1255
	GGCATAAGCCTATGCCT	1256
Cystic fibrosis H	TCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGT GAGGACACTGCTCCTACACCCAGCCATTTTTGGCCTTCATCA CATTGGAATGCAGATGAGAATAGCTATGTTTAGTTT	1257
	AACTAAACATAGCTATTCTCATCTGCATTCCAATGTGATGAA GGCCAAAAATGGCTGGGTGTAGGAGCAGTGTCTCACAATA AAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGA	1258
	GCTCCTACACCCAGCCA	1259
	TGGCTGGGTGTAGGAGC	1260
Cystic fibrosis Ala141A	TTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGTGAGGAC ACTGCTCCTACACCCAGCCATTTTTGGCCTTCATCACATTGG AATGCAGATGAGAATAGCTATGTTTAGTTTGATTTA	1261
	TAAATCAAACATAACATAGCTATTCTCATCTGCATTCCAATGT GATGAAGGCCAAAAATGGCTGGGTGTAGGAGCAGTGTCTC ACAATAAGAGAAGGCATAAGCCTATGCCTAGATAAA	1262
	ACACCCAGCCATTTTTG	1263
	CAAAAATGGCTGGGTGT	1264
Cystic fibrosis Ile148T	GCCTTCTCTTTATTGTGAGGACACTGCTCCTACACCCAGCCA TTTTTGGCCTTCATCACATTGGAATGCAGATGAGAATAGCTAT GTTTAGTTTGATTTATAAGAAGGTAATACTTCCTTG	1265
	CAAGGAAGTATTACCTTCTTATAAATCAAACATAACATAGCTA TTCTCATCTGCATTCCAATGTGATGAAGGCCAAAAATGGCTG GGTGTAGGAGCAGTGTCTCACAATAAAGAGAAGGC	1266
	TCATCACATTGGAATGC	1267
	GCATTCCAATGTGATGA	1268
Cystic fibrosis Gly149Ar	CTTCTCTTTATTGTGAGGACACTGCTCCTACACCCAGCCATTT TTGGCCTTCATCACATTGGAATGCAGATGAGAATAGCTATGT TTAGTTTGATTTATAAGAAGGTAATACTTCCTTGCA	1269

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGCAAGGAAGTATTACCTTCTTATAAATCAAACATAACATAGC TATTCTCATCTGCATTCC <u>CA</u> ATGTGATGAAGGCCAAAAATGGCT GGGTGTAGGAGCAGTGTCTCACAATAAAGAGAAG	1270
	ATCACATT <u>G</u> GAATGCAG	1271
	CTGCATTCC <u>CA</u> ATGTGAT	1272
Cystic fibrosis GI	TTTATTGTGAGGACACTGCTCCTACACCCAGCCATTTTTGGC CTTCATCACATTGGAATGCAGATGAGAATAGCTATGTTTAGTT TGATTATAAGAAGGTAATACTTCCTTGACAGGCC	1273
	GGCCTGTGCAAGGAAGTATTACCTTCTTATAAATCAAACATAA CATAGCTATTCTCATCTGCATTCCAATGTGATGAAGGCCAAAA ATGGCTGGGTGTAGGAGCAGTGTCTCACAATAA	1274
	TTGGAATGCAGATGAGA	1275
	TCTCATCTGCATTCCAA	1276
Cystic fibrosis	AATATATTTGTATTTTGTGTTGAAATTATCTAACTTTCCATTT TTCTTTTAGACTTTAAAGCTGTCAAGCCGTGTTCTAGATAAAA TAAGTATTGGACAACCTGTTAGTCTCCTTTCCA	1277
	TGGAAAGGAGACTAACAAGTTGTCCAATACTTATTTTATCTAG AACACGGCTTGACAGCTTTAAAGTCTAAAAGAAAAATGGAAA GTTAGATAATTTCAACAAACAAAATACAAATATATT	1278
	AGACTTTAAAGCTGTCA	1279
	TGACAGCTTTAAAGTCT	1280
Cystic fibrosis Ile175Val ATA-GTA	TTATCTAACTTTCCATTTTTCTTTTAGACTTTAAAGCTGTCAAG CCGTGTTCTAGATAAAAATAAGTATTGGACAACCTTGTTAGTCTC CTTTCCAACAACCTGAACAAATTTGATGAAGTAT	1281
	ATACTTCATCAAATTTGTTCAAGTTGTTGGAAAGGAGACTAAC AAGTTGTCCAATACTTATTTTATCTAGAACACGGCTTGACAGC TTTAAAGTCTAAAAGAAAAATGGAAAGTTAGATAA	1282
	TAGATAAAAATAAGTATT	1283
	AATACTTATTTTATCTA	1284
Cystic fibrosis G	TTTCCATTTTTCTTTTAGACTTTAAAGCTGTCAAGCCGTGTTCT AGATAAAATAAGTATTGGACAACCTTGTTAGTCTCCTTTCCAAC AACCTGAACAAATTTGATGAAGTATGTACCTATT	1285
	AATAGGTACATACTTCATCAAATTTGTTCAAGTTGTTGGAAAG GAGACTAACAAGTTGTCCAATACTTATTTTATCTAGAACACGG CTTGACAGCTTTAAAGTCTAAAAGAAAAATGGAAA	1286
	TAAGTATTGGACAACCT	1287

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AAGTTGTCCAATACTTA	1288
Cystic fibrosis His199G	AAGATACAATGACACCTGTTTTGCTGTGCTTTTATTTTCCAG GGACTTGCAATTGGCACATTTTCGTGTGGATCGCTCCTTTGCAA GTGGCACTCCTCATGGGGCTAATCTGGGAGTTGTTA	1289
	TAACAACTCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAA AGGAGCGATCCACACGAAATGTGCCAATGCAAGTCCCTGGA AAATAAAAGCACAGCAAAAACAGGTGTCATTGTATCTT	1290
	TTGGCACATTTTCGTGTG	1291
	CACACGAAATGTGCCAA	1292
Cystic fibrosis His199T	GGAAGATACAATGACACCTGTTTTGCTGTGCTTTTATTTTCC AGGGACTTGCAATTGGCACATTTTCGTGTGGATCGCTCCTTTGC AAGTGGCACTCCTCATGGGGCTAATCTGGGAGTTGT	1293
	ACAACTCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAAAG GAGCGATCCACACGAAATGTGCCAATGCAAGTCCCTGGAAA ATAAAAGCACAGCAAAAACAGGTGTCATTGTATCTTCC	1294
	CATTGGCACATTTTCGTG	1295
	CACGAAATGTGCCAATG	1296
Cystic fibrosis P	TGTTTTGCTGTGCTTTTATTTTCCAGGGACTTGCAATTGGCAC ATTTTCGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGG GGCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCT	1297
	AGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCCCATG AGGAGTGCCACTTGCAAAGGAGCGATCCACACGAAATGTGC CAATGCAAGTCCCTGGAAAATAAAAGCACAGCAAAAACA	1298
	GGATCGCTCCTTTGCAA	1299
	TTGCAAAGGAGCGATCC	1300
Cystic fibrosis L	TTTGCTGTGCTTTTATTTTCCAGGGACTTGCAATTGGCACATTT CGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGGGGC TAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTGG	1301
	CCACAGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCC CATGAGGAGTGCCACTTGCAAAAGGAGCGATCCACACGAAAT GTGCCAATGCAAGTCCCTGGAAAATAAAAGCACAGCAAA	1302
	CGCTCCTTTGCAAGTGG	1303
	CCACTTGCAAAAGGAGCG	1304
Cystic fibrosis Gln220Te	TTCGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGGGG CTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTGGACTT GGTTTCCTGATAGTCCTTGCCCTTTTTCAGGCTGGGC	1305

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCCCAGCCTGAAAAAGGGCAAGGACTATCAGGAAACCAAGT CCACAGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCC CATGAGGAGTGCCACTTGCAAAGGAGCGATCCACACGAA	1306
	AGTTGTTACAGGCGTCT	1307
	AGACGCCTGTAACAACT	1308
Cystic f	CCTTTGCAAGTGGCACTCCTCATGGGGCTAATCTGGGAGTTG TTACAGGCGTCTGCCTTCTGTGGACTTGGTTTCCTGATAGTC CTTGCCCTTTTTTCAGGCTGGGCTAGGGAGAATGATGA	1309
	TCATCATTCTCCCTAGCCCAGCCTGAAAAAGGGCAAGGACTA TCAGGAAACCAAGTCCACAAGAAGGCAGACGCCTGTAACAAC TCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAAAGG	1310
	CTGCCTTCTGTGGACTT	1311
	AAGTCCACAAGAAGGCAG	1312
Cystic fibrosis V	TGGGGCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTG GACTTGGTTTCCTGATAGTCCTTGCCCTTTTTTCAGGCTGGGC TAGGGAGAATGATGATGAAGTACAGGTAGCAACCTAT	1313
	ATAGGTTGCTACCTGTACTTCATCATCATTCTCCCTAGCCCAG CCTGAAAAAGGGCAAGGACTATCAGGAAACCAAGTCCACAG AAGGCAGACGCCTGTAACAACTCCCAGATTAGCCCCA	1314
	CCTGATAGTCCTTGCCC	1315
	GGGCAAGGACTATCAGG	1316
Cystic fibrosis Gly239A	GTTACAGGCGTCTGCCTTCTGTGGACTTGGTTTCCTGATAGT CCTTGCCCTTTTTTCAGGCTGGGCTAGGGAGAATGATGATGAA GTACAGGTAGCAACCTATTTTCATAACTTGAAAGTTT	1317
	AACTTTCAAGTTATGAAAATAGGTTGCTACCTGTACTTCATC ATCATTCTCCCTAGCCCAGCCTGAAAAAGGGCAAGGACTATC AGGAAACCAAGTCCACAGAAGGCAGACGCCTGTAAC	1318
	TTTCAGGCTGGGCTAGG	1319
	CCTAGCCCAGCCTGAAA	1320

EXAMPLE 11

Cyclin-dependent kinase inhibitor 2A - CDKN2A

[0221] The human CDKN2A gene was also designated MTS-1 for multiple tumor suppressor-1 and has been implicated in multiple cancers including, for example, malignant melanoma.

- 5 Malignant melanoma is a cutaneous neoplasm of melanocytes. Melanomas generally have features of asymmetry, irregular border, variegated color, and diameter greater than 6 mm. The precise cause of

melanoma is unknown, but sunlight and heredity are risk factors. Melanoma has been increasing during the past few decades.

[0222] The CDKN2A gene has been found to be homozygously deleted at high frequency in cell lines derived from tumors of lung, breast, brain, bone, skin, bladder, kidney, ovary, and lymphocyte. Melanoma cell lines carried at least one copy of CDKN2A in combination with a deleted allele. Melanoma cell lines that carried at least 1 copy of CDKN2A frequently showed nonsense, missense, or frameshift mutations in the gene. Thus, CDKN2A may rival p53 (see Example 6) in the universality of its involvement in tumorigenesis. The attached table discloses the correcting oligonucleotide base sequences for the CDKN2A oligonucleotides of the invention.

Table 13

CDKN2A Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Melanoma Trp15Term TGG-TAG	GGGCGGCGGGGAGCAGCATGGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGCCGGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGG	1321
	CCCGCCTCCAGCAGCGCCCGCACCTCCTCTACCCGACCCCGGGCCGCGGCCGTGGCCAGCCAGTCAGCCGAAGGCTCCATGTGCTCCCCGCCGCCGGCTCCATGCTGCTCCCCGCCGCC	1322
	GGCTGACTGGCTGGCCA	1323
	TGGCCAGCCAGTCAGCC	1324
Melanoma Leu16Pro CTG-CCG	CGGCGGGGAGCAGCATGGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGC	1325
	GCCCCGCCTCCAGCAGCGCCCGCACCTCCTCTACCCGACC CGGGGCCGCGGCCGTGGCCAGCCAGTCAGCCGAAGGCTCCA TGCTGCTCCCCGCCGCCGGCTCCATGCTGCTCCCCGCCG	1326
	TGACTGGCTGGCCACGG	1327
	CCGTGGCCAGCCAGTCA	1328
Melanoma Gly23Asp GGT-GAT	CGGCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTG GCCACGGCCGCGGCCCGGGGTCGGGTAGAGGAGGTGCGGG CGCTGCTGGAGGCGGGGGCGCTGCCAACGCACCGAATAG	1329
	CTATTCGGTGCGTTGGGCAGCGCCCCCGCCTCCAGCAGCGC CCGCACCTCCTCTACCCGACCCCGGGCCGCGGCCGTGGCCA GCCAGTCAGCCGAAGGCTCCATGCTGCTCCCCGCCGCCG	1330
	GGCCCGGGGTCGGGTAG	1331

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTACCCGAC <u>C</u> CCCCGGGCC	1332
Melanoma Arg24Pro CGG-CCG	CGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCC ACGGCCGCGGCCCGGGGTC <u>G</u> GGTAGAGGAGGTGCGGGCGC TGCTGGAGGCGGGGGCGCTGCCCAACGCACCGAATAGTTA	1333
	TAACCTATTCGGTGCGTTGGGACGCGCCCCGCCTCCAGCAGC GCCCCGACCTCCTCTACCC <u>G</u> ACCCCCGGGCCGCGGCCGTGGC CAGCCAGTCAGCCGAAGGCTCCATGCTGCTCCCCGCCG	1334
	CCGGGGTC <u>G</u> GGTAGAGG	1335
	CCTCTACCC <u>G</u> ACCCCCG	1336
Melanoma Leu32Pro CTG-CCG	CGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGGTGCGGT AGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGCGCTGCCC AACGCACCGAATAGTTACGGTCGGAGGCCGATCCAGGTGGG	1337
	CCCACCTGGATCGGCCTCCGACCGTAACTATTCGGTGCGTTG GGCAGCGCCCCCGCCTCC <u>A</u> GCAGCGCCCGCACCTCCTCTAC CCGACCCCCGGGCCGCGGCCGTGGCCAGCCAGTCAGCCG	1338
	GGCGCTGCT <u>T</u> GGAGGCGG	1339
	CCGCCTCC <u>A</u> GCAGCGCC	1340
Melanoma Gly35Ala GGG-GCG	GGCTGGCCACGGCCGCGGCCCGGGGTGCGGTAGAGGAGGT GCGGGCGCTGCTGGAGGCGGG <u>G</u> GGCGCTGCCCAACGCACCG AATAGTTACGGTCGGAGGCCGATCCAGGTGGGTAGAGGGTC	1341
	GACCCTCTACCCACCTGGATCGGCCTCCGACCGTAACTATTC GGTGCGTTGGGACGCGCC <u>C</u> CGCCTCCAGCAGCGCCCGCAC CTCCTCTACCCGACCCCGGGCCGCGGCCGTGGCCAGCC	1342
	GGAGGCGGG <u>G</u> GGCGCTGC	1343
	GCAGCGCC <u>C</u> CCGCCTCC	1344
Melanoma Tyr44Term TACg-TAA	GGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGCGCTG CCCAACGCACCGAATAGTTA <u>C</u> GGTCGGAGGCCGATCCAGGTG GGTAGAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGA	1345
	TCGCCCCGCCATCCCCTGCTCCCGCTGCAGACCCTCTACCCAC CTGGATCGGCCTCCGACC <u>G</u> TAACTATTCGGTGCGTTGGGCAG CGCCCCCGCCTCCAGCAGCGCCCGCACCTCCTCTACC	1346
	AATAGTTA <u>C</u> GGTCGGAG	1347
	CTCCGACC <u>G</u> TAACTATT	1348

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Melanoma Met53Ile ATGa-ATC	TCTCCCATACCTGCCCCACCCTGGCTCTGACCACTCTGCTCT CTCTGGCAGGTCATGATGATGGGCAGCGCCCGCTGGCGGA GCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCA	1349
	TGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCTCCG CCACGCGGGCGCTGCCCATCATCATGACCTGCCAGAGAGAG CAGAGTGGTCAGAGCCAGGGTGGGGGCAGGTATGGGAGA	1350
	GTCATGATGATGGGCAG	1351
	CTGCCCATCATCATGAC	1352
Melanoma Met54Ile ATGg-ATT	CCCATACCTGCCCCACCCTGGCTCTGACCACTCTGCTCTCTC TGGCAGGTCATGATGATGGGCAGCGCCCGCTGGCGGAGCT GCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCAGAC	1353
	GTCTGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCT CCGCCACGCGGGCGCTGCCCATCATCATGACCTGCCAGAGA GAGCAGAGTGGTCAGAGCCAGGGTGGGGGCAGGTATGGG	1354
	ATGATGATGGGCAGCGC	1355
	GCGCTGCCCATCATCAT	1356
Melanoma Ser56Ile AGC-ATC	GCCGGCCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGC AGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTG CTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGC	1357
	GCGGGGTGCGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCA GCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGACCTGCC AGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGGCCGGC	1358
	GATGGGCAGCGCCCGAG	1359
	CTCGGGCGCTGCCCATC	1360
Melanoma Ala57Val GCC-GTC	GGCCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGG TCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTG CTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCAC	1361
	GTGGCGGGGTGCGCGCAGTTGGGCTCCGCGCCGTGGAGCA GCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGACCT GCCAGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGGCC	1362
	GGGCAGCGCCCGAGTGG	1363
	CCACTCGGCGCTGCCC	1364

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Melanoma Arg58Term cCGA-TGA	CCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGGTCA TGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTC CACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTC	1365
	GAGTGGCGGGGTCTGGCGCAGTTGGGCTCCGCGCCGTGGAG CAGCAGCAGCTCCGCCACTCGGGCGCTGCCATCATCATGAC CTGCCAGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGG	1366
	GCAGCGCCCGAGTGGCG	1367
	CGCCACTCGGGCGCTGC	1368
Melanoma Val59Gly GTG-GGG	CACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGGTCATGAT GATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACG GCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCAC	1369
	GTGAGAGTGGCGGGGTCTGGCGCAGTTGGGCTCCGCGCCGTG GAGCAGCAGCAGCTCCGCCACTCGGGCGCTGCCATCATCAT GACCTGCCAGAGAGAACAGAATGGTCAGAGCCAGGGTG	1370
	CGCCCGAGTGGCGGAGC	1371
	GCTCCGCCACTCGGGCG	1372
Melanoma Leu62Pro CTG-CCG	TCTGACCACTCTGCTCTCTCTGGCAGGTCATGATGATGGGCA GCGCCCGCGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGAG CCCAACTGCGCAGACCCTGCCACTCTACCCGACCGGT	1373
	ACCGGTCGGGTGAGAGTGGCAGGGTCTGCGCAGTTGGGCTC CGCGCCGTGGAGCAGCAGCAGCTCCGCCACGCGGGCGCTGC CCATCATCATGACCTGCCAGAGAGAGCAGAGTGGTCAGA	1374
	GGCGGAGCTGCTGCTGC	1375
	GCAGCAGCAGCTCCGCC	1376
Melanoma Ala68Val GCG-GTG	TCTGGCAGGTCATGATGATGGGCAGCGCCCGCGTGGCGGAG CTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCAGACCC TGCCACTCTACCCGACCGGTGCATGATGCTGCCCGGGA	1377
	TCCCGGGCAGCATCATGCACCGGTCGGGTGAGAGTGGCAGG GTCTGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCT CCGCCACGCGGGCGCTGCCATCATCATGACCTGCCAGA	1378
	CCACGGCGCGGAGCCCA	1379
	TGGGCTCCGCGCCGTGG	1380

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Melanoma Asn71Lys AACT-AAA	CATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGC TCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTC ACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCTG	1381
	CAGGAAGCCCTCCCGGGCAGCGTCGTGCACGGGTCTGGGTGA GAGTGGCGGGGTCTGGCGCA G TTGGGCTCCGCGCCGTGGAG CAGCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATG	1382
	GAGCCCAACTGCGCCGA	1383
	TCGGCGCA G TTGGGCTC	1384
Melanoma Asn71Ser AAC-AGC	TCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTG CTCCACGGCGCGGAGCCCA A CTGCGCCGACCCCGCCACTCT CACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCT	1385
	AGGAAGCCCTCCCGGGCAGCGTCGTGCACGGGTCTGGGTGAG AGTGGCGGGGTCTGGCGCAG T TTGGGCTCCGCGCCGTGGAGCA GCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGA	1386
	GGAGCCCA A CTGCGCCG	1387
	CGGCGCAG T TTGGGCTCC	1388
Melanoma Pro81Leu CCC-CTC	AGCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGAC CCCGCCACTCTACCCGAC C CGTGCACGACGCTGCCCGGGA GGGCTTCCTGGACACGCTGGTGGTGTCTGCACCGGGCCGG	1389
	CCGGCCCGGTGCAGCACCACCAGCGTGTCCAGGAAGCCCTC CCGGGCAGCGTCGTGCACG G GTCTGGGTGAGAGTGGCGGGG TCGGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCT	1390
	CACCCGAC C CGTGCACG	1391
	CGTGCACG G GTCTGGGTG	1392
Melanoma Asp84Tyr cGAC-TAC	CTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCAC TCTACCCGACCCGTGCAC G ACGCTGCCCGGGAGGGCTTCCT GGACACGCTGGTGGTGTCTGCACCGGGCCGGGGCGCGGC	1393
	GCCGCGCCCCGGCCCGGTGCAGCACCACCAGCGTGTCCAGG AAGCCCTCCCGGGCAGCGT C GTGCACGGGTCTGGGTGAGAGT GGCGGGGTCTGGCGCAGTTGGGCTCCGCGCCGTGGAGCAG	1394
	CCGTGCAC G ACGCTGCC	1395
	GGCAGCGT C GTGCACGG	1396

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Melanoma Ala85Thr cGCT-ACT	CTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCT CACCCGACCCGTGCACGAC <u>G</u> CTGCCCGGGAGGGCTTCCTGG ACACGCTGGTGGTGTCTGCACCGGGCCGGGGCGCGGCTGG	1397
	CCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAGCGTGTCC AGGAAGCCCTCCCGGGCAG <u>C</u> GTCGTGCACGGGTTCGGGTGAG AGTGGCGGGGTCTGGCGCAGTTGGGCTCCGCGCCGTGGAG	1398
	TGCACGAC <u>G</u> CTGCCCGG	1399
	CCGGGCAG <u>C</u> GTCGTGCA	1400
Melanoma Arg87Pro CGG-CCG	GCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGA CCCGTGCACGACGCTGCC <u>C</u> GGGAGGGCTTCCTGGACACGCT GGTGGTGTCTGCACCGGGCCGGGGCGCGGCTGGACGTGCG	1401
	CGCACGTCCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAG CGTGTCCAGGAAGCCCTCC <u>C</u> GGGCAGCGTCGTGCACGGGTC GGGTGAGAGTGGCGGGGTCTGGCGCAGTTGGGCTCCGCGC	1402
	CGCTGCC <u>C</u> GGGAGGGCT	1403
	AGCCCTCC <u>C</u> GGGCAGCG	1404
Melanoma Arg87Trp cCGG-TGG	GGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCG ACCCGTGCACGACGCTGCC <u>C</u> GGGAGGGCTTCCTGGACACGC TGGTGGTGTCTGCACCGGGCCGGGGCGCGGCTGGACGTGC	1405
	GCACGTCCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAGC GTGTCCAGGAAGCCCTCC <u>C</u> GGGCAGCGTCGTGCACGGGTCTG GGTGAGAGTGGCGGGGTCTGGCGCAGTTGGGCTCCGCGCC	1406
	ACGCTGCC <u>C</u> GGGAGGGC	1407
	GCCCTCC <u>C</u> GGGCAGCGT	1408
Melanoma Leu97Arg CTG-CGG	CTCTACCCGACCGGTGCATGATGCTGCCCGGGAGGGCTTCC TGGACACGCTGGTGGTGTCTGCACCGGGCCGGGGCGCGGCTG GACGTGCGCATGCCTGGGGTCGTCTGCCCGTGGACTT	1409
	AAGTCCACGGGCAGACGACCCAGGCATCGCGCACGTCCAG CCGCGCCCCGGCCCGGTGC <u>A</u> GCACCACCAGCGTGTCCAGGA AGCCCTCCCGGGCAGCATCATGCACCGGTCGGGTGAGAG	1410
	GGTGGTGC <u>T</u> GCACCGGG	1411
	CCCGGTGC <u>A</u> GCACCACC	1412

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Melanoma Arg99Pro CGG-CCG	CCCGACCGGTGCATGATGCTGCCCGGGAGGGCTTCCTGGAC ACGCTGGTGGTGTGTCACCGGGCCGGGGCGCGGCTGGACGT GCGCGATGCCTGGGGTCGTCTGCCCGTGGACTTGGCCGA	1413
	TCGGCCAAGTCCACGGGCAGACGACCCCAGGCATCGCGCAC GTCCAGCCGCGCCCCGGGCCGGGTGCAGCACCACCAGCGTGT CCAGGAAGCCCTCCCGGGCAGCATCATGCACCGGTTCGGG	1414
	GCTGCACCGGGCCGGG	1415
	CCCCGGCCGGGTGCAGC	1416
Melanoma Gly101Trp cGGG-TGG	CCGGTGCATGATGCTGCCCGGGAGGGCTTCCTGGACACGCT GGTGGTGTGTCACCGGGGCCGGGGCGCGGCTGGACGTGCGC GATGCCTGGGGTCGTCTGCCCGTGGACTTGCCCGAGGAGC	1417
	GCTCCTCGGCCAAGTCCACGGGCAGACGACCCCAGGCATCG CGCACGTCCAGCCGCGCCCCGGGCCGGTGCAGCACCACCAG CGTGTCCAGGAAGCCCTCCCGGGCAGCATCATGCACCGG	1418
	ACCGGGCCGGGGCGCGG	1419
	CCGCGCCCCGGGCCGGT	1420
Melanoma Arg107Cys gCGC-TGC	CGGGAGGGCTTCCTGGACACGCTGGTGGTGTGTCACCGGGC CGGGGCGCGGCTGGACGTGCGCGATGCCTGGGGTCGTCTGC CCGTGGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTG	1421
	CAACGTGCGGTTGGCCCCGCTCCTCGGCCAAGTCCACGGGC AGACGACCCCAGGCATCGCGCACGTCCAGCCGCGCCCCGGC CCGGTGCAGCACCACCAGCGTGTCCAGGAAGCCCTCCCG	1422
	TGGACGTGCGCGATGCC	1423
	GGCATCGCGCACGTCCA	1424
Melanoma Ala118Thr gGCT-ACT	CACCGGGCCGGGGCGCGGCTGGACGTGCGCGATGCCTGGG GCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGC GATGTGCGACGGTACCTGCGCGCGGCTGCGGGGGGCACCA	1425
	TGGTGCCCCCGCAGCCGCGCGCAGGTACCGTGCGACATCG CGATGGCCCAGCTCCTCAGCCAGGTCCACGGGCAGACGGCC CCAGGCATCGCGCACGTCCAGCCGCGCCCCGGCCCCGGTG	1426
	TGGACCTGGCTGAGGAG	1427
	CTCCTCAGCCAGGTCCA	1428

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Melanoma Val126Asp GTC-GAC	TGCGCGATGCCTGGGGCCGTCTGCCCCTGGACCTGGCTGAG GAGCTGGGCCATCGCGATGTCGCACGGTACCTGCGCGCGGC TGCGGGGGGCACCAGAGGCAGTAACCATGCCCGCATAGA	1429
	TCTATGCGGGCATGGTACTGCCTCTGGTGCCCCCGCAGCC GCGCGCAGGTACCGTGCGACATCGCGATGGCCCAGCTCCTC AGCCAGGTCCACGGGCAGACGGCCCCAGGCATCGCGCA	1430
	TCGCGATGTCGCACGGT	1431
	ACCGTGCGACATCGCGA	1432

EXAMPLE 12

Adenomatous polyposis of the colon - APC

[0223] Adenomatous polyposis of the colon is characterized by adenomatous polyps of the colon and rectum; in extreme cases the bowel is carpeted with a myriad of polyps. This is a viciously premalignant disease with one or more polyps progressing through dysplasia to malignancy in untreated gene carriers with a median age at diagnosis of 40 years.

[0224] Mutations in the APC gene are an initiating event for both familial and sporadic colorectal tumorigenesis and many alleles of the APC gene have been identified. Carcinoma may arise at any age from late childhood through the seventh decade with presenting features including, for example, weight loss and inanition, bowel obstruction, or bloody diarrhea. Cases of new mutation still present in these ways but in areas with well organized registers most other gene carriers are detected. The attached table discloses the correcting oligonucleotide base sequences for the APC oligonucleotides of the invention.

Table 14

APC Mutations And Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Arg121Term AGA-TGA	GGATCTGTATCAAGCCGTTCTGGAGAGTGCAGTCCTGTTCTT ATGGGTTTCATTTCCAAGAAGAGGGTTTGTAAATGGAAGCAGA GAAAGTACTGGATATTTAGAAGAACTTGAGAAAGAGA	1433
	TCTCTTTCTCAAGTTCTTCTAAATATCCAGTACTTTCTCTGCTT CCATTTACAAACCCTCTTCTTGAAATGAACCCATAGGAACAG GACTGCACTCTCCAGAACGGCTTGATACAGATCC	1434
	TTCCAAGAAGAGGGTTT	1435
	AAACCCTCTTCTTGAA	1436

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Trp157Term TGG-TAG	AAAAAAAAAATAGGTCATTGCTTCTTGCTGATCTTGACAAAGAAGAAAAGGAAAAAGACTGGTATTACGCTCAACTTCAGAATCTC ACTAAAAGAATAGATAGTCTTCCTTTAACTGAAAA	1437
	TTTTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGAGATTCTG AAGTTGAGCGTAATACAGTCTTTTCTTTTCTTCTTTGTCAA GATCAGCAAGAAGCAATGACCTATTTTTTTTTT	1438
	AAAAGACTGGTATTACG	1439
	CGTAATACAGTCTTTT	1440
Adenomatous polyposis coli Tyr159Term TAC-TAG	AAATAGGTCATTGCTTCTTGCTGATCTTGACAAAGAAGAAAAG GAAAAAGACTGGTATTACGCTCAACTTCAGAATCTCACTAAAA GAATAGATAGTCTTCCTTTAACTGAAAATGTAAGT	1441
	ACTTACATTTTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGA GATTCTGAAGTTGAGCGTAATACCAGTCTTTTCTTTTCTTCT TTGTCAAGATCAGCAAGAAGCAATGACCTATTT	1442
	TGGTATTACGCTCAACT	1443
	AGTTGAGCGTAATACCA	1444
Adenomatous polyposis coli Gln163Term CAG-TAG	TTGCTTCTTGCTGATCTTGACAAAGAAGAAAAGGAAAAAGACT GGTATTACGCTCAACTTCAGAATCTCACTAAAAGAATAGATAG TCTTCCTTTAACTGAAAATGTAAGTAACTGGCAGT	1445
	ACTGCCAGTTACTTACATTTTCAGTTAAAGGAAGACTATCTATT CTTTTAGTGAGATTCTGAAGTTGAGCGTAATACCAGTCTTTTT CCTTTTCTTCTTTGTCAAGATCAGCAAGAAGCAA	1446
	CTCAACTTCAGAATCTC	1447
	GAGATTCTGAAGTTGAG	1448
Adenomatous polyposis coli Arg168Term AGA-TGA	CTTGACAAAGAAGAAAAGGAAAAAGACTGGTATTACGCTCAAC TTCAGAATCTCACTAAAAGAATAGATAGTCTTCCTTTAACTGAA AATGTAAGTAACTGGCAGTACAACCTATTTGAAA	1449
	TTTCAAATAAGTTGTACTGCCAGTTACTTACATTTTCAGTTAAA GGAAGACTATCTATTCTTTTAGTGAGATTCTGAAGTTGAGCGT AATACCAGTCTTTTTCTTTTCTTCTTTGTCAAG	1450
	TCACTAAAAGAATAGAT	1451
	ATCTATTCTTTTAGTGA	1452
Adenomatous polyposis coli Ser171Ile AGT-ATT	AAGAAAAGGAAAAAGACTGGTATTACGCTCAACTTCAGAATCT CACTAAAAGAATAGATAGTCTTCCTTTAACTGAAAATGTAAGTA ACTGGCAGTACAACCTATTTGAACTTTAATAAC	1453
	GTTATTAAAGTTTCAAATAAGTTGTACTGCCAGTTACTTACATT TTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGAGATTCTGAA GTTGAGCGTAATACCAGTCTTTTCTTTTCTT	1454
	AATAGATAGTCTTCCTT	1455
	AAGGAAGACTATCTATT	1456
Adenomatous polyposis coli Gln181Term	GATTAACGTAAATACAAGATATTGATACTTTTTTATTATTTGTG GTTTTAGTTTTCTTACAACAGATATGACCAGAAGGCAATTG GAATATGAAGCAAGGCAAATCAGAGTTGCGATGG	1457

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
CAA-TAA	CCATCGCAACTCTGATTTGCCTTGCTTCATATTCCAATTGCCT TCTGGTCATATCTGTTT <u>G</u> AAGGAAAACATAAAACCACAAATAAT AAAAAAGTATCAATATCTTGTATTTACGTTAATC	1458
	TTTCCTTACAAACAGAT ATCTGTTT <u>G</u> AAGGAAA	1459 1460
Adenomatous polyposis coli Glu190Term GAA-TAA	CTTTTTATTATTTGTGGTTTTAGTTTTCTTACAAACAGATATG ACCAGAAGGCAATTGGAATATGAAGCAAGGCAAATCAGAGTT GCGATGGAAGAACAACTAGGTACCTGCCAGGATA	1461
	TATCCTGGCAGGTACCTAGTTGTTCTTCCATCGCAACTCTGAT TTGCCTTGCTTCATATT <u>C</u> CAATTGCCTTCTGGTCATATCTGTTT GTAAGGAAAACATAAAACCACAAATAATAAAAAAG	1462
	GGCAATTGGAATATGAA	1463
	TTCATATT <u>C</u> CAATTGCC	1464
Adenomatous polyposis coli Gln208Term CAG-TAG	CAATTGGAATATGAAGCAAGGCAAATCAGAGTTGCGATGGAA GAACAACAGGTACCTGCCAGGATATGGAAAAACGAGCACAG GTAAGTTACTTGTCTTAAGTGATAAAACAGCGAAGA	1465
	TCTTCGCTGTTTTATCACTTAGAAACAAGTAACTTACCTGTGCT CGTTTTTCCATATCCT <u>G</u> GCAGGTACCTAGTTGTTCTTCCATCG CAACTCTGATTTGCCTTGCTTCATATTCCAATTG	1466
	GTACCTGCCAGGATATG	1467
	CATATCCT <u>G</u> GCAGGTAC	1468
Adenomatous polyposis coli Arg213Term CGA-TGA	GCAAGGCAAATCAGAGTTGCGATGGAAGAACAACAGGTACC TGCCAGGATATGGAAAAACGAGCACAGGTAAGTTACTTGTTTC TAAGTGATAAAACAGCGAAGAGCTATTAGGAATAAA	1469
	TTTATTCCTAATAGCTCTTCGCTGTTTTATCACTTAGAAACAAG TAACTTACCTGTGCTC <u>G</u> TTTTTCCATATCCTGGCAGGTACCTA GTTGTTCTTCCATCGCAACTCTGATTTGCCTTGC	1470
	TGGAAAAACGAGCACAG	1471
	CTGTGCTC <u>G</u> TTTTTCCA	1472
Adenomatous polyposis coli Arg232Term CGA-TGA	GTTTTATTTTAGCGAAGAATAGCCAGAATTCAGCAAATCGAAA AGGACATACTTCGTATACGACAGCTTTTACAGTCCCAAGCAAC AGAAGCAGAGGTTAGTAAATTGCCTTTCTTGTTTG	1473
	CAAACAAGAAAGGCAATTTACTAACCTCTGCTTCTGTTGCTTG GGACTGTAAAAGCTGT <u>C</u> GATACGAAGTATGTCCTTTTCGATT TGCTGAATTCTGGCTATTCTTCGCTAAAATAAAAC	1474
	TTCGTATACGACAGCTT	1475
	AAGCTGT <u>C</u> GATACGAA	1476
Adenomatous polyposis coli Gln233Term CAG-TAG	TTATTTTAGCGAAGAATAGCCAGAATTCAGCAAATCGAAAAGG ACATACTTCGTATACGACAGCTTTTACAGTCCCAAGCAACAGA AGCAGAGGTTAGTAAATTGCCTTTCTTGTTTGTGG	1477
	CCACAAACAAGAAAGGCAATTTACTAACCTCTGCTTCTGTTGC TTGGGACTGTAAAAGCT <u>G</u> TCGTATACGAAGTATGTCCTTTTCG ATTTGCTGAATTCTGGCTATTCTTCGCTAAAATAA	1478

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Gln247Term CAG-TAG	GTATACGAC <u>C</u> AGCTTTTA	1479
	TAAAAGCT <u>G</u> TCGTATAC	1480
	AGAAAGCCTACACCATTTTTGCATGTACTGATGTAACTCCATCTTAACAGAGGTCATCTCAGAACAAAGCATGAAACCGGCTCACATGATGCTGAGCGGCAGAATGAAGGTCAAGGAGTGG	1481
	CCACTCCTTGACCTTCATTCTGCCGCTCAGCATCATGTGAGCCGTTTCATGCTTGTCTGAGATGACCTCTGTAAAGATGGAGTTAACATCAGTACATGCAAAAATGGTGTAGGCTTTCT	1482
	GGTCATCTCAGAACAAAG	1483
	CTTGTTCTGAGATGACC	1484
Adenomatous polyposis coli Gly267Term GGA-TGA	CAGAACAAGCATGAAACCGGCTCACATGATGCTGAGCGGCAG AATGAAGGTCAAGGAGTGGGAGAAATCAACATGGCAACTTCTGGTAATGGTCAGGTAAATAAATTATTTTATCATATTT	1485
	AAATATGATAAAATAATTTATTTACCTGACCATTACCAGAAAGTTGCCATGTTGATTTCTCCCACTCCTTGACCTTCATTCTGCCGCTCAGCATCATGTGAGCCGGTTTCATGCTTGTCTG	1486
	AAGGAGTGGGAGAAATC	1487
	GATTTCTCCCACTCCTT	1488
Adenomatous polyposis coli Glu443Term GAA-TAA	CTTCAAATAACAAAGCATTATGGTTTATGTTGATTTTATTTTCA GTGCCAGCTCCTGTTGAACATCAGATCTGTCCTGCTGTGTGT GTTCTAATGAAACTTTTCATTTGATGAAGAGCATA	1489
	TATGCTCTTCATCAAATGAAAGTTTCATTAGAACACACACAGCAGGACAGATCTGATGTTCAACAGGAGCTGGCACTGAAAAATAAAATCAACATAAACCATAATGCTTTGTTATTTGAAG	1490
	CTCCTGTTGAACATCAG	1491
	CTGATGTTCAACAGGAG	1492
Adenomatous polyposis coli SER457TER TCA-TAA	CAGTGCCAGCTCCTGTTGAACATCAGATCTGTCCTGCTGTGTGTGTTCTAATGAAACTTTTCATTTGATGAAGAGCATAGACATGC AATGAATGAACTAGGTAAGACAAAAATGTTTTTTAA	1493
	TAAAAAACATTTTTGTCTTACCTAGTTCATTTCATTGCATGTCTATGCTCTTCATCAAATGAAAGTTTCATTAGAACACACACAGCAGGACAGATCTGATGTTCAACAGGAGCTGGCACTG	1494
	GAAACTTTTCATTTGATG	1495
	CATCAAATGAAAGTTTC	1496
Adenomatous polyposis coli Gln473Term CAG-TAG	AGTTGTTTTATTTTAGATGATTGTCTTTTCTCTTGCCCTTTTTAAATTAGGGGGACTACAGGCCATTGCAGAATTATTGCAAGTGACTGTGAAATGTACGGGCTTACTAATGACCACT	1497
	AGTGGTCATTAGTAAGCCCGTACATTTTACAGTCCACTTGCAATAATTCTGCAATGGCCTGTAGTCCCCCTAATTTAAAAGGGCAAGAGGAAAAAGACAATCATCTAAAATAAAACAACCT	1498
	GGGGACTACAGGCCATT	1499
	AATGGCCTGTAGTCCCC	1500

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Tyr486Term TAC-TAG	TTTAAATTAGGGGGACTACAGGCCATTGCAGAATTATTGCAA GTGGACTGTGAAATGTACGGGCTTACTAATGACCACTACAGT ATTACACTAAGACGATATGCTGGAATGGCTTTGACA	1501
	TGTCAAAGCCATTCCAGCATATCGTCTTAGTGTAATACTGTAG TGGTCATTAGTAAGCCCGTACATTTACAGTCCACTTGCAATA ATTCTGCAATGGCCTGTAGTCCCCCTAATTTAAAA	1502
	GAAATGTACGGGCTTAC	1503
	GTAAGCCCCGTACATTTT	1504
Adenomatous polyposis coli Arg499Term CGA-TGA	TTGCAAGTGGACTGTGAAATGTATGGGCTTACTAATGACCACT ACAGTATTACACTAAGACGATATGCTGGAATGGCTTTGACAAA CTTGACTTTTGGAGATGTAGCCAACAAGGTATGTT	1505
	AACATACCTTGTTGGCTACATCTCCAAAAGTCAAGTTTGTCAA AGCCATTCCAGCATATCGTCTTAGTGTAATACTGTAGTGGTCA TTAGTAAGCCCATACATTTACAGTCCACTTGCAA	1506
	CACTAAGACGATATGCT	1507
	AGCATATCGTCTTAGTG	1508
Adenomatous polyposis coli Tyr500Term TAT-TAG	AGTGGACTGTGAAATGTATGGGCTTACTAATGACCACTACAGT ATTACACTAAGACGATATGCTGGAATGGCTTTGACAACTTGA CTTTTGGAGATGTAGCCAACAAGGTATGTTTTTAT	1509
	ATAAAACATACCTTGTTGGCTACATCTCCAAAAGTCAAGTTT GTCAAAGCCATTCCAGCATATCGTCTTAGTGTAATACTGTAGT GGTCATTAGTAAGCCCATACATTTACAGTCCACT	1510
	AGACGATATGCTGGAAT	1511
	ATTCCAGCATATCGTCT	1512
Adenomatous polyposis coli Lys586Term AAA-TAA	GACAAATCCAACTCTAATTAGATGACCCATATTCTGTTTCTTA CTAGGAATCAACCCTCAAAAGCGTATTGAGTGCCATTATGGAAT TTGTCAGCACATTGCACTGAGAATAAAGCTGATA	1513
	TATCAGCTTTATTCTCAGTGCAATGTGCTGACAAATTCCATAA GGCACTCAATACGCTTTTGAGGGTTGATTCTAGTAAGAAACA GAATATGGGTCATCTAATTAGAGTTGGAATTTGTC	1514
	CAACCCTCAAAAGCGTA	1515
	TACGCTTTTGAGGGTTG	1516
Adenomatous polyposis coli Leu592Term TTA-TGA	TAGATGACCCATATTCTGTTTCTTACTAGGAATCAACCCTCAA AAGCGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACT GAGAATAAAGCTGATATATGTGCTGTAGATGGTGC	1517
	GCACCATCTACAGCACATATATCAGCTTTATTCTCAGTGCAAT GTGCTGACAAATTCCATAAGGCACTCAATACGCTTTTGAGGGT TGATTCTAGTAAGAAACAGAATATGGGTCATCTA	1518
	GAGTGCCTTATGGAATT	1519
	AATTCCATAAGGCACTC	1520

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Trp593Term TGG-TAG	ATGACCCATATTCTGTTTCTTACTAGGAATCAACCCTCAAAG CGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTGAG AATAAAGCTGATATATGTGCTGTAGATGGTGCACT	1521
	AGTGCACCATCTACAGCACATATATCAGCTTTATTCTCAGTGC AATGTGCTGACAAATTCATAAGGCACTCAATACGCTTTTGAG GGTTGATTCTAGTAAGAAACAGAATATGGGTCAT	1522
	TGCCTTATGGAATTTGT	1523
	ACAAATTCATAAGGCA	1524
Adenomatous polyposis coli Trp593Term TGG-TGA	TGACCCATATTCTGTTTCTTACTAGGAATCAACCCTCAAAGC GTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTGAGA ATAAAGCTGATATATGTGCTGTAGATGGTGCACTT	1525
	AAGTGCACCATCTACAGCACATATATCAGCTTTATTCTCAGTGC CAATGTGCTGACAAATTCATAAGGCACTCAATACGCTTTTGAG GGGTTGATTCTAGTAAGAAACAGAATATGGGTCA	1526
	GCCTTATGGAATTTGTC	1527
	GACAAATTCATAAGGC	1528
Adenomatous polyposis coli Tyr622Term TAC-TAA	TAAAGCTGATATATGTGCTGTAGATGGTGCACTTGCAATTTTGT GTTGGCACTCTTACTTACCGGAGCCAGACAAACACTTTAGCC ATTATTGAAAGTGGAGGTGGGATATTACGGAATGTG	1529
	CACATTCCGTAATATCCACCTCCACTTTCAATAATGGCTAAA GTGTTTGTCTGGCTCCGGTAAGTAAGAGTGCCAACCAAAAAT GCAAGTGCACCATCTACAGCACATATATCAGCTTTA	1530
	CTTACTTACCGGAGCCA	1531
	TGGCTCCGGTAAGTAAG	1532

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Gln625Term CAG-TAG	GATATATGTGCTGTAGATGGTGCACTTGCATTTTTGGTTGGCACTCTTACTTACCGGAGCCAGACAAACACTTTAGCCATTATTGA AAGTGGAGGTGGGATATTACGGAATGTGTCCAGCT	1533
	AGCTGGACACATTCCGTAATATCCACCTCCACTTTCAATAAT GGCTAAAGTGTTTGTCTGGCTCCGGTAAGTAAGAGTGCCAAC CAAAAATGCAAGTGACCATCTACAGCACATATATC	1534
	ACCGGAGCCAGACAAAC	1535
	GTTTGTCTGGCTCCGGT	1536
Adenomatous polyposis coli Leu629Term TTA-TAA	TAGATGGTGCACTTGCATTTTTGGTTGGCACTCTTACTTACCG GAGCCAGACAAACACTTTAGCCATTATTGAAAGTGGAGGTGG GATATTACGGAATGTGTCCAGCTTGATAGCTACAAA	1537
	TTTGTAGCTATCAAGCTGGACACATTCCGTAATATCCACCTC CACTTTCAATAATGGCTAAAGTGTTTGTCTGGCTCCGGTAAGT AAGAGTGCCAACCAAAAATGCAAGTGACCATCTA	1538
	AAACACTTTAGCCATTA	1539
	TAATGGCTAAAGTGTTT	1540
Adenomatous polyposis coli Glu650Term GAG-TAG	GCCATTATTGAAAGTGGAGGTGGGATATTACGGAATGTGTCC AGCTTGATAGCTACAAATGAGGACCACAGGTATATATAGAGTT TTATATTACTTTTAAAGTACAGAATTCATACTCTCA	1541
	TGAGAGTATGAATTCTGTACTTTAAAAGTAATATAAACTCTAT ATATACCTGTGGTCCTCATTGTAGCTATCAAGCTGGACACAT TCCGTAATATCCACCTCCACTTTCAATAATGGC	1542
	CTACAAATGAGGACCAC	1543
	GTGGTCCTCATTGTAG	1544
Adenomatous polyposis coli Trp699Term TGG-TGA	TGCATGTGGAACCTTTGTGGAATCTCTCAGCAAGAAATCCTAAA GACCAGGAAGCATTATGGGACATGGGGGCAGTTAGCATGCTC AAGAACCTCATTCAATCAAAAGCACAAAATGATTGCT	1545
	AGCAATCATTTTGTGCTTTGAATGAATGAGGTTCTTGAGCATG CTAACTGCCCCCATGTCCATAATGCTTCCTGGTCTTTAGGAT TTCTTGCTGAGAGATTCCACAAAGTTCCACATGCA	1546
	GCATTATGGGACATGGG	1547
	CCCATGTCCATAATGC	1548
Adenomatous polyposis coli Ser713Term TCA-TGA	AAGACCAGGAAGCATTATGGGACATGGGGGCAGTTAGCATGC TCAAGAACCTCATTCAATCAAAGCACAAAATGATTGCTATGGG AAGTGCTGCAGCTTTAAGGAATCTCATGGCAAATAG	1549
	CTATTTGCCATGAGATTCCTTAAAGCTGCAGCACTTCCCATAG CAATCATTTTGTGCTTTGAATGAATGAGGTTCTTGAGCATGCT AACTGCCCCCATGTCCATAATGCTTCCTGGTCTT	1550
	CATTCATTCAAAGCACA	1551
	TGTGCTTTGAATGAATG	1552

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Ser722Gly AGT-GGT	GGGGCAGTTAGCATGCTCAAGAACCTCATTCAATCAAAGCAC AAAATGATTGCTATGGGA <u>A</u> GTGCTGCAGCTTTAAGGAATCTCA TGGCAAATAGGCCTGCGAAGTACAAGGATGCCAATA	1553
	TATTGGCATCCTTGTACTTCGCAGGCCTATTTGCCATGAGATT CCTTAAAGCTGCAGCACTTCCCATAGCAATCATTTTGTGCTTT GAATGAATGAGGTTCTTGAGCATGCTAACTGCCCC	1554
	CTATGGGA <u>A</u> GTGCTGCA	1555
	TGCAGCACTTCCCATAG	1556
Adenomatous polyposis coli Leu764Term TTA-TAA	TCTCCTGGCTCAGCTTGCCATCTCTTCATGTTAGGAAACAAA AGCCCTAGAAGCAGAATT <u>A</u> GATGCTCAGCACTTATCAGAACT TTTGACAATATAGACAATTTAAGTCCCAAGGCATC	1557
	GATGCCTTGGGACTTAAATTGTCTATATTGTCAAAAGTTTCTG ATAAGTGCTGAGCATCT <u>A</u> ATTCTGCTTCTAGGGCTTTTTGTTT CCTAACATGAAGAGATGGCAAGCTGAGCCAGGAGA	1558
	AGCAGAATTAGATGCTC	1559
	GAGCATCT <u>A</u> ATTCTGCT	1560
Adenomatous polyposis coli Ser784Thr TCT-ACT	TTAGATGCTCAGCACTTATCAGAACTTTTGACAATATAGACA ATTTAAGTCCCAAGGCATCTCATCGTAGTAAGCAGAGACACA GCAAGTCTCTATGGTGATTATGTTTTTGACACCATC	1561
	GATGGTGTCAAAACATAATCACCATAGAGACTTGCTGTGTCT CTGCTTACTACGATGAG <u>A</u> TGCCTTGGGACTTAAATTGTCTATA TTGTCAAAAGTTTCTGATAAGTGCTGAGCATCTAA	1562
	CCAAGGCATCTCATCGT	1563
	ACGATGAG <u>A</u> TGCCTTGG	1564
Adenomatous polyposis coli Arg805Term CGA-TGA	CTCATCGTAGTAAGCAGAGACACAGCAAGTCTCTATGGTGATT ATGTTTTTGACACCAAT <u>C</u> GACATGATGATAATAGGTCAGACAT TTTAATACTGGCACATGACTGTCCTTTCACCATAT	1565
	ATATGGTGAAAGGACAGTCATGTGCCAGTATTAATGTCTGA CCTATTATCATCATGT <u>C</u> GATTGGTGTCAAAACATAATCACCAT AGAGACTTGCTGTGTCTCTGCTTACTACGATGAG	1566
	ACACCAAT <u>C</u> GACATGAT	1567
	ATCATGT <u>C</u> GATTGGTGT	1568
Adenomatous polyposis coli Gln879Term CAG-TAG	GGTCTAGGCAACTACCATCCAGCAACAGAAAATCCAGGAACT TCTTCAAAGCGAGGTTTG <u>C</u> AGATCTCCACCACTGCAGCCCAG ATTGCCAAAGTCATGGAAGAAGTGTCAGCCATTCTATA	1569
	TATGAATGGCTGACACTTCTCCATGACTTTGGCAATCTGGGC TGCAGTGGTGGAGATCT <u>G</u> CAAACCTCGCTTTGAAGAAGTTCC TGGATTTTCTGTTGCTGGATGGTAGTTGCCTAGACC	1570
	GAGGTTTG <u>C</u> AGATCTCC	1571
	GGAGATCT <u>G</u> CAAACCTC	1572

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Ser932Term TCA-TAA	TACATTGTGTGACAGATGAGAGAAATGCACTTAGAAGAAGCTC TGCTGCCCATACACATTCAAACACTTACAATTTCACTAAGTCG GAAAATTCAAATAGGACATGTTCTATGCCTTATGC	1573
	GCATAAGGCATAGAACATGTCCTATTTGAATTTTCCGACTTAG TGAAATTGTAAGTGTGGAATGTGTATGGGCAGCAGAGCTTCT TCTAAGTGCATTTCTCTCATCTGTCACACAATGTA	1574
	TACACATTCAAACACTT	1575
	AAGTGTTTGAATGTGTA	1576
Adenomatous polyposis coli Ser932Term TCA-TGA	TACATTGTGTGACAGATGAGAGAAATGCACTTAGAAGAAGCTC TGCTGCCCATACACATTCAAACACTTACAATTTCACTAAGTCG GAAAATTCAAATAGGACATGTTCTATGCCTTATGC	1577
	GCATAAGGCATAGAACATGTCCTATTTGAATTTTCCGACTTAG TGAAATTGTAAGTGTGGAATGTGTATGGGCAGCAGAGCTTCT TCTAAGTGCATTTCTCTCATCTGTCACACAATGTA	1578
	TACACATTCAAACACTT	1579
	AAGTGTTTGAATGTGTA	1580
Adenomatous polyposis coli Tyr935Term TAC-TAG	GACAGATGAGAGAAATGCACTTAGAAGAAGCTCTGCTGCCCA TACACATTCAAACACTTACAATTTCACTAAGTCGGAAAATTCAA ATAGGACATGTTCTATGCCTTATGCCAAATTAGAA	1581
	TTCTAATTTGGCATAAGGCATAGAACATGTCCTATTTGAATTTT CCGACTTAGTGAAATTGTAAGTGTGTTGAATGTGTATGGGCAGC AGAGCTTCTTCTAAGTGCATTTCTCTCATCTGTC	1582
	AACACTTACAATTTAC	1583
	GTGAAATTGTAAGTGTT	1584
Adenomatous polyposis coli Tyr935Term TAC-TAA	GACAGATGAGAGAAATGCACTTAGAAGAAGCTCTGCTGCCCA TACACATTCAAACACTTACAATTTCACTAAGTCGGAAAATTCAA ATAGGACATGTTCTATGCCTTATGCCAAATTAGAA	1585
	TTCTAATTTGGCATAAGGCATAGAACATGTCCTATTTGAATTTT CCGACTTAGTGAAATTGTAAGTGTGTTGAATGTGTATGGGCAGC AGAGCTTCTTCTAAGTGCATTTCTCTCATCTGTC	1586
	AACACTTACAATTTAC	1587
	GTGAAATTGTAAGTGTT	1588
Adenomatous polyposis coli Tyr1000Term TAC-TAA	ACCCTCGATTGAATCCTATTCTGAAGATGATGAAAGTAAGTTT TGCAGTTATGGTCAATACCCAGCCGACCTAGCCCATAAAATAC ATAGTGCAATCATATGGATGATAATGATGGAGAA	1589
	TTCTCCATCATTATCATCCATATGATTTGCACTATGTATTTTAT GGGCTAGGTCGGCTGGGTATTGACCATAACTGCAAACTTAC TTTCATCATCTTCAGAATAGGATTCAATCGAGGGT	1590
	GGTCAATACCCAGCCGA	1591
	TCGGCTGGGTATTGACC	1592
Adenomatous polyposis coli Glu1020Term	TACCCAGCCGACCTAGCCCATAAAATACATAGTGCAAATCATA TGGATGATAATGATGGAGAAGTAGATACACCAATAAATTATAG TCTTAAATATTCAGATGAGCAGTTGAACTCTGGAA	1593

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
GAA-TAA	TTCCAGAGTTCAACTGCTCATCTGAATATTTAAGACTATAATTT ATTGGTGTATCTAGTTCTCCATCATTATCATCCATATGATTTGC ACTATGTATTTTATGGGCTAGGTCTGGCTGGGTA	1594
	ATGATGGAGAACTAGAT	1595
	ATCTAGTTCTCCATCAT	1596
Adenomatous polyposis coli Ser1032Term TCA-TAA	ATGAAACCCTCGATTGAATCCTATTCTGAAGATGATGAAAGTA AGTTTTGCAGTTATGGTCAATACCCAGCCGACCTAGCCCATAA AATACATAGTGCAAATCATATGGATGATAATGATG	1597
	CATCATTATCATCCATATGATTTGCACTATGTATTTTATGGGCT AGGTCGGCTGGGTATTGACCATAACTGCAAACTTACTTTTCAT CATCTTCAGAATAGGATTCAATCGAGGGTTTCAT	1598
	GTTATGGTCAATACCCA	1599
	TGGGTATTGACCATAAC	1600
Adenomatous polyposis coli Gln1041Term CAA-TAA	TGAAGATGATGAAAGTAAGTTTTGCAGTTATGGTCAATACCCA GCCGACCTAGCCCATAAATAACATAGTGCAAATCATATGGATG ATAATGATGGAGAACTAGATACACCAATAAATTAT	1601
	ATAATTTATTGGTGTATCTAGTTCTCCATCATTATCATCCATAT GATTTGCACTATGTATTTTATGGGCTAGGTCTGGCTGGGTATTG ACCATAACTGCAAACTTACTTTTCATCATCTTCA	1602
	GCCCATAAATAACATAG	1603
	CTATGTATTTTATGGGC	1604
Adenomatous polyposis coli Gln1045Term CAG-TAG	ATAAATTATAGTCTTAAATATTCAGATGAGCAGTTGAACTCTGG AAGGCAAAGTCCTTCAAGAATGAAAGATGGGCAAGACCCAA ACACATAATAGAAGATGAAATAAAACAAAGTGAGC	1605
	GCTCACTTTGTTTTATTTTCATCTTCTATTATGTGTTTGGGTCTT GCCCATCTTTCACTTCTGTGAAGGACTTTGCCTTCCAGAGTTCA ACTGCTCATCTGAATATTTAAGACTATAATTTAT	1606
	GTCCTTCAAGAATGAA	1607
	TTCATTCTGTGAAGGAC	1608
Adenomatous polyposis coli Gln1067Term CAA-TAA	GAAAGATGGGCAAGACCCAAACACATAATAGAAGATGAAATA AAACAAAGTGAGCAAAGACAATCAAGGAATCAAAGTACAACCTT ATCCTGTTTATACTGAGAGCACTGATGATAAACACC	1609
	GGTGTATATCATCAGTGCTCTCAGTATAAACAGGATAAGTTGT ACTTTGATTCCTTGATTGTCTTTGCTCACTTTGTTTTATTTTCATC TTCTATTATGTGTTTGGGTCTTGCCCATCTTTC	1610
	AGCAAAGACAATCAAGG	1611
	CCTTGATTGTCTTTGCT	1612
Adenomatous polyposis coli Tyr1075Term TAT-TAG	AATAGAAGATGAAATAAAACAAAGTGAGCAAAGACAATCAAGG AATCAAAGTACAACCTTATCCTGTTTATACTGAGAGCACTGATG ATAAACACCTCAAGTTCCAACCACATTTTGGACAG	1613
	CTGTCCAAATGTGGTTGGAAGTTGAGGTGTTTATCATCAGTG CTCTCAGTATAAACAGGATAAGTTGTACTTTGATTCCTTGATT GTCTTTGCTCACTTTGTTTTATTTTCATCTTCTATT	1614

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACAACTTATCCTGTTTA	1615
	TAAACAGGATAAGTTGT	1616
Adenomatous polyposis coli Tyr1102Term TAC-TAG	TGATGATAAACACCTCAAGTTCCAACCACATTTTGGACAGCAG GAATGTGTTTCTCCATACAGGTCACGGGGAGCCAATGGTTCA GAAACAAATCGAGTGGGTTCTAATCATGGAATTAAT	1617
	ATTAATTCCATGATTAGAACCCACTCGATTTGTTTCTGAACCAT TGGCTCCCCGTGACCTGTATGGAGAAACACATTCCTGCTGTC CAAATGTGGTTGGAACCTGAGGTGTTTATCATCA	1618
	TCTCCATACAGGTCACG	1619
	CGTGACCTGTATGGAGA	1620
Adenomatous polyposis coli Ser1110Term TCA-TGA	AACCACATTTTGGACAGCAGGAATGTGTTTCTCCATACAGGTC ACGGGGAGCCAATGGTTGAGAAACAAATCGAGTGGGTTCTAA TCATGGAATTAATCAAAATGTAAGCCAGTCTTTGTG	1621
	CACAAAGACTGGCTTACATTTTGATTAATTCCATGATTAGAAC CCACTCGATTTGTTTCTGAACCATTTGGCTCCCCGTGACCTGTA TGGAGAAACACATTCCTGCTGTCCAAAATGTGGTT	1622
	CAATGGTTGAGAAACAA	1623
	TTGTTTCTGAACCATTG	1624
Adenomatous polyposis coli Arg1114Term CGA-TGA	GGACAGCAGGAATGTGTTTCTCCATACAGGTCACGGGGAGCC AATGGTTCAGAAACAAATCGAGTGGGTTCTAATCATGGAATTA ATCAAAATGTAAGCCAGTCTTTGTGTCAAGAAGATG	1625
	CATCTTCTTGACACAAAGACTGGCTTACATTTTGATTAATTCCA TGATTAGAACCCACTCGATTTGTTTCTGAACCATTTGGCTCCCC GTGACCTGTATGGAGAAACACATTCCTGCTGTCC	1626
	AAACAAATCGAGTGGGT	1627
	ACCCACTCGATTTGTTT	1628
Adenomatous polyposis coli Tyr1135Term TAT-TAG	GGGTTCTAATCATGGAATTAATCAAAATGTAAGCCAGTCTTTG TGTCAGAAGATGACTATGAAGATGATAAGCCTACCAATTATA GTGAACGTTACTCTGAAGAAGAACAGCATGAAGAA	1629
	TTCTTCATGCTGTTCTTCTTCAGAGTAACGTTCACTATAATTGG TAGGCTTATCATCTTCTAGTCATCTTCTTGACACAAAGACTG GCTTACATTTTGATTAATTCCATGATTAGAACCC	1630
	GATGACTATGAAGATGA	1631
	TCATCTTCTAGTCATC	1632
Adenomatous polyposis coli Gln1152Term CAG-TAG	GAAGATGACTATGAAGATGATAAGCCTACCAATTATAGTGAAC GTTACTCTGAAGAAGAACAGCATGAAGAAGAGAGACCAA CAAATTATAGCATAAATATAATGAAGAGAAACGTC	1633
	GACGTTTCTCTTCATTATATTTATGCTATAATTTGTTGGTCTC TCTTCTTCTTCATGCTGTTCTTCTTCAGAGTAACGTTCACTATA ATTGGTAGGCTTATCATCTTCATAGTCATCTTC	1634
	AAGAAGAACAGCATGAA	1635
	TTCATGCTGTTCTTCTT	1636

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Gln1175Term CAG-TAG	GAAGAAGAGAGACCAACAAATTATAGCATAAAATATAATGAAG AGAAACGTCATGTGGATCAGCCTATTGATTATAGTTTAAAATAT GCCACAGATATTCCTTCATCACAGAAACAGTCAT	1637
	ATGACTGTTTCTGTGATGAAGGAATATCTGTGGCATATTTTAA ACTATAATCAATAGGCTGATCCACATGACGTTTCTCTTCATTAT ATTTATGCTATAATTTGTTGGTCTCTCTTCTTC	1638
	ATGTGGATCAGCCTATT	1639
	AATAGGCTGATCCACAT	1640
Adenomatous polyposis coli Pro1176Leu CCT-CTT	AAGAGAGACCAACAAATTATAGCATAAAATATAATGAAGAGAA ACGTCATGTGGATCAGCCTATTGATTATAGTTTAAAATATGCC ACAGATATTCCTTCATCACAGAAACAGTCATTTTC	1641
	GAAAATGACTGTTTCTGTGATGAAGGAATATCTGTGGCATATT TTAAACTATAATCAATAGGCTGATCCACATGACGTTTCTCTTCA TTATATTTTATGCTATAATTTGTTGGTCTCTCTT	1642
	GGATCAGCCTATTGATT	1643
	AATCAATAGGCTGATCC	1644
Adenomatous polyposis coli Ala1184Pro GCC-CCC	ATAAAATATAATGAAGAGAAACGTCATGTGGATCAGCCTATTG ATTATAGTTTAAAATATGCCACAGATATTCCTTCATCACAGAAA CAGTCATTTTCATTCTCAAAGAGTTCATCTGGAC	1645
	GTCCAGATGAACTCTTTGAGAATGAAAATGACTGTTTCTGTGA TGAAGGAATATCTGTGGCATATTTTAACTATAATCAATAGGCT GATCCACATGACGTTTCTCTTCATTATATTTTAT	1646
	TAAAATATGCCACAGAT	1647
	ATCTGTGGCATATTTTA	1648
Adenomatous polyposis coli Ser1194Term TCA-TGA	ATCAGCCTATTGATTATAGTTTAAAATATGCCACAGATATTCCT TCATCACAGAAACAGTCATTTTCATTCTCAAAGAGTTCATCTG GACAAAGCAGTAAACCGAACATATGTCTTCAAG	1649
	CTTGAAGACATATGTTTCGGTTTTACTGCTTTGTCCAGATGAAC TCTTTGAGAATGAAAATGACTGTTTCTGTGATGAAGGAATATC TGTGGCATATTTTAACTATAATCAATAGGCTGAT	1650
	GAAACAGTCATTTTCAT	1651
	ATGAAAATGACTGTTTC	1652
Adenomatous polyposis coli Ser1198Term TCA-TGA	ATTATAGTTTAAAATATGCCACAGATATTCCTTCATCACAGAAA CAGTCATTTTCATTCTCAAAGAGTTCATCTGGACAAAGCAGTA AAACCGAACATATGTCTTCAAGCAGTGAGAATAC	1653
	GTATTCTCACTGCTTGAAGACATATGTTTCGGTTTTACTGCTTT GTCCAGATGAACTCTTTGAGAATGAAAATGACTGTTTCTGTGA TGAAGGAATATCTGTGGCATATTTTAACTATAAT	1654
	TTCATTCTCAAAGAGTT	1655
	AACTCTTTGAGAATGAA	1656

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Gln1228Term CAG-TAG	ACCGAACATATGTCTTCAAGCAGTGAGAATACGTCCACACCTT CATCTAATGCCAAGAGGCAGAATCAGCTCCATCCAGTTCTGC ACAGAGTAGAAGTGGTCAGCCTCAAAGGCTGCCACT	1657
	AGTGGCAGCCTTTGAGGCTGACCACTTCTACTCTGTGCAGAA CTGGATGGAGCTGATTCTGCCTCTTGGCATTAGATGAAGGTG TGGACGTATTCTCACTGCTTGAAGACATATGTTCCGT	1658
	CCAAGAGGCAGAATCAG	1659
	CTGATTCTGCCTCTTGG	1660
Adenomatous polyposis coli Gln1230Term CAG-TAG	CATATGTCTTCAAGCAGTGAGAATACGTCCACACCTTCATCTA ATGCCAAGAGGCAGAATCAGCTCCATCCAGTTCTGCACAGAG TAGAAGTGGTCAGCCTCAAAGGCTGCCACTTGCAAG	1661
	CTTGCAAGTGGCAGCCTTTGAGGCTGACCACTTCTACTCTGT GCAGAACTGGATGGAGCTGATTCTGCCTCTTGGCATTAGATG AAGGTGTGGACGTATTCTCACTGCTTGAAGACATATG	1662
	GGCAGAATCAGCTCCAT	1663
	ATGGAGCTGATTCTGCC	1664
Adenomatous polyposis coli Cys1249Term TGC-TGA	TCAGCTCCATCCAAGTTCTGCACAGAGTAGAAGTGGTCAGCC TCAAAAGGCTGCCACTTGCAAAGTTTCTTCTATTAACCAAGAA ACAATACAGACTTATTGTGTAGAAGATACTCCAATA	1665
	TATTGGAGTATCTTCTACACAATAAGTCTGTATTGTTTCTTGGT TAATAGAAGAACTTTGCAAGTGGCAGCCTTTTGAGGCTGAC CACTTCTACTCTGTGCAGAACTTGGATGGAGCTGA	1666
	GCCACTTGCAAAGTTTC	1667
	GAAACTTTGCAAGTGGC	1668
Adenomatous polyposis coli Cys1270Term TGT-TGA	AGTTTCTTCTATTAACCAAGAAACAATACAGACTTATTGTGTAG AAGATACTCCAATATGTTTTTCAAGATGTAGTTCAATTATCATCT TTGTCATCAGCTGAAGATGAAATAGGATGTAAT	1669
	ATTACATCCTATTTTCATCTTCAGCTGATGACAAAGATGATAATG AACTACATCTTGAAAAACATATTGGAGTATCTTCTACACAATAA GTCTGTATTGTTTCTTGGTTAATAGAAGAACT	1670
	CCAATATGTTTTTCAAG	1671
	CTTGAAAAACATATTGG	1672
Adenomatous polyposis coli Ser1276Term TCA-TGA	AAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATATG TTTTTCAAGATGTAGTTCAATTATCATCTTTGTCATCAGCTGAAG ATGAAATAGGATGTAATCAGACGACACAGGAAGC	1673
	GCTTCCTGTGTCGTCTGATTACATCCTATTTTCATCTTCAGCTG ATGACAAAGATGATAATGAACATACATCTTGAAAAACATATTGG AGTATCTTCTACACAATAAGTCTGTATTGTTTCTT	1674
	ATGTAGTTCAATTATCAT	1675
	ATGATAATGAACATACAT	1676

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Glu1286Term GAA-TAA	GATACTCCAATATGTTTTCAAGATGTAGTTCATTATCATCTTT GTCATCAGCTGAAGATGAAATAGGATGTAATCAGACGACACA GGAAGCAGATTCTGCTAATACCCTGCAAATAGCAG	1677
	CTGCTATTTGCAGGGTATTAGCAGAATCTGCTTCCTGTGTCGT CTGATTACATCCTATTTTCATCTTCAGCTGATGACAAAGATGATA ATGAACTACATCTTGAAAAACATATTGGAGTATC	1678
	CTGAAGATGAAATAGGA	1679
	TCCTATTTTCATCTTCAG	1680
Adenomatous polyposis coli Gln1294Term CAG-TAG	TGTAGTTCATTATCATCTTTGTCATCAGCTGAAGATGAAATAG GATGTAATCAGACGACACAGGAAGCAGATTCTGCTAATACCC TGCAAATAGCAGAAATAAAAGAAAAGATTGGAACTA	1681
	TAGTTCCAATCTTTTCTTTTATTTCTGCTATTTGCAGGGTATTA GCAGAATCTGCTTCCTGTGTCGTCTGATTACATCCTATTTTCAT CTTCAGCTGATGACAAAGATGATAATGAACTACA	1682
	AGACGACACAGGAAGCA	1683
	TGCTTCCTGTGTCGTCT	1684
Predisposition to, association with, colorectal cancer Ile1307Lys ATA-AAA	TAGGATGTAATCAGACGACACAGGAAGCAGATTCTGCTAATA CCCTGCAAATAGCAGAAATAAAAGAAAAGATTGGAACTAGGTC AGCTGAAGATCCTGTGAGCGAAGTTCCAGCAGTGTC	1685
	GACACTGCTGGAACCTCGCTCACAGGATCTTCAGCTGACCTA GTTCCAATCTTTTCTTTTATTTCTGCTATTTGCAGGGTATTAGC AGAATCTGCTTCCTGTGTCGTCTGATTACATCCTA	1686
	AGCAGAAATAAAAGAAA	1687
	TTTCTTTTATTTCTGCT	1688
Adenomatous polyposis coli Glu1309Term GAA-TAA	CCAAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATA TGTTTTTCAAGATGTAGTTCATTATCATCTTTGTCATCAGCTGA AGATGAAATAGGATGTAATCAGACGACACAGGAA	1689
	TTCCTGTGTCGTCTGATTACATCCTATTTTCATCTTCAGCTGATG ACAAAGATGATAATGA A CTACATCTTGAAAAACATATTGGAGT ATCTTCTACACAATAAGTCTGTATTGTTTCTTGG	1690
	AGATGTAGTTCATTATC	1691
	GATAATGA A CTACATCT	1692
Predisposition to Colorectal Cancer Glu1317Gln GAA-CAA	GATTCTGCTAATACCCTGCAAATAGCAGAAATAAAAGAAAAGA TTGGAAGTACAGCTGAAGATCCTGTGAGCGAAGTTCCAG CAGTGTCACAGCACCCCTAGAACCAAATCCAGCAGAC	1693
	GTCTGCTGGATTTGGTTCTAGGGTGCTGTGACACTGCTGGAA CTTCGCTCACAGGATCTTCAGCTGACCTAGTTCCAATCTTTTC TTTTATTTCTGCTATTTGCAGGGTATTAGCAGAATC	1694
	GGTCAGCTGAAGATCCT	1695
	AGGATCTTCAGCTGACC	1696
Adenomatous polyposis coli Gln1328Term	AAAGAAAAGATTGGAAGTACAGCTGAAGATCCTGTGAGC GAAGTTCCAGCAGTGTCAGCACCCTAGAACCAAATCCAGC AGACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCA	1697

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
CAG-TAG	TGGCTGATTCTGAAGATAAACTAGAACCCCTGCAGTCTGCTGG ATTTGGTTCTAGGGTGCTGTGACACTGCTGGAACCTCGCTCA CAGGATCTTCAGCTGACCTAGTTCCAATCTTTTCTTT	1698
	CAGTGTCACAGCACCCCT	1699
	AGGGTGCTGTGACACTG	1700
Adenomatous polyposis coli Gln1338Term CAG-TAG	GATCCTGTGAGCGAAGTTCCAGCAGTGTACAGCACCCCTAGA ACCAAATCCAGCAGACTGCAGGGTTCTAGTTTATCTTCAGAAT CAGCCAGGCACAAAGCTGTTGAATTTTCTTCAGGAG	1701
	CTCCTGAAGAAAATTCAACAGCTTTGTGCCTGGCTGATTCTGA AGATAAACTAGAACCCTGCAGTCTGCTGGATTTGGTTCTAGG GTGCTGTGACACTGCTGGAACCTTCGCTCACAGGATC	1702
	GCAGACTGCAGGGTTCT	1703
	AGAACCCTGCAGTCTGC	1704
Adenomatous polyposis coli Leu1342Term TTA-TAA	AAGTTCCAGCAGTGTACAGCACCCCTAGAACCAAATCCAGCA GACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACA AAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTC	1705
	GAGGGAGATTTGCTCCTGAAGAAAATTCAACAGCTTTGTGC CTGGCTGATTCTGAAGATAAACTAGAACCCTGCAGTCTGCTG GATTTGGTTCTAGGGTGCTGTGACACTGCTGGAACCT	1706
	TTCTAGTTTATCTTCAG	1707
	CTGAAGATAAACTAGAA	1708
Adenomatous polyposis coli Arg1348Trp AGG-TGG	CAGCACCCCTAGAACCAAATCCAGCAGACTGCAGGGTTCTAGT TTATCTTCAGAATCAGCCAGGCACAAAGCTGTTGAATTTCTT CAGGAGCGAAATCTCCCTCCCGAAAGTGGTGCTCAG	1709
	CTGAGCACCACTTTGCGGAGGGAGATTTGCTCCTGAAGAAA ATTCAACAGCTTTGTGCTGGCTGATTCTGAAGATAAACTAGA ACCCTGCAGTCTGCTGGATTTGGTTCTAGGGTGCTG	1710
	AATCAGCCAGGCACAAA	1711
	TTTGTGCTGGCTGATT	1712
Adenomatous polyposis coli Gly1357Term GGA-TGA	CTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACAAA GCTGTTGAATTTCTTCAGGAGCGAAATCTCCCTCCCGAAAGT GGTGCTCAGACACCCCAAAGTCCACCTGAACACTAT	1713
	ATAGTGTTCAAGTGGACTTTGGGGTGTCTGAGCACCACTTTC GGGAGGGAGATTTGCTCCTGAAGAAAATTCAACAGCTTTGT GCCTGGCTGATTCTGAAGATAAACTAGAACCCTGCAG	1714
	TTTCTTCAGGAGCGAAA	1715
	TTTCGCTCCTGAAGAAA	1716
Adenomatous polyposis coli Gln1367Term CAG-TAG	CCAGGCACAAAGCTGTTGAATTTCTTCAGGAGCGAAATCTCC CTCCCGAAAGTGGTGCTCAGACACCCCAAAGTCCACCTGAAC ACTATGTTCAAGAGACCCCACTCATGTTTAGCAGAT	1717
	ATCTGCTAAACATGAGTGGGGTCTCCTGAACATAGTGTTTCA GTGGACTTTGGGGTGTCTGAGCACCACTTTGGGAGGGAGAT TTCGCTCCTGAAGAAAATTCAACAGCTTTGTGCCTGG	1718

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTGGTGCTCAGACACCC	1719
	GGGTGTCTGAGCACCAC	1720
Adenomatous polyposis coli Lys1370Term AAA-TAA	AAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTCCAAAA GTGGTGCTCAGACACCCAAAAGTCCACCTGAACACTATGTTC AGGAGACCCCACTCATGTTTAGCAGATGTACTTCTG	1721
	CAGAAGTACATCTGCTAAACATGAGTGGGGTCTCCTGAACAT AGTGTTTCAGGTGGACTTTGGGGTGTCTGAGCACCACCTTTTGG AGGGAGATTTTCGCTCCTGAAGAAAATTCAACAGCTTT	1722
	AGACACCCBAAAGTCCA	1723
	TGGACTTTTGGGTGTCT	1724
Adenomatous polyposis coli Ser1392Term TCA-TAA	CACCTGAACACTATGTTTCAGGAGACCCCACTCATGTTTAGCA GATGTACTTCTGTTCAGTTCACTTGATAGTTTTGAGAGTCGTTT GATTGCCAGCTCCGTTTCAGAGTGAACCATGCAGTGG	1725
	CCACTGCATGGTTCACTCTGAACGGAGCTGGCAATCGAACGA CTCTCAAACTATCAAGTGAAGTACAGAGTACATCTGCTAA ACATGAGTGGGGTCTCCTGAACATAGTGTTTCAGGTG	1726
	TGTCAGTTCACTTGATA	1727
	TATCAAGTGAAGTACAG	1728
Adenomatous polyposis coli Ser1392Term TCA-TGA	CACCTGAACACTATGTTTCAGGAGACCCCACTCATGTTTAGCA GATGTACTTCTGTTCAGTTCACTTGATAGTTTTGAGAGTCGTTT GATTGCCAGCTCCGTTTCAGAGTGAACCATGCAGTGG	1729
	CCACTGCATGGTTCACTCTGAACGGAGCTGGCAATCGAACGA CTCTCAAACTATCAAGTGAAGTACAGAGTACATCTGCTAA ACATGAGTGGGGTCTCCTGAACATAGTGTTTCAGGTG	1730
	TGTCAGTTCACTTGATA	1731
	TATCAAGTGAAGTACAG	1732
Adenomatous polyposis coli Glu1397Term GAG-TAG	GTTTCAGGAGACCCCACTCATGTTTAGCAGATGTACTTCTGTCA GTTCACTTGATAGTTTTGAGAGTCGTTTCGATTGCCAGCTCCGT TCAGAGTGAACCATGCAGTGGGAATGGTAGGTGGCA	1733
	TGCCACCTACCATTCCTGCTGTTCACTCTGAACGGAGC TGGCAATCGAACGACTCTCAAACTATCAAGTGAAGTACAGAG AGTACATCTGCTAAACATGAGTGGGGTCTCCTGAAC	1734
	ATAGTTTTGAGAGTCGT	1735
	ACGACTCTCAAACTAT	1736
Adenomatous polyposis coli Lys1449Term AAG-TAG	CAAACCATGCCACCAAGCAGAAGTAAACACCTCCACCACCT CCTCAAACAGCTCAAACCAAGCGAGAAGTACCTAAAAATAAA GCACCTACTGCTGAAAAGAGAGAGAGTGGACCTAAGC	1737
	GCTTAGGTCCACTCTCTCTTTTCAGCAGTAGGTGCTTTATT TTTAGGTACTTCTCGCTTGGTTTGAGCTGTTTGAGGAGGTGGT GGAGGTGTTTTACTTCTGCTTGGTGGCATGGTTTG	1738
	CTCAAACCAAGCGAGAA	1739
	TTCTCGCTTGGTTTGAG	1740

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Arg1450Term CGA-TGA	ACCATGCCACCAAGCAGAAGTAAACACCTCCACCACCTCCT CAAACAGCTCAAACCAAGCGAGAAGTACCTAAAAATAAGCA CCTACTGCTGAAAAGAGAGAGAGTGGACCTAAGCAAG	1741
	CTTGCTTAGGTCCACTCTCTCTTTTCAGCAGTAGGTGCTTT ATTTTtaggtacttctCGCTTGGTTTGAGCTGTTTGAGGAGGT GGTGGAGGTGTTTACTTCTGCTTGGTGGCATGGT	1742
	AAACCAAGCGAGAAGTA	1743
	TACTTCTCGCTTGGTTT	1744
Adenomatous polyposis coli Ser1503Term TCA-TAA	CAGATGCTGATACTTTATTACATTTTCCACGGAAAGTACTCC AGATGGATTTTCTTGTTCTATCCAGCCTGAGTGCTCTGAGCCTC GATGAGCCATTATACAGAAAGATGTGGAATTAAG	1745
	CTTAATTCCACATCTTTCTGTATAAATGGCTCATCGAGGCTCA GAGCACTCAGGCTGGATGAACAAGAAAATCCATCTGGAGTAC TTCCGTGGCAAATGTAATAAAGTATCAGCATCTG	1746
	TTCTTGTTCTATCCAGCC	1747
	GGCTGGATGAACAAGAA	1748
Adenomatous polyposis coli Gln1529Term CAG-TAG	CTGAGCCTCGATGAGCCATTATACAGAAAGATGTGGAATTAA GAATAATGCCTCCAGTTGAGGAAAATGACAATGGGAATGAAA CAGAATCAGAGCAGCCTAAAGAATCAAATGAAAACC	1749
	GGTTTTCATTTGATTCTTTAGGCTGCTCTGATTCTGTTTCATTC CCATTGTCATTTTCTGAACTGGAGGCATTATTCTTAATTCCAC ATCTTTCTGTATAAATGGCTCATCGAGGCTCAG	1750
	CTCCAGTTGAGGAAAAT	1751
	ATTTTCCTGAACTGGAG	1752
Adenomatous polyposis coli Ser1539Term TCA-TAA	ATGTGGAATTAAGAATAATGCCTCCAGTTCAGGAAAATGACAA TGGAATGAAACAGAATCAGAGCAGCCTAAAGAATCAAATGA AAACCAAGAGAAAGAGGCAGAAAAAACTATTGATTC	1753
	GAATCAATAGTTTTTCTGCCTCTTTCTCTTGGTTTTCATTTGA TTCTTTAGGCTGCTCTGATTCTGTTTCATTCCCATTGTCATTTT CCTGAACTGGAGGCATTATTCTTAATTCCACAT	1754
	AACAGAATCAGAGCAGC	1755
	GCTGCTCTGATTCTGTT	1756
Adenomatous polyposis coli Ser1567Term TCA-TGA	AAAACCAAGAGAAAGAGGCAGAAAAAACTATTGATTCTGAAAA GGACCTATTAGATGATTGAGATGATGATATTGAAATACTA GAAGAATGTATTATTTCTGCCATGCCAACAAAGTC	1757
	GACTTTGTTGGCATGGCAGAAATAATACATTCTTCTAGTATTTT AATATCATCATCATCTGAATCATCTAATAGGTCCTTTTCAGAAT CAATAGTTTTTCTGCCTCTTTCTTGGTTTT	1758
	AGATGATTGAGATGATG	1759
	CATCATCTGAATCATCT	1760

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Asp1822Val GAC-GTC	AGAGAGTTTTCTCAGACAACAAAGATTCAAAGAAACAGAATTT GAAAAATAATTCCAAGG <u>A</u> CTTCAATGATAAGCTCCCAAATAAT GAAGATAGAGTCAGAGGAAGTTTTGCTTTTGATTCT	1761
	GAATCAAAGCAAACTTCCTCTGACTCTATCTTCATTATTTGG GAGCTTATCATTGAAGT <u>C</u> CTTGGGAATTATTTTTCAAATTCTGTT TCTTTGAATCTTTGTTGTCTGAGAAACTCTCT	1762
	TTCCAAGG <u>A</u> CTTCAATG	1763
	CATTGAAGT <u>C</u> CTTGGAA	1764
Adenomatous polyposis coli Leu2839Phe CTT-TTT	AAAACTGACAGCACAGAATCCAGTGGAACCCAAAGTCCTAAG CGCCATTCTGGGTCTTAC <u>C</u> TTGTGACATCTGTTTAAAGAGAG GAAGAATGAACTAAGAAAATTCTATGTTAATTACA	1765
	TGTAATTAACATAGAATTTTCTTAGTTTCATTCTTCCTCTCTTTT AAACAGATGTCACAAG <u>G</u> TAAGACCCAGAATGGCGCTTAGGAC TTTGGGTTCCACTGGATTCTGTGCTGTCAGTTTT	1766
	GGTCTTAC <u>C</u> TTGTGACA	1767
	TGTCACAAG <u>G</u> TAAGACC	1768

EXAMPLE 13

Parahemophilia - Factor V Deficiency

[0225] Deficiency in clotting Factor V is associated with a lifelong predisposition to thrombosis. The disease typically manifests itself with usually mild bleeding, although bleeding times and clotting times are consistently prolonged. Individuals that are heterozygous for a mutation in Factor V have lowered levels of factor V but probably never have abnormal bleeding. A large number of alleles with a range of presenting symptoms have been identified. The attached table discloses the correcting oligonucleotide base sequences for the Factor V oligonucleotides of the invention.

Table 15

Factor V Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Factor V deficiency Ala221Val GCC-GTC	TTGACTGAATGCTTATTTTGGCCTGTGTCTCTCCCTCTTTCTCA GATATAACAGTTTGTG <u>C</u> CCATGACCACATCAGCTGGCATCTGC TGGGAATGAGCTCGGGGCCAGAATTATTCTCCAT	4340
	ATGGAGAATAATTCTGGCCCCGAGCTCATTCCCAGCAGATGC CAGCTGATGTGGTCATGG <u>G</u> CACAACTGTTATATCTGAGAAA GAGGGAGAGACACAGGCCAAAATAAGCATTCAAGTCAA	1769
	AGTTTGTG <u>C</u> CCATGACC	1770
	GGTCATGGG <u>C</u> CACAACT	1771

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thrombosis Arg306Gly AGG-GGG	TGTCCTAACTCAGCTGGGATGCAGGCTTACATTGACATTAAAA ACTGCCCAAAGAAAACCA <u>AG</u> GAAATCTTAAGAAAATAACTCGTGA GCAGAGGCGGCACATGAAGAGGTGGGAATACTTCA	1772
	TGAAGTATTCCACCTCTTCATGTGCCGCCTCTGCTCACGAGT TATTTTCTTAAGATTCC <u>T</u> GGTTTTCTTTGGGCAGTTTTTAATGT CAATGTAAGCCTGCATCCAGCTGAGTTAGGACA	1773
	AGAAAACCA <u>AG</u> GAAATCTT	1774
	AAGATTCC <u>T</u> GGTTTTCT	1775
Thrombosis Arg306Thr AGG-ACG	GTCCTAACTCAGCTGGGATGCAGGCTTACATTGACATTAAAA CTGCCCAAAGAAAACCA <u>G</u> GAAATCTTAAGAAAATAACTCGTGAG CAGAGGCGGCACATGAAGAGGTGGGAATACTTCAT	1776
	ATGAAGTATTCCACCTCTTCATGTGCCGCCTCTGCTCACGAG TTATTTTCTTAAGATTCC <u>T</u> GGTTTTCTTTGGGCAGTTTTTAATG TCAATGTAAGCCTGCATCCAGCTGAGTTAGGAC	1777
	GAAAACCA <u>G</u> GAAATCTTA	1778
	TAAGATTCC <u>T</u> GGTTTTCT	1779
Increased Risk Thrombosis Arg485Lys AGA-AAA	CCACAGAAAATGATGCCCAGTGCTTAACAAGACCATACTACAG TGACGTGGACATCATGA <u>G</u> AGACATCGCCTCTGGGCTAATAGG ACTACTTCTAATCTGTAAGAGCAGATCCCTGGACAG	1780
	CTGTCCAGGGATCTGCTCTTACAGATTAGAAGTAGTCCTATTA GCCCAGAGGCGATGTCT <u>C</u> TCATGATGTCCACGTCACTGTAGT ATGGTCTTGTTAAGCACTGGGCATCATTTTCTGTGG	1781
	CATCATGA <u>G</u> AGACATCG	1782
	CGATGTCT <u>C</u> TCATGATG	1783
Increased Risk Thrombosis Arg506Gln CGA-CAA	ACATCGCCTCTGGGCTAATAGGACTACTTCTAATCTGTAAGAG CAGATCCCTGGACAGGC <u>G</u> AGGAATACAGGTATTTTGTCTTG AAGTAACCTTTTCAGAAATTCTGAGAATTTCTTCTGG	1784
	CCAGAAGAAATTCTCAGAATTTCTGAAAGGTTACTTCAAGGAC AAAATACCTGTATTCCT <u>C</u> GCCTGTCCAGGGATCTGCTCTTACA GATTAGAAGTAGTCCTATTAGCCCAGAGGCGATGT	1785
	GGACAGGC <u>G</u> AGGAATAC	1786
	GTATTCCT <u>C</u> GCCTGTCC	1787
Factor V Deficiency Arg506Term CGA-TGA	GACATCGCCTCTGGGCTAATAGGACTACTTCTAATCTGTAAGA GCAGATCCCTGGACAGGC <u>G</u> AGGAATACAGGTATTTTGTCTT GAAGTAACCTTTTCAGAAATTCTGAGAATTTCTTCTG	1788
	CAGAAGAAATTCTCAGAATTTCTGAAAGGTTACTTCAAGGACA AAATACCTGTATTCCT <u>C</u> GCCTGTCCAGGGATCTGCTCTTACAG ATTAGAAGTAGTCCTATTAGCCCAGAGGCGATGTC	1789
	TGGACAGGC <u>G</u> AGGAATA	1790
	TATTCCTC <u>G</u> CCTGTCCA	1791

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thrombosis Arg712Term CGA-TGA	AGTGATGCTGACTATGATTACCAGAACAGACTGGCTGCAGCA TTAGGAATCAGGTCATTCCGAAACTCATCATTGAATCAGGAAG AAGAAGAGTTCAATCTTACTGCCCTAGCTCTGGAGA	1792
	TCTCCAGAGCTAGGGCAGTAAGATTGAACTCTTCTTCTTCCTG ATTCAATGATGAGTTTCGGAATGACCTGATTCCCTAATGCTGCA GCCAGTCTGTTCTGGTAATCATAGTCAGCATCACT	1793
	GGTCATTCCGAAACTCA	1794
	TGAGTTTCGGAATGACC	1795
Thrombosis His1299Arg CAT-CGT	TCAGTCAGACAAACCTTTCCCCAGCCCTCGGTCAGATGCCCA TTTCTCCAGACCTCAGCCATACAACCTTTCTCTAGACTTCAG CCAGACAAACCTCTCTCCAGAACTCAGTCAAACAAA	1796
	TTTGTGTTGACTGAGTTCTGGAGAGAGGTTTGTCTGGCTGAAGT CTAGAGAAAGGGTTGTATGGCTGAGGTCTGGAGAAATGGGCA TCTGACCGAGGGCTGGGGAAGGTTTGTCTGACTGA	1797
	CCTCAGCCATACAACCC	1798
	GGTTGTATGGCTGAGG	1799

EXAMPLE 14

Hemophilia - Factor VIII Deficiency

[0226] The attached table discloses the correcting oligonucleotide base sequences for the Factor VIII oligonucleotides of the invention.

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Table 16

Factor VIII Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia A TyrSCys TAC-TGC	AGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGCGATTCTGCTT TAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAAGTGC ATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCC	1800
	GGCAGCTCACCGAGATCACTTTGCATATAGTCCCATGACAGT TCCACTGCACCCAGGTAGTATCTTCTGGTGGCACTAAAGCAG AATCGCAAAGGCACAGAAAGAAGCAGGTGGAGAGCT	1801
	CAGAAGATACTACCTGG	1802
	CCAGGTAGTATCTTCTG	1803
Haemophilia A Leu7Arg CTG-CGG	CCACCTGCTTCTTTCTGTGCCTTTTGCGATTCTGCTTTAGTGC CACCAGAAGATACTACCTGGGTGCAGTGGAAGTGCATGGGA CTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGA	1804

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCCACAGGCAGCTCACCGAGATCACTTTGCATATAGTCCCAT GACAGTTCCACTGCACCC <u>A</u> GGTAGTATCTTCTGGTGGCACTA AAGCAGAATCGCAAAGGCACAGAAAGAAGCAGGTGG	1805
	ATACTACCTGGGTGCAG	1806
	CTGCACCC <u>A</u> GGTAGTAT	1807
Haemophilia A Ser(-1)Arg AGTg-AGG	AGTCATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTT TTGCGATTCTGCTTTAGIGCCACCAGAAGATACTACCTGGGT GCAGTGGAAGTGTCTATGGGACTATATGCAAAGTGAT	1808
	ATCACTTTGCATATAGTCCCATGACAGTTCCACTGCACCCAGG TAGTATCTTCTGGTGGC <u>A</u> CTAAAGCAGAATCGCAAAGGCAC AGAAAGAAGCAGGTGGAGAGCTCTATTTGCATGACT	1809
	TGCTTTAGT <u>G</u> CCACCAG	1810
	CTGGTGGC <u>A</u> CTAAAGCA	1811
Haemophilia A Arg(-5)Term gCGA-TGA	CATTTGTAGCAATAAGTCATGCAAATAGAGCTCTCCACCTGCT TCTTTCTGTGCCTTTTGC <u>G</u> ATTCTGCTTTAGTGCCACCAGAAG ATACTACCTGGGTGCAGTGGAAGTGTCTATGGGACT	1812
	AGTCCCATGACAGTTCCACTGCACCCAGGTAGTATCTTCTGG TGGCACTAAAGCAGAATC <u>G</u> CAAAGGCACAGAAAGAAGCAG GTGGAGAGCTCTATTTGCATGACTTATTGCTACAAATG	1813
	GCCTTTTGC <u>G</u> ATTCTGC	1814
	GCAGAATC <u>G</u> CAAAGGC	1815

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia A Glu11Val GAA-GTA	TTCTGTGCCTTTTGCATTCTGCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAGGTAAAG	1816
	CTTTACCTTTCGTCCACAGGCAGCTCACCGAGATCACTTTGCATATAGTCCCATGACAGTTCCACTGCACCCAGGTAGTATCTTCTGGTGGCACTAAAGCAGAATCGCAAAAGGCACAGAA	1817
	TGCAGTGGAACTGTCAT	1818
	ATGACAGTTCCACTGCA	1819
Haemophilia A Trp14Gly aTGG-GGG	CTTTTGCATTCTGCTTTAGTGCCACCAGAAGATACTACCTGGTGTCAGTGGAACTGTCAATGGGACTATATGCAAAGTGATCTCGTGAGCTGCCTGTGGACGCAAGGTAAAGGCATGTCC	1820
	GGACATGCCTTTACCTTTCGTCCACAGGCAGCTCACCGAGATCACTTTGCATATAGTCCCATGACAGTTCCACTGCACCCAGGTAGTATCTTCTGGTGGCACTAAAGCAGAATCGCAAAAG	1821
	AACTGTCAATGGGACTAT	1822
	ATAGTCCCATGACAGTT	1823
Haemophilia A Tyr46Term TACa-TAA	TTCACGCAGATTTCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCCGGATCACCTTTTCAACATCGCTAAGCCAAGGCCA	1824
	TGGCCTTGGCTTAGCGATGTTGAAAAGGTGATCCGTGAATTCACAAACAGAGTCTTTTTGTACACGACTGAGGTGTTGAATGGA	1825
	AAAGATTTTGGCACTCTAGGAGGAAATCTGCGTGAA	1826
	GTCGTGTACAAAAAGAC	1827
Haemophilia A Asp56Glu GATc-GAA	ATCTTTTCCATTCAACACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTACGGATCACCTTTTCAACATCGCTAAGCCAA	1828
	GGCCACCCTGGATGGGTAATGAAAACAATGTTGAA	1829
	TTCAACATTGTTTTATTACCCATCCAGGGTGGCCTTGGCTTAGCGATGTTGAAAAGGTGATCCGTGAATTCTACAAACAGAGCTTTTTGTACACGACTGAGGTGTTGAATGGAAAAGAT	1830
	TTCACGGATCACCTTTT	1831
Haemophilia A Gly73Val GGT-GTT	AAAAGGTGATCCGTGAA	1832
	TTCTGGAGTACTATCCCCAAGTAACCTTTGGCGGACATCTCATCTTACAGGTCTGCTAGTTCCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCTTC	1833
	GAAGCCATGTTCTTAAGTGAATGACCACTGTATCATAAACCTCAGCCTGGATGGTAGGACCTAGCAGACCTGTAAGAATGAGATGTCCGCCAAAGGTTACTTGGGGATAGTACTCCAGAA	1834
	TCTGCTAGGTCCTACCA	1835
	TGGTAGGACCTAGCAGA	

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia A Glu79Lys tGAG-AAG	CAAGTAACCTTTGGCGGACATCTCATTCTTACAGGTCTGCTAG GTCCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTAC ACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTC	1836
	GAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAAATGA CCACTGTATCATAAACCTCAGCCTGGATGGTAGGACCTAGCA GACCTGTAAGAATGAGATGTCCGCCAAAGGTTACTTG	1837
	TCCAGGCTGAGGTTTAT	1838
	ATAAACCTCAGCCTGGA	1839
Haemophilia A Val50Asp GTT-GAT	TAACCTTTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCC TACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACACTT AAGAACATGGCTTCCCATCCTGTCAGTCTTCATGC	1840
	GCATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAA ATGACCACTGTATCATAAACCTCAGCCTGGATGGTAGGACCT AGCAGACCTGTAAGAATGAGATGTCCGCCAAAGGTTA	1841
	GGCTGAGGTTTATGATA	1842
	TATCATAAACCTCAGCC	1843
Haemophilia A Asp82Val GAT-GTT	TTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCCCTACCAT CCAGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAA CATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG	1844
	CCAACAGCATGAAGACTGACAGGATGGGAAGCCATGTTCTTA AGTGTAATGACCACTGTATCATAAACCTCAGCCTGGATGGTA GGACCTAGCAGACCTGTAAGAATGAGATGTCCGCCAA	1845
	GGTTTATGATACAGTGG	1846
	CCACTGTATCATAAACCC	1847
Haemophilia A Asp82Gly GAT-GGT	TTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCCCTACCAT CCAGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAA CATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG	1848
	CCAACAGCATGAAGACTGACAGGATGGGAAGCCATGTTCTTA AGTGTAATGACCACTGTATCATAAACCTCAGCCTGGATGGTA GGACCTAGCAGACCTGTAAGAATGAGATGTCCGCCAA	1849
	GGTTTATGATACAGTGG	1850
	CCACTGTATCATAAACCC	1851
Haemophilia A Val85Asp GTC-GAC	ATCTCATTCTTACAGGTCTGCTAGGTCCCTACCATCCAGGCTGA GGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCTTCC CATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTA	1852
	TAGGATACACCAACAGCATGAAGACTGACAGGATGGGAAGCC ATGTTCTTAAGTGTAAATGACCACTGTATCATAAACCTCAGCCT GGATGGTAGGACCTAGCAGACCTGTAAGAATGAGAT	1853
	TACAGTGGTCATTACAC	1854
	GTGTAATGACCACTGTA	1855
Haemophilia A Lys89Thr AAG-ACG	CAGGTCTGCTAGGTCCCTACCATCCAGGCTGAGGTTTATGATA CAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAG TCTTCATGCTGTTGGTGTATCCTACTGGAAAGCTTC	1856

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAAGCTTTCCAGTAGGATACACCAACAGCATGAAGACTGACA GGATGGGAAGCCATGTTCTTAAGTGTAAATGACCACTGTATCAT AAACCTCAGCCTGGATGGTAGGACCTAGCAGACCTG	1857
	TACACTTAAGAACATGG	1858
	CCATGTTCTTAAGTGTAA	1859
Haemophilia A Met91Val cATG-GTG	CTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATACAGTG GTCATTACACTTAAGAACAATGGCTTCCCATCCTGTCAGTCTTC ATGCTGTTGGTGTATCCTACTGGAAAGCTTCTGAGG	1860
	CCTCAGAAGCTTTCCAGTAGGATACACCAACAGCATGAAGAC TGACAGGATGGGAAGCCATGTTCTTAAGTGTAAATGACCACTG TATCATAAACCTCAGCCTGGATGGTAGGACCTAGCAG	1861
	TTAAGAACAATGGCTTCC	1862
	GGAAGCCATGTTCTTAA	1863
Haemophilia A His94Arg CAT-CGT	CTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACACT TAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGGT GTATCCTACTGGAAAGCTTCTGAGGGTGAGTAAAA	1864
	TTTTACTCACCTCAGAAGCTTTCCAGTAGGATACACCAACAG CATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAA TGACCACTGTATCATAAACCTCAGCCTGGATGGTAG	1865
	GGCTTCCCATCCTGTCA	1866
	TGACAGGATGGGAAGCC	1867
Haemophilia A His94Tyr cCAT-TAT	CCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACAC TTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG TGTATCCTACTGGAAAGCTTCTGAGGGTGAGTAAA	1868
	TTTACTCACCTCAGAAGCTTTCCAGTAGGATACACCAACAGC ATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAA GACCACTGTATCATAAACCTCAGCCTGGATGGTAGG	1869
	TGGCTTCCCATCCTGTC	1870
	GACAGGATGGGAAGCCA	1871
Haemophilia A Leu98Arg CTT-CGT	CTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGC TTCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGG AAAGCTTCTGAGGGTGAGTAAAATACCCTCCTATT	1872
	AATAGGAGGGTATTTTACTCACCTCAGAAGCTTTCCAGTAG GATACACCAACAGCATGAAGACTGACAGGATGGGAAGCCAT GTTCTTAAGTGTAAATGACCACTGTATCATAAACCTCAG	1873
	TGTCAGTCTTCATGCTG	1874
	CAGCATGAAGACTGACA	1875
Haemophilia A Gly102Ser tGGT-AGT	GATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTG TCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCTTCTGA GGGTGAGTAAAATACCCTCCTATTGTCCTGTCATT	1876
	AATGACAGGACAATAGGAGGGTATTTTACTCACCTCAGAAG CTTTCCAGTAGGATACACCAACAGCATGAAGACTGACAGGAT GGGAAGCCATGTTCTTAAGTGTAAATGACCACTGTATC	1877

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGCTGTTGGTGTATCC	1878
	GGATACACCAACAGCAT	1879
Haemophilia A Glu113Asp GAA-T-GAC	CTTTGAGTGTACAGTGGATATAGAAAGGACAATTTTATTTCTT CCTGCTATAGGAGCTGAATATGATGATCAGACCAGTCAAAGG GAGAAAGAAGATGATAAAGTCTTCCCTGGTGGAAAGC	1880
	GCTTCCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTTGA CTGGTCTGATCATCATATTCAGCTCCTATAGCAGGAAGAAATA AAATTGTCCTTTCTATATCCACTGTACACTCAAAG	1881
	GGAGCTGAATATGATGA	1882
	TCATCATATTCAGCTCC	1883
Haemophilia A Tyr114Cys TAT-TGT	TTGAGTGTACAGTGGATATAGAAAGGACAATTTTATTTCTTCC TGCTATAGGAGCTGAATATGATGATCAGACCAGTCAAAGGGA GAAAGAAGATGATAAAGTCTTCCCTGGTGGAAAGCCA	1884
	TGGCTTCCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTT GACTGGTCTGATCATCATATTCAGCTCCTATAGCAGGAAGAAA TAAATTGTCCTTTCTATATCCACTGTACACTCAA	1885
	AGCTGAATATGATGATC	1886
	GATCATCATATTCAGCT	1887
Haemophilia A Asp116Gly GAT-GGT	GTACAGTGGATATAGAAAGGACAATTTTATTTCTTCCCTGCTAT AGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAGA AGATGATAAAGTCTTCCCTGGTGGAAAGCCATACATA	1888
	TATGTATGGCTTCCACCAGGGAAGACTTTATCATCTTCTTTCT CCCTTTGACTGGTCTGATCATCATATTCAGCTCCTATAGCAGG AAGAAATAAAATTGTCCTTTCTATATCCACTGTAC	1889
	ATATGATGATCAGACCA	1890
	TGGTCTGATCATCATAT	1891
Haemophilia A Gln 117Term tCAG-TAG	ACAGTGGATATAGAAAGGACAATTTTATTTCTTCCCTGCTATAG GAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAGAAG ATGATAAAGTCTTCCCTGGTGGAAAGCCATACATATG	1892
	CATATGTATGGCTTCCACCAGGGAAGACTTTATCATCTTCTTT CTCCCTTTGACTGGTCTGATCATCATATTCAGCTCCTATAGCA GGAAGAAATAAAATTGTCCTTTCTATATCCACTGT	1893
	ATGATGATCAGACCAGT	1894
	ACTGGTCTGATCATCAT	1895
Haemophilia A Thr118Ile ACC-ATC	TGGATATAGAAAGGACAATTTTATTTCTTCCCTGCTATAGGAGC TGAATATGATGATCAGACCAGTCAAAGGGAGAAAGAAGATGA TAAAGTCTTCCCTGGTGGAAAGCCATACATATGTCTG	1896
	CAGACATATGTATGGCTTCCACCAGGGAAGACTTTATCATCTT CTTTCTCCCTTTGACTGGTCTGATCATCATATTCAGCTCCTATA GCAGGAAGAAATAAAATTGTCCTTTCTATATCCA	1897
	TGATCAGACCAGTCAAA	1898
	TTTGACTGGTCTGATCA	1899

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia A Glu122Term gGAG-TAG	AGGACAATTTTATTTCTTCCTGCTATAGGAGCTGAATATGATG ATCAGACCAGTCAAAGGGAGAGAAAGAAGATGATAAAGTCTTCC CTGGTGGAAGCCATACATATGTCTGGCAGGTCCTGA	1900
	TCAGGACCTGCCAGACATATGTATGGCTTCCACCAGGGAAGA CTTTATCATCTTCTTTCTCCCTTTGACTGGTCTGATCATCATAT TCAGCTCCTATAGCAGGAAGAAATAAAATTGTCCT	1901
	GTCAAAGGGAGAGAAAGAA	1902
	TTCTTTCTCCCTTTGAC	1903
Haemophilia A Asp126His tGAT-CAT	TTTCTTCCTGCTATAGGAGCTGAATATGATGATCAGACCAGTC AAAGGGAGAGAAAGAAGATGATAAAGTCTTCCCTGGTGGAAGCC ATACATATGTCTGGCAGGTCCTGMAGAGAATGGTC	1904
	GACCATTTCTTTTCAGGACCTGCCAGACATATGTATGGCTTCC ACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTTGACTGGTC TGATCATCATATTCAGCTCCTATAGCAGGAAGAAA	1905
	AAGAAGATGATAAAGTC	1906
	GACTTTATCATCTTCTT	1907
Haemophilia A Gln139Term gCAG-TAG	AGTCAAAGGGAGAGAAAGAAGATGATAAAGTCTTCCCTGGTGGA AGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCA ATGGCCTCTGACCCACTGTGCCTTACCTACTCATATC	1908
	GATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTGGA CCATTCTCTTTTCAGGACCTGCCAGACATATGTATGGCTTCCAC CAGGGAAGACTTTATCATCTTCTTTCTCCCTTTGACT	1909
	ATGTCTGGCAGGTCCTG	1910
	CAGGACCTGCCAGACAT	1911
Haemophilia A Val140Ala GTC-GCC	AAAGGGAGAGAAAGAAGATGATAAAGTCTTCCCTGGTGGAAGCC ATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGG CCTCTGACCCACTGTGCCTTACCTACTCATATCTTTTC	1912
	GAAAGATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATT GGACCATTCTCTTTTCAGGACCTGCCAGACATATGTATGGCTT CCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTT	1913
	CTGGCAGGTCCTGAAAG	1914
	CTTTCAGGACCTGCCAG	1915
Haemophilia A Asn144Lys AATg-AAA	AGATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTG GCAGGTCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACT GTGCCTTACCTACTCATATCTTTCTCATGTGGACCTG	1916
	CAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGTGG GTCAGAGGCCATTGGACCAATTCTCTTTTCAGGACCTGCCAGAC ATATGTATGGCTTCCACCAGGGAAGACTTTATCATCT	1917
	AAAGAGAATGGTCCAAT	1918
	ATTGGACCAATTCTCTTT	1919
Haemophilia AG Gly145Asp GGT-GAT	ATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGC AGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGT GCCTTACCTACTCATATCTTTCTCATGTGGACCTGGT	1920

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGT GGGTCAGAGGCCATTGGA <u>C</u> CATTCTCTTTTCAGGACCTGCCAG ACATATGTATGGCTTCCACCAGGGAAGACTTTATCAT	1921
	AGAGAATGGTCCAATGG	1922
	CCATTGGAC <u>C</u> CATTCTCT	1923
Haemophilia A Gly145Val GGT-GTT	ATGATAAAGTCTTCCCTGGTGGGAAGCCATACATATGTCTGGC AGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGT GCCTTACCTACTCATATCTTTCTCATGTGGACCTGGT	1924
	ACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGT GGGTCAGAGGCCATTGGA <u>C</u> CATTCTCTTTTCAGGACCTGCCAG ACATATGTATGGCTTCCACCAGGGAAGACTTTATCAT	1925
	AGAGAATGGTCCAATGG	1926
	CCATTGGAC <u>C</u> CATTCTCT	1927
Haemophilia A Pro146Ser tCCA-TCA	GATAAAGTCTTCCCTGGTGGGAAGCCATACATATGTCTGGCAG GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGC CTTACCTACTCATATCTTTCTCATGTGGACCTGGTAA	1928
	TTACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACA GTGGGTCAGAGGCCATTGG <u>G</u> ACCATTCTCTTTTCAGGACCTGCC AGACATATGTATGGCTTCCACCAGGGAAGACTTTATC	1929
	AGAATGGTCCAATGGCC	1930
	GGCCATTGG <u>G</u> ACCATTCT	1931
Haemophilia A Cys153Trp TGCc-TGG	CCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAAT GGCCTCTGACCCACTGTGC <u>C</u> CTTACCTACTCATATCTTTCTCAT GTGGACCTGGTAAAGACTTGAATTCAGGCCTCATT	1932
	AATGAGGCCTGAATTCAGTCTTTTACCAGGTCCACATGAGAA AGATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTGG ACCATTCTCTTTTCAGGACCTGCCAGACATATGTATGG	1933
	CCACTGTGCCTTACCTA	1934
	TAGGTAAGGCACAGTGG	1935
Haemophilia A Tyr156Term TACT-TAA	TGTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGA CCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTG GTAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTA	1936
	TAGGGCTCCAATGAGGCCTGAATTCAGTCTTTTACCAGGTC CACATGAGAAAGATATGA <u>G</u> TAGGTAAGGCACAGTGGGTCAGA GGCCATTGGACCATTCTCTTTTCAGGACCTGCCAGACA	1937
	CTTACCTACTCATATCT	1938
	AGATATGAGTAGGTAAG	1939
Haemophilia A Ser157Pro cTCA-CCA	GTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGAC CCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTGG TAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTAC	1940
	GTAGGGCTCCAATGAGGCCTGAATTCAGTCTTTTACCAGGT CCACATGAGAAAGATATGA <u>G</u> TAGGTAAGGCACAGTGGGTCAG AGGCCATTGGACCATTCTCTTTTCAGGACCTGCCAGAC	1941

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTACCTACTCATATCTT	1942
	AAGATATGAGTAGGTAA	1943
Haemophilia A Ser160Pro TCT-CCT	GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTACTAGTATGTA	1944
	TACATACTAGTAGGGCTCCAATGAGGCCTGAATTCAGTCTTTTACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTGGACCATTCTCTTTCAGGAC	1945
	CATATCTTTCTCATGTG	1946
	CACATGAGAAAGATATG	1947
Haemophilia A Val162Met GTG-ATG	AAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTACTAGTATGTAGAGAAG	1948
	CTTCTCTACATACTAGTAGGGCTCCAATGAGGCCTGAATTCAGTCTTTTACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTGGACCATTCTCTTT	1949
	TTTCTCATGTGGACCTG	1950
	CAGGTCCACATGAGAAA	1951
Haemophilia A Lys166Thr AAA-ACA	CAATGGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTGGTAAAGACTTGAATTCAGGCCTCATTGGAGCCCTACTAGTATGTAGAGAAGGTAAGTGTATGAA	1952
	TTCATACACTTACCTTCTCTACATACTAGTAGGGCTCCAATGAGGCCTGAATTCAGTCTTTTACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTG	1953
	CCTGGTAAAGACTTGA	1954
	TCAAGTCTTTTACCAGG	1955
Haemophilia A Ser170Leu TCA-TTA	ACCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTACTAGTATGTAGAGAAGGTAAGTGTATGAAAGCGTAGGATTG	1956
	CAATCCTACGCTTTCATACACTTACCTTCTCTACATACTAGTAGGGCTCCAATGAGGCCTGAATTCAGTCTTTTACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGTGGGT	1957
	CTTGAATTCAGGCCTCA	1958
	TGAGGCCTGAATTCAG	1959
Haemophilia A Phe195Val aTTT-GTT	AATGTTCTCACTTCTTTTTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCTTGCACAAATTATACTACTTTTTGCTGTATTTGATGAAGGTTAGTGAGTCTTAATCTGAATTTTGGATT	1960
	AATCCAAAATTGAGTTAAGACTCACTAACCTTCATCAAATACAGCAAAAAGTAGTATAAATTTGTGCAAGGTCTGTGTCTTTTCTTGGCCAGACTCCCTGAAAAAGAAGTGAGAACATT	1961
	TGCACAAATTTATACTA	1962
	TAGTATAAATTTGTGCA	1963

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia A Leu198His CTT-CAT	CTTCTTTTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCT TGCACAAATTTATACTACTTTTGGCTGTATTTGATGAAGGTTAG TGAGTCTTAATCTGAATTTTGGATTCCCTGAAAGAA	1964
	TTCTTTTCAGGAATCCAAAATTCAGATTAAGACTCACTAACCTTC ATCAAATACAGCAAAAAGTAGTATAAATTTGTGCAAGGTCTGT GTCTTTTCCTTGGCCAGACTCCCTGAAAAAGAAG	1965
	TATACTACTTTTGGCTG	1966
	CAGCAAAAAGTAGTATA	1967
Haemophilia A Ala200Asp GCT-GAT	TTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCTTGCACA AATTTATACTACTTTTTGCTGTATTTGATGAAGGTTAGTGAGTC TTAATCTGAATTTTGGATTCCCTGAAAGAAATCCTC	1968
	GAGGATTTCTTTTCAGGAATCCAAAATTCAGATTAAGACTCACT AACCTTCATCAAATACAGCAAAAAGTAGTATAAATTTGTGCAA GGTCTGTGTCTTTTCCTTGGCCAGACTCCCTGAAA	1969
	ACTTTTTGCTGTATTTG	1970
	CAAATACAGCAAAAAGT	1971
Haemophilia A Ala200Thr tGCT-ACT	TTTTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCTTGCAC AAATTTATACTACTTTTTGCTGTATTTGATGAAGGTTAGTGAGT CTTAATCTGAATTTTGGATTCCCTGAAAGAAATCCT	1972
	AGGATTTCTTTTCAGGAATCCAAAATTCAGATTAAGACTCACTA ACCTTCATCAAATACAGCAAAAAGTAGTATAAATTTGTGCAAG GTCTGTGTCTTTTCCTTGGCCAGACTCCCTGAAAA	1973
	TACTTTTTGCTGTATTT	1974
	AAATACAGCAAAAAGTA	1975
Haemophilia A Val234Phe aGTC-TTC	AACTCCTTGATGCAGGATAGGGATGCTGCATCTGCTCGGGCC TGGCCTAAAATGCACACAGTCAATGGTTATGTAAACAGGTCTC TGCCAGGTATGTACACACCTGCTCAACAATCCTCAG	1976
	CTGAGGATTGTTGAGCAGGTGTGTACATACCTGGCAGAGACC TGTTTACATAACCATGACTGTGTGCATTTTAGGCCAGGCCCG AGCAGATGCAGCATCCCTATCCTGCATCAAGGAGTT	1977
	TGCACACAGTCAATGGT	1978
	ACCATTGACTGTGTGCA	1979
Haemophilia A Gly247Glu GGA-GAA	ATTTTCAGATTCTCTACTTCATAGCCATAGGTGTCTTATTCCTAC TTTACAGGTCTGATTGGATGCCACAGGAAATCAGTCTATTGG CATGTGATTGGAATGGGCACCACTCCTGAAGTGCA	1980
	TGCACTTCAGGAGTGGTGCCCATTCGAATCACATGCCAATAG ACTGATTTCTGTGGCATCCAATCAGACCTGTAAAGTAGGAAT AAGACACCTATGGCTATGAAGTAGAGAATCTGAAAT	1981
	TCTGATTGGATGCCACA	1982
	TGTGGCATCCAATCAGA	1983
Haemophilia A Trp255Cys TGGc-TGT	ATAGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCAC AGGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACT CCTGAAGTGCACTCAATATTCCTCGAAGGTCACACA	1984

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGTGTGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGGT GCCCATTCCAATCACATGCCAATAGACTGATTTCTGTGGCAT CCAATCAGACCTGTAAAGTAGGAATAAGACACCTAT	1985
	GTCTATTGGCATGTGAT	1986
	ATCACATGCCAATAGAC	1987
Haemophilia A Trp255Term TGGc-TGA	ATAGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCAC AGGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACT CCTGAAGTGCACTCAATATTCCTCGAAGGTCACACA	1988
	TGTGTGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGGT GCCCATTCCAATCACATGCCAATAGACTGATTTCTGTGGCAT CCAATCAGACCTGTAAAGTAGGAATAAGACACCTAT	1989
	GTCTATTGGCATGTGAT	1990
	ATCACATGCCAATAGAC	1991
Haemophilia A His256Leu CAT-CTT	AGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCACAG GAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCC TGAAGTGCACTCAATATTCCTCGAAGGTCACACATT	1992
	AATGTGTGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTG GTGCCCATTCCAATCACATGCCAATAGACTGATTTCTGTGGC ATCCAATCAGACCTGTAAAGTAGGAATAAGACACCT	1993
	CTATTGGCATGTGATTG	1994
	CAATCACATGCCAATAG	1995
Haemophilia A Gly259Arg tGGA-AGA	TATTCCTACTTTACAGGTCTGATTGGATGCCACAGGAAATCAG TCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAAGTGC ACTCAATATTCCTCGAAGGTCACACATTTCTTGTGA	1996
	TCACAAGAAATGTGTGACCTTCGAGGAATATTGAGTGCACTTC AGGAGTGGTGCCCATTCGAATCACATGCCAATAGACTGATT CCTGTGGCATCCAATCAGACCTGTAAAGTAGGAATA	1997
	ATGTGATTGGAATGGGC	1998
	GCCCATTCCAATCACAT	1999
Haemophilia A Val266Gly GTG-GGG	TTGGATGCCACAGGAAATCAGTCTATTGGCATGTGATTGGAA TGGGCACCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTC ACACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTT	2000
	AAGGACGCCTGGCGATGGTTCCTCACAAGAAATGTGTGACCT TCGAGGAATATTGAGTGCACTTCAGGAGTGGTGCCCATTC ATCACATGCCAATAGACTGATTTCTGTGGCATCCAA	2001
	TCCTGAAGTGCACTCAA	2002
	TTGAGTGCACTTCAGGA	2003
Haemophilia A Glu272Gly GAA-GGA	CAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAAG TGCACTCAATATTCCTCGAAGGTCACACATTTCTTGTGAGGAA CCATCGCCAGGCGTCCTTGGAATCTCGCCAATAAC	2004
	GTTATTGGCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTC ACAAGAAATGTGTGACCTTCGAGGAATATTGAGTGCACTTCA GGAGTGGTGCCCATTCGAATCACATGCCAATAGACTG	2005
	ATTCCTCGAAGGTCACA	2006

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGTGACCTTCGAGGAAT	2007
Haemophilia A Glu272Lys cGAA-AAA	TCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA GTGCACTCAATATTCCTC <u>G</u> AAGGTCACACATTTCTTGTGAGGA ACCATCGCCAGGCGTCCTTGGAATCTCGCCAATAA	2008
	TTATTGGCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTCA CAAGAAATGTGTGACCTTC <u>G</u> GAGGAATATTGAGTGCACCTTCAG GAGTGGTGCCCATTCGAATCACATGCCAATAGACTGA	2009
	TATTCCTC <u>G</u> AAGGTCAC	2010
	GTGACCTTCGAGGAATA	2011
Haemophilia A Thr275Ile ACA-ATA	GGCATGTGATTGGAATGGGCACCACTCCTGAAGTGCACCTCAA TATTCCTCGAAGGTCACA <u>C</u> ATTTCTTGTGAGGAACCATCGCCA GGCGTCCTTGGAATCTCGCCAATAACTTTTCCTTAC	2012
	GTAAGGAAAGTTATTGGCGAGATTTCCAAGGACGCCTGGCGA TGGTTCCTCACAAGAAAT <u>G</u> TGTGACCTTCGAGGAATATTGAGT GCACTTCAGGAGTGGTGCCCATTCGAATCACATGCC	2013
	AGGTCACA <u>C</u> ATTTCTTG	2014
	CAAGAAAT <u>G</u> TGTGACCT	2015
Haemophilia A Val278Ala GTG-GCG	TTGGAATGGGCACCACTCCTGAAGTGCACCTCAATATTCCTCG AAGGTCACACATTTCTT <u>G</u> TGAGGAACCATCGCCAGGCGTCCT TGGAATCTCGCCAATAACTTTCTTACTGCTCAAAC	2016
	GTTTGAGCAGTAAGGAAAGTTATTGGCGAGATTTCCAAGGAC GCCTGGCGATGGTTCCTC <u>A</u> CAAGAAATGTGTGACCTTCGAGG AATATTGAGTGCACCTCAGGAGTGGTGCCCATTCGAA	2017
	ATTTCTTG <u>T</u> GAGGAACC	2018
	GGTTCCTC <u>A</u> CAAGAAAT	2019
Haemophilia A Asn280Ile AAC-ATC	TGGGCACCACTCCTGAAGTGCACCTCAATATTCCTCGAAGGTC ACACATTTCTTGTGAGGA <u>A</u> CCATCGCCAGGCGTCCTTGGA TCTCGCCAATAACTTTCTTACTGCTCAAACACTCTT	2020
	AAGAGTGTGAGCAGTAAGGAAAGTTATTGGCGAGATTTCC AAGGACGCCTGGCGATGGTTCCTCACAAGAAATGTGTGACCT TCGAGGAATATTGAGTGCACCTCAGGAGTGGTGCCCA	2021
	TGTGAGGA <u>A</u> CCATCGCC	2022
	GGCGATGGTTCCTCACA	2023
Haemophilia A Arg282Cys tCGC-TGC	ACCACTCCTGAAGTGCACCTCAATATTCCTCGAAGGTCACACAT TTCTTGTGAGGAACCATC <u>G</u> CCAGGCGTCCTTGGAATCTCGC CAATAACTTTCTTACTGCTCAAACACTCTTGATGG	2024
	CCATCAAGAGTGTGAGCAGTAAGGAAAGTTATTGGCGAGA TTTCCAAGGACGCCTGGC <u>G</u> ATGGTTCCTCACAAGAAATGTGT GACCTTCGAGGAATATTGAGTGCACCTCAGGAGTGGT	2025
	GGAACCATC <u>G</u> CCAGGCG	2026
	CGCCTGGC <u>G</u> ATGGTTC	2027

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia A Arg282His CGC-CAC	CCACTCCTGAAGTGCACCTCAATATTCCTCGAAGGTCACACATT TCTTGTGAGGAACCATC <u>G</u> CCAGGCGTCCTTGAAATCTCGCC AATAACTTTCTTACTGCTCAAACACTCTTGATGGA	2028
	TCCATCAAGAGTGTGTTGAGCAGTAAGGAAAGTTATTGGCGAG ATTTCCAAGGACGCCTGG <u>C</u> GATGGTTCCTCACAAGAAATGTG TGACCTTCGAGGAATATTGAGTGCACCTTCAGGAGTGG	2029
	GAACCATC <u>G</u> CCAGGCGT	2030
	ACGCCTGG <u>C</u> GATGGTTC	2031
Haemophilia A Arg282Leu CGC-CTC	CCACTCCTGAAGTGCACCTCAATATTCCTCGAAGGTCACACATT TCTTGTGAGGAACCATC <u>G</u> CCAGGCGTCCTTGAAATCTCGCC AATAACTTTCTTACTGCTCAAACACTCTTGATGGA	2032
	TCCATCAAGAGTGTGTTGAGCAGTAAGGAAAGTTATTGGCGAG ATTTCCAAGGACGCCTGG <u>C</u> GATGGTTCCTCACAAGAAATGTG TGACCTTCGAGGAATATTGAGTGCACCTTCAGGAGTGG	2033
	GAACCATC <u>G</u> CCAGGCGT	2034
	ACGCCTGG <u>C</u> GATGGTTC	2035
Haemophilia A Ala284Glu GCG-GAG	CTGAAGTGCACCTCAATATTCCTCGAAGGTCACACATTTCTTGT GAGGAACCATCGCCAGG <u>G</u> CGTCCTTGAAATCTCGCCAATAAC TTTCCTTACTGCTCAAACACTCTTGATGGACCTTG	2036
	CCAAGGTCCATCAAGAGTGTGTTGAGCAGTAAGGAAAGTTATT GGCGAGATTTCCAAGGAC <u>G</u> CCTGGCGATGGTTCCTCACAAG AAATGTGTGACCTTCGAGGAATATTGAGTGCACCTTCAG	2037
	TCGCCAGG <u>G</u> CGTCCTTG	2038
	CCAAGGAC <u>G</u> CCTGGCGA	2039
Haemophilia A Ala284Pro gGCG-CCG	CCTGAAGTGCACCTCAATATTCCTCGAAGGTCACACATTTCTTG TGAGGAACCATCGCCAG <u>G</u> CGTCCTTGAAATCTCGCCAATAA CTTTCCTTACTGCTCAAACACTCTTGATGGACCTTG	2040
	CAAGGTCCATCAAGAGTGTGTTGAGCAGTAAGGAAAGTTATTG GCGAGATTTCCAAGGAC <u>G</u> CCTGGCGATGGTTCCTCACAAGAA ATGTGTGACCTTCGAGGAATATTGAGTGCACCTTCAGG	2041
	ATCGCCAG <u>G</u> CGTCCTTG	2042
	CAAGGAC <u>G</u> CCTGGCGAT	2043
Haemophilia A Ser289Leu TCG-TTG	TATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCATCGCCA GGCGTCCTTGAAATCT <u>C</u> GCCAATAACTTTCTTACTGCTCAA ACACTCTTGATGGACCTTGACAGTTTCTACTGTT	2044
	AACAGTAGAACTGTCCAAGGTCCATCAAGAGTGTGTTGAGCA GTAAGGAAAGTTATTGGC <u>G</u> AGATTTCCAAGGACGCCTGGCGA TGGTTCCTCACAAGAAATGTGTGACCTTCGAGGAATA	2045
	GGAAATCT <u>C</u> GCCAATAA	2046
	TTATTGGC <u>G</u> AGATTTCC	2047
Haemophilia A Phe293Ser TTC-TCC	GTCACACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTG AAATCTCGCCAATAACTT <u>T</u> CCTTACTGCTCAAACACTCTTGAT GGACCTTGACAGTTTCTACTGTTTTGTCATATCTC	2048

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAGATATGACAAAACAGTAGAACTGTCCAAGGTCCATCAAG AGTGTTTGAGCAGTAAGGA <u>A</u> AGTTATTGGCGAGATTTCCTCAAG GACGCCTGGCGATGGTTCTCACAAGAAATGTGTGAC	2049
	AATAACTTTCCTTACTG	2050
	CAGTAAGGA <u>A</u> AGTTATT	2051
Haemophilia A Thr295Ala tACT-GCT	ACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATC TCGCCAATAACTTTCCTT <u>A</u> CTGCTCAAACACTCTTGATGGACC TTGGACAGTTTCTACTGTTTTGTCATATCTCTTCCC	2052
	GGGAAGAGATATGACAAAACAGTAGAACTGTCCAAGGTCCA TCAAGAGTGTTTGAGCAGT <u>A</u> AGGAAAGTTATTGGCGAGATT CCAAGGACGCCTGGCGATGGTTCTCACAAGAAATGT	2053
	CTTTCCTT <u>A</u> CTGCTCAA	2054
	TTGAGCAGT <u>A</u> AGGAAAG	2055
Haemophilia A Thr295Ile ACT-ATT	CATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATCT CGCCAATAACTTTCCTT <u>A</u> CTGCTCAAACACTCTTGATGGACCT TGGACAGTTTCTACTGTTTTGTCATATCTCTTCCCA	2056
	TGGGAAGAGATATGACAAAACAGTAGAACTGTCCAAGGTCC ATCAAGAGTGTTTGAGCAGT <u>G</u> AAGGAAAGTTATTGGCGAGATT CCAAGGACGCCTGGCGATGGTTCTCACAAGAAATG	2057
	TTTCCTT <u>A</u> CTGCTCAA	2058
	TTTGAGCAGT <u>G</u> AAGGAAA	2059
Haemophilia A Ala296Val GCT-GTT	TTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATCTCGC CAATAACTTTCCTTACTG <u>C</u> TCAAACACTCTTGATGGACCTTGG ACAGTTTCTACTGTTTTGTCATATCTCTTCCCACCA	2060
	TGGTGGGAAGAGATATGACAAAACAGTAGAACTGTCCAAGG TCCATCAAGAGTGTTTGAGCAGT <u>A</u> AGGAAAGTTATTGGCGAG ATTCCAAGGACGCCTGGCGATGGTTCTCACAAGAA	2061
	CCTTACTG <u>C</u> TCAAACAC	2062
	GTGTTTGAGCAGT <u>A</u> AGG	2063
Haemophilia A Leu308Pro CTG-CCG	TCTCGCCAATAACTTTCCTTACTGCTCAAACACTCTTGATGGA CCTTGGACAGTTTCTACTGTTTTGTCATATCTCTTCCCACCA CATGGTAATATCTTGATCTTTAAATGAATATTA	2064
	TAATATTCATTTTAAAGATCCAAGATATTACCATGTTGGTGGG AAGAGATATGACAAAAC <u>A</u> GTAGAACTGTCCAAGGTCCATCA AGAGTGTTTGAGCAGT <u>A</u> AGGAAAGTTATTGGCGAGA	2065
	GTTTCTACTGTTTTGTC	2066
	GACAAAAC <u>A</u> GTAGAAAC	2067
Haemophilia A Glu321Lys gGAA-AAA	ACAGCCTAATATAGCAAGACACTCTGACATTGTTTGGTTTGTG TGACTCCAGATGGCATG <u>G</u> AAGCTTATGTCAAAGTAGACAGCT GTCCAGAGGAACCCCACTACGAATGAAAAATAATG	2068
	CATTATTTTTCATTTCGTAGTTGGGGTTCTCTGGACAGCTGTC TACTTTGACATAAGCTT <u>C</u> CATGCCATCTGGAGTCAGACAAACC AAACAATGTCAGAGTGTCTTGCTATATTAGGCTGT	2069
	ATGGCATG <u>G</u> AAGCTTAT	2070

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATAAGCTT <u>C</u> CATGCCAT	2071
Haemophilia A Tyr323Term TATg-TAA	ATATAGCAAGACACTCTGACATTGTTTGGTTTGTCTGACTCCA GATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGTCCAGAG GAACCCCAACTACGAATGAAAAATAATGAAGAAGCG	2072
	CGCTTCTTCATTATTTTTCATTTCGTAGTTGGGGTTCCTCTGGA CAGCTGTCTACTTTGACATAAGCTTCCATGCCATCTGGAGTCA GACAAACCAACAATGTCAGAGTGTCTTGCTATAT	2073
	GAAGCTTATGTCAAAGT	2074
	ACTTTGACATAAGCTTC	2075
Haemophilia A Val326Leu aGTA-CTA	AAGACACTCTGACATTGTTTGGTTTGTCTGACTCCAGATGGCA TGGAAGCTTATGTCAAAGTAGACAGCTGTCCAGAGGAACCCC AACTACGAATGAAAAATAATGAAGAAGCGGAAGACT	2076
	AGTCTTCCGCTTCTTCATTATTTTTCATTTCGTAGTTGGGGTTC TCTGGACAGCTGTCTACTTTGACATAAGCTTCCATGCCATCTG GAGTCAGACAAACCAACAATGTCAGAGTGTCTT	2077
	ATGTCAAAGTAGACAGC	2078
	GCTGTCTACTTTGACAT	2079
Haemophilia A Cys329Arg cTGT-CGT	TGACATTGTTTGGTTTGTCTGACTCCAGATGGCATGGAAGCTT ATGTCAAAGTAGACAGCTGTCCAGAGGAACCCCAACTACGAA TGAAAAATAATGAAGAAGCGGAAGACTATGATGATG	2080
	CATCATCATAGTCTTCCGCTTCTTCATTATTTTTCATTTCGTAGT TGGGGTTCCTCTGGACAGCTGTCTACTTTGACATAAGCTTCC ATGCCATCTGGAGTCAGACAAACCAACAATGTCA	2081
	TAGACAGCIGTCCAGAG	2082
	CTCTGGACAGCTGTCTA	2083
Haemophilia A Cys329Tyr TGT-TAT	GACATTGTTTGGTTTGTCTGACTCCAGATGGCATGGAAGCTTA TGTCAAAGTAGACAGCTGTCCAGAGGAACCCCAACTACGAAT GAAAAATAATGAAGAAGCGGAAGACTATGATGATGA	2084
	TCATCATCATAGTCTTCCGCTTCTTCATTATTTTTCATTTCGTAG TTGGGGTTCCTCTGGACAGCTGTCTACTTTGACATAAGCTTCC ATGCCATCTGGAGTCAGACAAACCAACAATGTC	2085
	AGACAGCTGTCCAGAGG	2086
	CCTCTGGACAGCTGTCT	2087
Haemophilia A Arg336Term aCGA-TGA	ACTCCAGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCG GAAGACTATGATGATGATCTTACTGATTCTGAAATGG	2088
	CCATTTCAGAATCAGTAAGATCATCATCATAGTCTTCCGCTTC TTCATTATTTTTCATTCTGTAGTTGGGGTTCCTCTGGACAGCTG TCTACTTTGACATAAGCTTCCATGCCATCTGGAGT	2089
	CCCAACTACGAATGAAA	2090
	TTTCATTCTGTAGTTGGG	2091
Haemophilia A Arg372Cys tCGC-TGC	GATTCTGAAATGGATGTGGTCAGGTTTGTATGATGACAACTCTC CTTCCTTTATCCAAATTGCTCAGTTGCCAAGAAGCATCCTAA AACTTGGGTACATTACATTGCTGCTGAAGAGGAGG	2092

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGATG CTTCTTGGCAACTGAGC <u>G</u> AATTTGGATAAAGGAAGGAGAGTT GTCATCATCAAACCTGACCACATCCATTTCAGAATC	2093
	TCCAAATT <u>C</u> GCTCAGTT	2094
	AACTGAGC <u>G</u> AATTTGGA	2095
Haemophilia A Arg372His CGC-CAC	ATTCTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCC TTCCTTTATCCAAATTC <u>G</u> CTCAGTTGCCAAGAAGCATCCTAAA ACTTGGGTACATTACATTGCTGCTGAAGAGGAGGA	2096
	TCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGAT GCTTCTTGGCAACTGAG <u>C</u> G AATTTGGATAAAGGAAGGAGAGT TGTCATCATCAAACCTGACCACATCCATTTCAGAAT	2097
	CCAAATTC <u>G</u> CTCAGTTG	2098
	CAACTGAGC <u>G</u> AATTTGG	2099
Haemophilia A Ser373Leu TCA-TTA	CTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTTC CTTTATCCAAATTCGCT <u>C</u> AGTTGCCAAGAAGCATCCTAAAAC TGGGTACATTACATTGCTGCTGAAGAGGAGGACTG	2100
	CAGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAG GATGCTTCTTGGCAACT <u>G</u> AGCGAATTTGGATAAAGGAAGGAG AGTTGTCATCATCAAACCTGACCACATCCATTTCAG	2101
	AATTCGCT <u>C</u> AGTTGCCA	2102
	TGGCAACT <u>G</u> AGCGAATT	2103
Haemophilia A Ser373Pro cTCA-CCA	TCTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTT CCTTTATCCAAATTCGCT <u>C</u> AGTTGCCAAGAAGCATCCTAAAAC TTGGGTACATTACATTGCTGCTGAAGAGGAGGACT	2104
	AGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGG ATGCTTCTTGGCAACT <u>G</u> AGCGAATTTGGATAAAGGAAGGAGA GTTGTCATCATCAAACCTGACCACATCCATTTCAGA	2105
	AAATTCGCT <u>C</u> AGTTGCC	2106
	GGCAACT <u>G</u> AGCGAATT	2107
Haemophilia A Ser373Term TCA-TAA	CTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTTC CTTTATCCAAATTCGCT <u>C</u> AGTTGCCAAGAAGCATCCTAAAAC TGGGTACATTACATTGCTGCTGAAGAGGAGGACTG	2108
	CAGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAG GATGCTTCTTGGCAACT <u>G</u> AGCGAATTTGGATAAAGGAAGGAG AGTTGTCATCATCAAACCTGACCACATCCATTTCAG	2109
	AATTCGCT <u>C</u> AGTTGCCA	2110
	TGGCAACT <u>G</u> AGCGAATT	2111
Haemophilia A Ile386Phe cATT-TTT	CCTTCCTTTATCCAAATTCGCTCAGTTGCCAAGAAGCATCCTA AACTTGGGTACATTAC <u>A</u> TTGCTGCTGAAGAGGAGGACTGGG ACTATGCTCCCTTAGTCCTCGCCCCCGATGACAGGT	2112
	ACCTGTCATCGGGGGCGAGGACTAAGGGAGCATAGTCCCAG TCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGAT GCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAGG	2113
	TACATTAC <u>A</u> TTGCTGCT	2114

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGCAGCAATGTAATGTA	2115
Haemophilia A Ile386Ser ATT-AGT	CTTCCTTTATCCAAATTCGCTCAGTTGCCAAGAAGCATCCTAA AACTTGGGTACATTACATTGCTGCTGAAGAGGAGGACTGGGA CTATGCTCCCTTAGTCCTCGCCCCGATGACAGGTA	2116
	TACCTGTCATCGGGGGCGAGGACTAAGGGAGCATAGTCCCA GTCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGA TGCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAG	2117
	ACATTACATTGCTGCTG	2118
	CAGCAGCAATGTAATGT	2119
Haemophilia A Glu390Gly GAG-GGG	AAATTCGCTCAGTTGCCAAGAAGCATCCTAAAACCTTGGGTACA TTACATTGCTGCTGAAGAGGAGGACTGGGACTATGCTCCCTT AGTCCTCGCCCCGATGACAGGTAAGCACTTTTTGA	2120
	TCAAAAAGTGCTTACCTGTCATCGGGGGCGAGGACTAAGGGA GCATAGTCCCAGTCTCTCTTTCAGCAGCAATGTAATGTACC CAAGTTTTAGGATGCTTCTTGGCAACTGAGCGAATTT	2121
	TGCTGAAGAGGAGGACT	2122
	AGTCCTCTCTTCAGCA	2123
Haemophilia A Trp393Gly cTGG-GGG	TCAGTTGCCAAGAAGCATCCTAAAACCTTGGGTACATTACATTG CTGCTGAAGAGGAGGACTGGGACTATGCTCCCTTAGTCCTCG CCCCCGATGACAGGTAAGCACTTTTTGACTATTGGT	2124
	ACCAATAGTCAAAAAGTGCTTACCTGTCATCGGGGGCGAGGA CTAAGGGAGCATAGTCCCAGTCCTCTCTTCAGCAGCAATGT AATGTACCCAAGTTTTAGGATGCTTCTTGGCAACTGA	2125
	AGGAGGACTGGGACTAT	2126
	ATAGTCCCAGTCCTCT	2127
Haemophilia A Lys408Ile AAA-ATA	GCCTACCTAGAATTTTTCTTCCCAACCTCTCATCTTTTTTCTC TTATACAGAAGTTATAAAGTCAATATTTGAACAATGGCCCTC AGCGGATTGGTAGGAAGTACAAAAAAGTCCGATT	2128
	AATCGGACTTTTTTGTACTTCCTACCAATCCGCTGAGGGCCAT TGTTCAAATATTGACTTTTATAAATTCTGTATAAGAGAAAAAA GATGAGAGGTTGGGAAGAAAAATTCTAGGTAGGC	2129
	AAGTTATAAAGTCAAT	2130
	ATTGACTTTTATAAATT	2131
Haemophilia A Leu412Phe TTGa-TTT	TTTTCTTCCCAACCTCTCATCTTTTTTCTCTTATACAGAAGTT ATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAG GAAGTACAAAAAAGTCCGATTTATGGCATAACACA	2132
	TGTGTATGCCATAAATCGGACTTTTTTGTACTTCCTACCAATC CGCTGAGGGCCATTGTTCAAATATTGACTTTTATAAATTCTGT ATAAGAGAAAAAAGATGAGAGGTTGGGAAGAAAA	2133
	CAATATTTGAACAATGG	2134
	CCATTGTTCAAATATTG	2135

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia A Arg418Trp gCGG-TGG	TCATCTTTTTTCTCTTATACAGAAGTTATAAAAGTCAATATTTG AACAATGGCCCTCAGCGGATTGGTAGGAAGTACAAAAAGTC CGATTTATGGCATAACAGATGAAACCTTTAAGA	2136
	TCTTAAAGGTTTCATCTGTGTATGCCATAAATCGGACTTTTTTG TACTTCCTACCAATCCGCTGAGGGCCATTGTTCAAATATTGAC TTTTATAACTTCTGTATAAGAGAAAAAAGATGA	2137
	GCCCTCAGCGGATTGGT	2138
	ACCAATCCGCTGAGGGC	2139
Haemophilia A Gly420Val GGT-GTT	TTTTCTCTTATACAGAAGTTATAAAAGTCAATATTTGAACAAT GGCCCTCAGCGGATTGGTAGGAAGTACAAAAAGTCCGATTT ATGGCATAACAGATGAAACCTTTAAGACTCGTGA	2140
	TCACGAGTCTTAAAGGTTTCATCTGTGTATGCCATAAATCGGA CTTTTTGTACTTCCTACCAATCCGCTGAGGGCCATTGTTCAA ATATTGACTTTTATAACTTCTGTATAAGAGAAAAA	2141
	GCGGATTGGTAGGAAGT	2142
	ACTTCCTACCAATCCGC	2143
Haemophilia A Lys425Arg AAA-AGA	GAAGTTATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGAT TGGTAGGAAGTACAAAAAGTCCGATTTATGGCATAACAGAG TGAAACCTTTAAGACTCGTGAAGCTATTCAGCATGA	2144
	TCATGCTGAATAGCTTCACGAGTCTTAAAGGTTTCATCTGTGT ATGCCATAAATCGGACTTTTTGTACTTCCTACCAATCCGCTG AGGGCCATTGTTCAAATATTGACTTTTATAACTTC	2145
	GTACAAAAAGTCCGAT	2146
	ATCGGACTTTTTGTAC	2147
Haemophilia A Arg427Term cCGA-TGA	TATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTA GGAAGTACAAAAAGTCCGATTTATGGCATAACAGATGAAA CCTTTAAGACTCGTGAAGCTATTCAGCATGAATCAG	2148
	CTGATTCATGCTGAATAGCTTCACGAGTCTTAAAGGTTTCATC TGTGTATGCCATAAATCGGACTTTTTGTACTTCCTACCAATC CGCTGAGGGCCATTGTTCAAATATTGACTTTTATA	2149
	AAAAAGTCCGATTTATG	2150
	CATAAATCGGACTTTTT	2151
Haemophilia A Tyr431Asn aTAC-AAC	TATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAAA AAAGTCCGATTTATGGCATACACAGATGAAACCTTTAAGACTC GTGAAGCTATTCAGCATGAATCAGGAATCTTGGGAC	2152
	GTCCCAAGATTCCTGATTCATGCTGAATAGCTTCACGAGTCTT AAAGGTTTCATCTGTGTATGCCATAAATCGGACTTTTTGTAC TTCTACCAATCCGCTGAGGGCCATTGTTCAAATA	2153
	TTATGGCATACACAGAT	2154
	ATCTGTGTATGCCATAA	2155
Haemophilia A Thr435Ile ACC-ATC	GCCCTCAGCGGATTGGTAGGAAGTACAAAAAGTCCGATTTA TGGCATAACAGATGAAACCTTTAAGACTCGTGAAGCTATTCA GCATGAATCAGGAATCTTGGGACCTTTACTTTATGG	2156

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTGAATAG CTTCACGAGTCTTAAAGGTTTCATCTGTGTATGCCATAAATCG GACTTTTTTGTACTTCCTACCAATCCGCTGAGGGC	2157
	AGATGAAACCTTTAAGA	2158
	TCTTAAAGGTTTCATCT	2159
Haemophilia A Pro451Leu CCT-CTT	ACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCAGCATGA ATCAGGAATCTTGGGACCTTTACTTTATGGGGAAGTTGGAGA CACACTGTTGGTAAGTTGAAGAAAAGATTTAAGGTC	2160
	GACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGTCTCCAA CTTCCCATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTG AATAGCTTCACGAGTCTTAAAGGTTTCATCTGTGT	2161
	CTTGGGACCTTTACTTT	2162
	AAAGTAAAGGTCCCAAG	2163
Haemophilia A Pro451Thr aCCT-ACT	TACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCAGCATG AATCAGGAATCTTGGGACCTTTACTTTATGGGGAAGTTGGAG ACACACTGTTGGTAAGTTGAAGAAAAGATTTAAGGT	2164
	ACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGTCTCCAACT TCCCATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTGAA TAGCTTCACGAGTCTTAAAGGTTTCATCTGTGTA	2165
	TCTTGGGACCTTTACTT	2166
	AAGTAAAGGTCCCAAGA	2167
Haemophilia A Gly455Arg tGGG-AGG	ACCTTTAAGACTCGTGAAGCTATTCAGCATGAATCAGGAATCT TGGGACCTTTACTTTATGGGGAAGTTGGAGACACACTGTTGG TAAGTTGAAGAAAAGATTTAAGGTCAGGTAAGAAGA	2168
	TCTTCTTACCTGACCTTAAATCTTTTCTTCAACTTACCAACAGT GTGTCTCCAACTTCCCATAAAGTAAAGGTCCCAAGATTCCTG ATTCATGCTGAATAGCTTCACGAGTCTTAAAGGT	2169
	TACTTTATGGGGAAGTT	2170
	AACTTCCCATAAAGTA	2171
Haemophilia A Gly455Glu GGG-GAG	CCTTTAAGACTCGTGAAGCTATTCAGCATGAATCAGGAATCTT GGGACCTTTACTTTATGGGGAAGTTGGAGACACACTGTTGGT AAGTTGAAGAAAAGATTTAAGGTCAGGTAAGAAGAA	2172
	TTCTTCTTACCTGACCTTAAATCTTTTCTTCAACTTACCAACAG TGTGTCTCCAACTTCCCATAAAGTAAAGGTCCCAAGATTCCT GATTCATGCTGAATAGCTTCACGAGTCTTAAAGG	2173
	ACTTTATGGGGAAGTTG	2174
	CAACTTCCCATAAAGT	2175
Haemophilia A Asp459Asn aGAC-AAC	CGTGAAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTA CTTTATGGGGAAGTTGGAGACACACTGTTGGTAAGTTGAAGA AAAGATTTAAGGTCAGGTAAGAAGAAAAGTCTGGAG	2176
	CTCCAGACTTTTTCTTCTTACCTGACCTTAAATCTTTTCTTCAA CTTACCAACAGTGTGTCTCCAACTTCCCATAAAGTAAAGGTC CCAAGATTCCTGATTCATGCTGAATAGCTTCACG	2177
	AAGTTGGAGACACACTG	2178

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAGTGTGTCTCCAACCTT	2179
Haemophilia A Phe465Cys TTT-TGT	TGTTGATCCTAGTCGTTTTAGGATTTGATCTTAGATCTCGCTTA TACTTTTCAGATTATATTTAAGAATCAAGCAAGCAGACCATATAA CATCTACCCTCACGGAATCACTGATGTCCGTCC	2180
	GGACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGT CTGCTTGCTTGATTCTTAATATAATCTGAAAGTATAAGCGAG ATCTAAGATCAAATCCTAAAACGACTAGGATCAACA	2181
	GATTATATTTAAGAATC	2182
	GATTCTTAATATAATC	2183
Haemophilia A Ala469Gly GCA-GGA	TCGTTTTAGGATTTGATCTTAGATCTCGCTTATACTTTTCAGATT ATATTTAAGAATCAAGCAAGCAGACCATATAACATCTACCCTC ACGGAATCACTGATGTCCGTCTTTGTATTCAAG	2184
	CTTGAATACAAAGGACGGACATCAGTGATTCCGTGAGGGTAG ATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATCTGAAA GTATAAGCGAGATCTAAGATCAAATCCTAAAACGA	2185
	GAATCAAGCAAGCAGAC	2186
	GTCTGCTTGCTTGATTG	2187
Haemophilia A Arg471Gly cAGA-GGA	TTAGGATTTGATCTTAGATCTCGCTTATACTTTTCAGATTATATT TAAGAATCAAGCAAGCAGACCATATAACATCTACCCTCACGG AATCACTGATGTCCGTCTTTGTATTCAAGGAGAT	2188
	ATCTCCTTGAATACAAAGGACGGACATCAGTGATTCCGTGAG GGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATC TGAAAGTATAAGCGAGATCTAAGATCAAATCCTAA	2189
	AAGCAAGCAGACCATAT	2190
	ATATGGTCTGCTTGCTT	2191
Haemophilia A Tyr473Cys TAT-TGT	TTGATCTTAGATCTCGCTTATACTTTTCAGATTATATTTAAGAAT CAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACT GATGTCCGTCTTTGTATTCAAGGAGATTACCAA	2192
	TTTGGTAATCTCCTTGAATACAAAGGACGGACATCAGTGATTCC CGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAA TATAATCTGAAAGTATAAGCGAGATCTAAGATCAA	2193
	CAGACCATATAACATCT	2194
	AGATGTTATATGGTCTG	2195
Haemophilia A Tyr473His aTAT-CAT	TTTGATCTTAGATCTCGCTTATACTTTTCAGATTATATTTAAGAA TCAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACT GATGTCCGTCTTTGTATTCAAGGAGATTACCAA	2196
	TTGGTAATCTCCTTGAATACAAAGGACGGACATCAGTGATTCC GTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAAT ATAATCTGAAAGTATAAGCGAGATCTAAGATCAA	2197
	GCAGACCATATAACATC	2198
	GATGTTATATGGTCTGC	2199
Haemophilia A Ile475Thr ATC-ACC	TTAGATCTCGCTTATACTTTTCAGATTATATTTAAGAATCAAGCA AGCAGACCATATAACATCTACCCTCACGGAATCACTGATGTCC GTCCTTTGTATTCAAGGAGATTACCAAAGGTAA	2200

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTACCTTTTGGTAATCTCCTTGAATACAAAGGACGGACATCAG TGATTCCGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATT CTTAAATATAATCTGAAAGTATAAGCGAGATCTAA	2201
	ATATAACATCTACCCTC	2202
	GAGGGTAGATGTTATAT	2203
Haemophilia A Gly479Arg cGGA-AGA	TTATACTTTTCAGATTATATTTAAGAATCAAGCAAGCAGACCATA TAACATCTACCCTCACGGAATCACTGATGTCCGTCCCTTTGTAT TCAAGGAGATTACCAAAGGTAAATATTCCTCG	2204
	CGAGGGAATATTTACCTTTTGGTAATCTCCTTGAATACAAAGG ACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGTCT GCTTGCTTGATTCTTAAATATAATCTGAAAGTATAA	2205
	ACCCTCACGGAATCACT	2206
	AGTGATTCCGTGAGGGT	2207
Haemophilia A Thr522Ser aACT-TCT	CCAATTCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGA CTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGA CCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAG	2208
	CTCTCTCCATATTAACGAACTAGAGTAATAGCGGGTCAGGC ACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGT CCATTTATATTTGAATATTTCTCCTGGCAGAATTGG	2209
	ATGGGCCAACTAAATCA	2210
	TGATTTAGTTGGCCCAT	2211
Haemophilia A Asp525Asn aGAT-AAT	CCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAG ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATT ACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTT	2212
	AAGCTAGATCTCTCCATATTAACGAACTAGAGTAATAGCG GGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTAC AGTCACTGTCCATTTATATTTGAATATTTCTCCTGG	2213
	CTAAATCAGATCCTCGG	2214
	CCGAGGATCTGATTTAG	2215
Haemophilia A Arg527Trp tCGG-TGG	GAAATATTCAAATATAAATGGACAGTGACTGTAGAAGATGGGC CAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAG TTTCGTTAATATGGAGAGAGATCTAGCTTCAGGAC	2216
	GTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGAGTA ATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATC TTCTACAGTCACTGTCCATTTATATTTGAATATTTCT	2217
	CAGATCCTCGGTGCCTG	2218
	CAGGCACCGAGGATCTG	2219
Haemophilia A Arg531Cys cCGC-TGC	TATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCA GATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATA TGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC	2220
	GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAA CGAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATT TAGTTGGCCCATCTTCTACAGTCACTGTCCATTTATA	2221
	GCCTGACCCGCTATTAC	2222

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTAATAGC <u>G</u> GGTCAGGC	2223
Haemophilia A Arg531Gly cCGC-GGC	TATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCC <u>G</u> GCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC	2224
	GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAGAGTAATAGC <u>G</u> GGTCAGGCACCGAGGATCTGATTAGTTGGCCCATCTTCTACAGTCACTGTCCATTATA	2225
	GCCTGACCC <u>G</u> GCTATTAC	2226
	GTAATAGC <u>G</u> GGTCAGGC	2227
Haemophilia A Arg531His CGC-CAC	ATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCC <u>G</u> GCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCT	2228
	AGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAGAGTAATAGC <u>G</u> GGTCAGGCACCGAGGATCTGATTAGTTGGCCCATCTTCTACAGTCACTGTCCATTAT	2229
	CCTGACCC <u>G</u> GCTATTACT	2230
	AGTAATAGC <u>G</u> GGTCAGG	2231
Haemophilia A Ser534Pro cTCT-CCT	ACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACT <u>T</u> CTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCT	2232
	AGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAG <u>A</u> GTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGT	2233
	GCTATTACT <u>T</u> CTAGTTTC	2234
	GAACTAG <u>A</u> GTAATAGC	2235
Haemophilia A Ser535Gly tAGT-GGT	GTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCT <u>A</u> GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCT	2236
	AGCAGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCAC	2237
	ATTACTCT <u>A</u> GTTTCGTT	2238
	AACGAACTAGAGTAAT	2239
Haemophilia A Val537Asp GTT-GAT	TAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCG <u>T</u> TAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCTACAAAGA	2240
	TCTTTGTAGCAGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAGAGTAATAGCGGGTCAAGCACCAGAGGATCTGATTTAGTTGGCCCATCTTCTA	2241
	TAGTTTCG <u>T</u> TAATATGG	2242
	CCATATTAAACGAACTA	2243
Haemophilia A Arg541Thr AGA-ACA	CAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCTACAAAGAATCTGTAGATCA	2244

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAATG AGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGAGT AATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTG	2245
	TATGGAGAGAGATCTAG	2246
	CTAGATCTCTCTCCATA	2247
Haemophilia A Asp542Gly GAT-GGT	CTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTT CGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCC TCTCCTCATCTGCTACAAAGAATCTGTAGATCAAA	2248
	CTTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCA ATGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAG AGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAG	2249
	GGAGAGAGATCTAGCTT	2250
	AAGCTAGATCTCTCTCC	2251
Haemophilia A Asp542His aGAT-CAT	ACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTT TCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCC CTCTCCTCATCTGCTACAAAGAATCTGTAGATCAAA	2252
	TTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAA TGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGA GTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGT	2253
	TGGAGAGAGATCTAGCT	2254
	AGCTAGATCTCTCTCCA	2255
Haemophilia A Asp542Tyr aGAT-TAT	ACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTT TCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCC CTCTCCTCATCTGCTACAAAGAATCTGTAGATCAAA	2256
	TTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAA TGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGA GTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGT	2257
	TGGAGAGAGATCTAGCT	2258
	AGCTAGATCTCTCTCCA	2259
Haemophilia A Glu557Term aGAA-TAA	GTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCT CTCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACC AGGTGAGTTCTTGCCCTTTCCAAGTGCTGGGTTTCAT	2260
	ATGAAACCCAGCACTTGAAAGGCAAGAACTCACCTGGTTTC CTCTTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGC CAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAC	2261
	GCTACAAAGAATCTGTA	2262
	TACAGATTCTTTGTAGC	2263
Haemophilia A Ser558Phe TCT-TTT	ATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCC TCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGG TGAGTTCTTGCCCTTTCCAAGTGCTGGGTTTCATTCTC	2264
	GAGAATGAAACCCAGCACTTGAAAGGCAAGAACTCACCTGG TTTCCTCTTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAG GGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATAT	2265

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia A Val559Ala GTA-GCA	CAAAGAATCTGTAGATC	2266
	GATCTACAGATTCTTTG	2267
	TGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCA TCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGGTGA GTTCTTGCCTTTCCAAGTGCTGGGTTTCATTCTCAGT	2268
	ACTGAGAATGAAACCCAGCACTTGGAAAGGCAAGAACTCACC TGGTTTCCTCTTTGATCTACAGATTCTTTGTAGCAGATGAGGA GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCA	2269
	AGAATCTGTAGATCAAA	2270
	TTTGATCTACAGATTCT	2271

EXAMPLE 15

Hemophilia – Factor IX Deficiency

[0227] The attached table discloses the correcting oligonucleotide base sequences for the Factor IX oligonucleotides of the invention.

5

Table 17

Factor IX Mutations And Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia B Asn2Asp tAAT-GAT	ATTTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAA TCGGCCAAAGAGGTATAATTTCAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA	2272
	TTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCT TCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTT GTTGGCGTTTTTCATGATCAAGAAAACTGAAAT	2273
	AGAGGTATAATTTCAGGT	2274
	ACCTGAATTATACCTCT	2275
Haemophilia B Asn2Ile AAT-ATT	TTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAAT CGGCCAAAGAGGTATAATTTCAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA	2276
	TTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTC TTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTT TGTTGGCGTTTTTCATGATCAAGAAAACTGAAA	2277
	GAGGTATAATTTCAGGTA	2278
	TACCTGAATTATACCTC	2279
Haemophilia B Asn2Tyr tAAT-TAT	ATTTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAA TCGGCCAAAGAGGTATAATTTCAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA	2280

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCT TCCAATTTACCTGAATTATACCTCTTTGGCCGATTGAGAATTTT GTTGGCGTTTTTCATGATCAAGAAAACTGAAAT	2281
	AGAGGTAT <u>A</u> ATTTCAGGT	2282
	ACCTGAATTATACCTCT	2283
Haemophilia B Ser3Pro tTCA-CCA	TCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATC GGCCAAAGAGGTATAATT <u>C</u> AGGTAAATTGGAAGAGTTTGTTT AAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT	2284
	ACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAAC TCTTCCAATTTACCTG <u>A</u> ATTATACCTCTTTGGCCGATTGAGAAT TTTGTTGGCGTTTTTCATGATCAAGAAAACTGA	2285
	GGTATAATT <u>C</u> AGGTAAA	2286
	TTTACCTG <u>A</u> ATTATACC	2287
Haemophilia B Gly4Asp GGT-GAT	TTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCC AAAGAGGTATAATT <u>CAG</u> GTAATTGGAAGAGTTTGTTCAAGG GAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAG	2288
	CTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC AACTCTTCCAATTTAC <u>C</u> TGAATTATACCTCTTTGGCCGATTCA GAATTTTGTTGGCGTTTTTCATGATCAAGAAAA	2289
	TAATTCAG <u>G</u> TAAATTGG	2290
	CCAATTTAC <u>C</u> TGAATTA	2291
Haemophilia B Gly4Ser aGGT-AGT	GTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGC CAAAGAGGTATAATT <u>CAG</u> GTAATTGGAAGAGTTTGTTCAAGG GAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAG	2292
	TACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACA AACTCTTCCAATTTAC <u>C</u> TGAATTATACCTCTTTGGCCGATTCA GAATTTTGTTGGCGTTTTTCATGATCAAGAAAAAC	2293
	ATAATTCAG <u>G</u> TAAATTG	2294
	CAATTTAC <u>C</u> TGAATTAT	2295
Haemophilia B LysSGlu tAAA-GAA	TTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAA AGAGGTATAATT <u>CAGGT</u> <u>A</u> AATTGGAAGAGTTTGTTCAAGGGA ACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTT	2296
	AACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGA ACAACTCTTCCAATTT <u>A</u> CTGAATTATACCTCTTTGGCCGATT CAGAATTTTGTTGGCGTTTTTCATGATCAAGAAA	2297
	ATTCAGGT <u>A</u> AATTGGAA	2298
	TTCCAATTTACCTGAAT	2299
Haemophilia B Glu7Ala GAA-GCA	ATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGT ATAATTCAGGTAAATTGG <u>A</u> AGAGTTTGTTCAAGGGAACCTTGA GAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGA	2300
	TCTTCAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTT CCCTTGAACAACTCT <u>T</u> CCAATTTACCTGAATTATACCTCTTTG GCCGATTGAGAATTTTGTTGGCGTTTTTCATGAT	2301
	TAAATTGG <u>A</u> AGAGTTTG	2302

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAA <u>A</u> CTCTTCCMTTTA	2303
Haemophilia B Glu7Lys gGAA-AAA	GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGG TATAATTCAGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTG AGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAG	2304
	CTTCAAACTACACTTTTTCTTCCATACATTCTCTCTCAAGGTT CCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTGG CCGATTCAGAAATTTGTGGCGTTTTTCATGATC	2305
	GTAAATTGGAAGAGTTT	2306
	AACTCTTCCAATTTAC	2307
Haemophilia B Glu7Val GAA-GTA	ATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGT ATAATTCAGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTGA GAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGA	2308
	TCTTCAAACTACACTTTTTCTTCCATACATTCTCTCTCAAGGTT CCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTG GCCGATTCAGAAATTTGTGGCGTTTTTCATGAT	2309
	TAAATTGGAAGAGTTTG	2310
	CAA <u>A</u> CTCTTCCAATTTA	2311
Haemophilia B Glu8Ala GAG-GCG	ATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATA ATTCAGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTGAGA GAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGC	2312
	GCTTCTTCAAACTACACTTTTTCTTCCATACATTCTCTCTCAAG GTTCCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCT TTGGCCGATTCAGAAATTTGTGGCGTTTTTCAT	2313
	ATTGGAAGAGTTTGTTC	2314
	GAACAACTCTTCCAAT	2315
Haemophilia B Glu8Gly GAG-GGG	ATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATA ATTCAGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTGAGA GAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGC	2316
	GCTTCTTCAAACTACACTTTTTCTTCCATACATTCTCTCTCAAG GTTCCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCT TTGGCCGATTCAGAAATTTGTGGCGTTTTTCAT	2317
	ATTGGAAGAGTTTGTTC	2318
	GAACAACTCTTCCAAT	2319
Haemophilia B Phe9Cys TTT-TGT	AAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTC AGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTGAGAGAGA ATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACG	2320
	CGTGCTTCTTCAAACTACACTTTTTCTTCCATACATTCTCTCTC AAGGTTCCCTTGAACA <u>A</u> ACTCTTCCAATTTACCTGAATTATAC CTCTTTGGCCGATTCAGAAATTTGTGGCGTTTT	2321
	GGAAGAGTTTGTTCAG	2322
	CTTGAACA <u>A</u> ACTCTTCC	2323
Haemophilia B Phe9Ile ATT-ATT	GAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAAT TCAGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTGAGAGA GAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCAC	2324

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
gTTT-ATT	GTGCTTCTTCAAACTACACTTTTCTTCCATACATTCTCTCTCA AGGTTCCCTTGAACAA <u>ACT</u> CTTCCAATTTACCTGAATTATACC TCTTTGGCCGATTTCAGAAATTTGTTGGCGTTTTTC	2325
	TGGAAGAGTTTGTTCAA	2326
	TTGAACAA <u>ACT</u> CTTCCA	2327
Haemophilia B Arg(-1)Ser AGGt-AGC	TTACATTTTCAGTTTTCTTGATCATGAAAACGCCAACAAAATTC TGAATCGGCCAAAGAG <u>G</u> TATAATTCAGGTAAATTGGAAGAGT TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAA	2328
	TTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCC AATTTACCTGAATTATAC <u>C</u> CTCTTTGGCCGATTTCAGAAATTTGTT GGCGTTTTTCATGATCAAGAAAACTGAAATGTAA	2329
	CCAAAGAG <u>G</u> TATAATTC	2330
	GAATTATAC <u>C</u> CTCTTTGG	2331
Haemophilia B Arg(-1)Thr AGG-ACG	TTTACATTTTCAGTTTTCTTGATCATGAAAACGCCAACAAAATT CTGAATCGGCCAAAGAG <u>G</u> TATAATTCAGGTAAATTGGAAGAG TTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGA	2332
	TCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCA ATTTACCTGAATTATAC <u>C</u> CTCTTTGGCCGATTTCAGAAATTTGTTG GCGTTTTTCATGATCAAGAAAACTGAAATGTAAA	2333
	GCCAAAGAG <u>G</u> TATAATT	2334
	AATTATAC <u>C</u> CTCTTTGGC	2335
Haemophilia B Lys(-2)Asn AAGa-AAT	CTTTTACATTTTCAGTTTTCTTGATCATGAAAACGCCAACAAAA TTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAG AGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATG	2336
	CATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATT TACCTGAATTATACCT <u>C</u> TTTGGCCGATTTCAGAAATTTGTTGGC GTTTTTCATGATCAAGAAAACTGAAATGTAAAAG	2337
	CGGCCAAAGAGGTATAA	2338
	TTATACCT <u>C</u> TTTGGCCG	2339
Haemophilia B Arg(-4)Gln CGG-CAG	AATTATTCTTTTACATTTTCAGTTTTCTTGATCATGAAAACGCC AACAAAATTCTGAATC <u>G</u> GCCAAAGAGGTATAATTCAGGTAAAT TGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGA	2340
	TCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTG AATTATACCTCTTTGGC <u>C</u> GATTTCAGAAATTTGTTGGCGTTTTC ATGATCAAGAAAACTGAAATGTAAAAGAATAATT	2341
	TCTGAATC <u>G</u> GCCAAAGA	2342
	TCTTTGGC <u>C</u> GATTTCAGA	2343
Haemophilia B Arg(-4)Leu CGG-CTG	AATTATTCTTTTACATTTTCAGTTTTCTTGATCATGAAAACGCC AACAAAATTCTGAATC <u>G</u> GCCAAAGAGGTATAATTCAGGTAAAT TGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGA	2344
	TCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTG AATTATACCTCTTTGGC <u>C</u> GATTTCAGAAATTTGTTGGCGTTTTC ATGATCAAGAAAACTGAAATGTAAAAGAATAATT	2345
	TCTGAATC <u>G</u> GCCAAAGA	2346
	TCTTTGGC <u>C</u> GATTTCAGA	2347

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia B Arg(-4)Trp tCGG-TGG	GAATTATTCTTTTACATTTTCAGTTTTCTTGATCATGAAAACGC CAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAA TTGGAAGAGTTTGTTCAGGGAACCTTGAGAGAG	2348
	CTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTGA ATTATACCTCTTTGGCCGATTGAGAATTTTGTGGCGTTTTTCAT GATCAAGAAAACTGAAATGTAAAAGAATAATTC	2349
	TTCTGAATCGGCCAAAG	2350
	CTTTGGCCGATTGAGAA	2351
Haemophilia B GinII Term tCAA-TAA	GCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGT AAATTGGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGT ATGGAAGAAAAGTGTAGTTTGAAGAAGCACGAGAAG	2352
	CTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACATTCT CTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTGAAT TATACCTCTTTGGCCGATTGAGAATTTTGTGGC	2353
	AGTTTGTTCAGGGAAC	2354
	GTTCCCTTGAACAACT	2355
Haemophilia B Gly12Ala GGG-GCG	ACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATT GGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATGGA AGAAAAGTGTAGTTTGAAGAAGCACGAGAAGTTT	2356
	AAAATTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACA TTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCT GAATTATACCTCTTTGGCCGATTGAGAATTTTGT	2357
	TGTTCAAGGGAACCTTG	2358
	CAAGGTTCCCTTGAACA	2359
Haemophilia B Gly12Arg aGGG-AGG	AACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATT TGGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATGG AAGAAAAGTGTAGTTTGAAGAAGCACGAGAAGTTT	2360
	AACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACAT TCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTG AATTATACCTCTTTGGCCGATTGAGAATTTTGT	2361
	TTGTTCAAGGGAACCTT	2362
	AAGGTTCCCTTGAACAA	2363
Haemophilia B Gly12Glu GGG-GAG	ACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATT GGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATGGA AGAAAAGTGTAGTTTGAAGAAGCACGAGAAGTTT	2364
	AAAATTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACA TTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCT GAATTATACCTCTTTGGCCGATTGAGAATTTTGT	2365
	TGTTCAAGGGAACCTTG	2366
	CAAGGTTCCCTTGAACA	2367
Haemophilia B Glu17Gln aGAA-CAA	CGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGT TTTGAAGAAGCACGAGAAGTTTTTGAACAACTGAAA	2368

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAAAACCTACAC TTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTC TTCCAATTTACCTGAATTATACCTCTTTGGCCG	2369
	TTGAGAGAGAATGTATG	2370
	CATACATTCTCTCTCAA	2371
Haemophilia B Glu17Lys aGAA-AAA	CGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGT TTTGAAGAAGCAGGAGAAGTTTTTGAACAACTGAAA	2372
	TTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAAAACCTACAC TTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTC TTCCAATTTACCTGAATTATACCTCTTTGGCCG	2373
	TTGAGAGAGAATGTATG	2374
	CATACATTCTCTCTCAA	2375
Haemophilia B Cys18Arg aTGT-CGT	CCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAG GGAACCTTGAGAGAGAAATGTATGGAAGAAAAGTGTAGTTTTG AAGAAGCACGAGAAGTTTTTGAACAACTGAAAGAA	2376
	TTCTTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAAAACCTA CACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAA CTCTTCCAATTTACCTGAATTATACCTCTTTGG	2377
	AGAGAGAATGTATGGAA	2378
	TTCCATACATTCTCTCT	2379
Haemophilia B Cys18Tyr TGT-TAT	CAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGG GAACCTTGAGAGAGAAATGTATGGAAGAAAAGTGTAGTTTTGA AGAAGCACGAGAAGTTTTTGAACAACTGAAAGAAC	2380
	GTTCTTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAAAACCT ACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAA ACTCTTCCAATTTACCTGAATTATACCTCTTTG	2381
	GAGAGAATGTATGGAA	2382
	CTTCCATACATTCTCTCT	2383
Haemophilia B Glu20Val GAA-GTA	GGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCT TGAGAGAGAAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGC ACGAGAAGTTTTTGAACAACTGAAAGAACAGTGAG	2384
	CTCACTGTTCTTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTC AAAACCTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTT GAACAACTCTTCCAATTTACCTGAATTATACC	2385
	ATGTATGGAAGAAAAGT	2386
	ACTTTTCTTCCATACAT	2387
Haemophilia B Glu21Lys aGAA-AAA	TATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTG AGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCAC GAGAAGTTTTTGAACAACTGAAAGAACAGTGAGTA	2388
	TACTCACTGTTCTTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCT TCAAAAACCTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCC TTGAACAACTCTTCCAATTTACCTGAATTATA	2389
	GTATGGAAGAAAAGTGT	2390

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACACTTTT <u>C</u> TTCCATAC	2391
Haemophilia B Cys23Arg gTGT-CGT	TCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGA GAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAA GTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCA	2392
	TGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACCTTCTCGT GCTTCTTCAAACTAC <u>A</u> CTTTTCTTCCATACATTCTCTCTCAAG GTTCCCTTGAACAAACTCTTCCAATTTACCTGA	2393
	AAGAAAAGTGTAGTTTT	2394
	AAAACACTAC <u>A</u> CTTTTCTT	2395
Haemophilia B Cys23Tyr TGT-TAT	CAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAG AATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAG TTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCAC	2396
	GTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACCTTCTC GTGCTTCTTCAAACTAC <u>A</u> CTTTTCTTCCATACATTCTCTCTCA AGGTTCCCTTGAACAAACTCTTCCAATTTACCTG	2397
	AGAAAAGTGTAGTTTTG	2398
	CAAAACTAC <u>A</u> CTTTTCTT	2399
Haemophilia B Phe25Ser TTT-TCT	AATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAATGTA TGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTG AAAACACTGAAAGAACAGTGAGTATTTCCACATAATA	2400
	TATTATGTGGAATACTCACTGTTCTTTCAGTGTTTTCAAAAAC TTCTCGTGCTTCTTCA <u>A</u> AACTACACTTTTCTTCCATACATTCTC TCTCAAGGTTCCCTTGAACAAACTCTTCCAATT	2401
	GTGTAGTTTTGAAGAAG	2402
	CTTCTTCA <u>A</u> AACTACAC	2403
Haemophilia B Glu26Gln tGAA-CAA	TTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAATGTATG GAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAA ACACTGAAAGAACAGTGAGTATTTCCACATAATACC	2404
	GGTATTATGTGGAATACTCACTGTTCTTTCAGTGTTTTCAAAA ACTTCTCGTGCTTCTTCA <u>A</u> AACTACACTTTTCTTCCATACATTCTC TCTCTCAAGGTTCCCTTGAACAAACTCTTCCAA	2405
	GTAGTTTTGAAGAAGCA	2406
	TGCTTCTTCA <u>A</u> AACTAC	2407
Haemophilia B Glu27Ala GAA-GCA	AAGAGTTTGTTC AAGGGAACCTTGAGAGAGAATGTATGGAAG AAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACAC TGAAAGAACAGTGAGTATTTCCACATAATACCCTTC	2408
	GAAGGGTATTATGTGGAATACTCACTGTTCTTTCAGTGTTTT CAAAAACCTTCTCGTGCTTCTTCA <u>A</u> AACTACACTTTTCTTCCATA CATTCTCTCTCAAGGTTCCCTTGAACAAACTCTT	2409
	TTTTGAAGAAGCACGAG	2410
	CTCGTGCTTCTTCAAAA	2411
Haemophilia B Glu27Asp GAAg-GAC	AGAGTTTGTTC AAGGGAACCTTGAGAGAGAATGTATGGAAGA AAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACT GAAAGAACAGTGAGTATTTCCACATAATACCCTTCA	2412
	TGAAGGGTATTATGTGGAATACTCACTGTTCTTTCAGTGTTT	2413

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCAAAACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCAT ACATTCTCTCTCAAGGTTCCCTTGAACAACTCT	
	TTTGAAGAAAGCACGAGA	2414
	TCTCGTGCTTCTTCAAA	2415
Haemophilia B Glu27Lys aGAA-AAA	GAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAA GAAAAGTGTAGTTTTGAAGAAAGCACGAGAAGTTTTTGAACA CTGAAAGAACAGTGAGTATTTCCACATAATACCCTT	2416
	AAGGGTATTATGTGGAAATACTCACTGTTCTTTTCACTGTTTTT AAAACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATAC ATTCTCTCTCAAGGTTCCCTTGAACAACTCTT	2417
	GTTTTGAAGAAAGCACGA	2418
	TCGTGCTTCTTCAAAAC	2419
Haemophilia B Glu27Val GAA-GTA	AAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAG AAAAGTGTAGTTTTGAAGAAAGCACGAGAAGTTTTTGAACAC TGAAAGAACAGTGAGTATTTCCACATAATACCCTTC	2420
	GAAGGGTATTATGTGGAAATACTCACTGTTCTTTTCACTGTTTT CAAAACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATA CATTCTCTCTCAAGGTTCCCTTGAACAACTCTT	2421
	TTTTGAAGAAAGCACGAG	2422
	CTCGTGCTTCTTCAAAA	2423
Haemophilia B Arg29Gln CGA-CAA	TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT GTAGTTTTGAAGAAAGCACGAGAAGTTTTTGAACAACTGAAAG AACAGTGAGTATTTCCACATAATACCCTTCAGATGC	2424
	GCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTTCACT TGTTTTCAAAACTTCTCGTGCTTCTTCAAACTACACTTTTCT TCCATACATTCTCTCTCAAGGTTCCCTTGAACAA	2425
	AGAAGCACGAGAAGTTT	2426
	AACTTCTCGTGCTTCT	2427
Haemophilia B Arg29Pro CGA-CCA	TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT GTAGTTTTGAAGAAAGCACGAGAAGTTTTTGAACAACTGAAAG AACAGTGAGTATTTCCACATAATACCCTTCAGATGC	2428
	GCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTTCACT TGTTTTCAAAACTTCTCGTGCTTCTTCAAACTACACTTTTCT TCCATACATTCTCTCTCAAGGTTCCCTTGAACAA	2429
	AGAAGCACGAGAAGTTT	2430
	AACTTCTCGTGCTTCT	2431
Haemophilia B Arg29Term aCGA-TGA	TTTGTTCAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAG TGTAGTTTTGAAGAAAGCACGAGAAGTTTTTGAACAACTGAAA GAACAGTGAGTATTTCCACATAATACCCTTCAGATG	2432
	CATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTTCACT GTTTTCAAAACTTCTCGTGCTTCTTCAAACTACACTTTTCTT CCATACATTCTCTCTCAAGGTTCCCTTGAACAA	2433
	AAGAAGCACGAGAAGTT	2434

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AACTTCTC <u>G</u> TGCTTCTT	2435
Haemophilia B Glu30Lys aGAA-AAA	GTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGT AGTTTTGAAGAAGCACGAGAAAGTTTTTAAAAACACTGAAAGAA CAGTGAGTATTTCCACATAATACCCTTCAGATGCAG	2436
	CTGCATCTGAAGGGTATTATGTGGAATACTCACTGTTCTTTC AGTGTTTTCAAAAACCTT <u>C</u> TCGTGCTTCTTCAAACTACACTTTT CTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC	2437
	AAGCACGAGAAAGTTTTT	2438
	AAAAACTT <u>C</u> TCGTGCTT	2439
Haemophilia B Glu30Term aGAA-TAA	GTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGT AGTTTTGAAGAAGCACGAGAAAGTTTTTAAAAACACTGAAAGAA CAGTGAGTATTTCCACATAATACCCTTCAGATGCAG	2440
	CTGCATCTGAAGGGTATTATGTGGAATACTCACTGTTCTTTC AGTGTTTTCAAAAACCTT <u>C</u> TCGTGCTTCTTCAAACTACACTTTT CTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC	2441
	AAGCACGAGAAAGTTTTT	2442
	AAAAACTT <u>C</u> TCGTGCTT	2443
Haemophilia B Glu33Asp GAAa-GAC	CCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGA AGCACGAGAAGTTTTTGA <u>A</u> AACACTGAAAGAACAGTGAGTAT TTCCACATAATACCCTTCAGATGCAGAGCATAGAATA	2444
	TATTCTATGCTCTGCATCTGAAGGGTATTATGTGGAATACTC ACTGTTCTTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAA ACTACACTTTTCTTCCATACATTCTCTCTCAAGG	2445
	GTTTTTGA <u>A</u> AACACTGA	2446
	TCAGTGTTTTCAAAAAC	2447
Haemophilia B Glu33Term tGAA-TAA	AACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAA GAAGCACGAGAAGTTTTT <u>G</u> AAAAACACTGAAAGAACAGTGAGT ATTTCCACATAATACCCTTCAGATGCAGAGCATAGAA	2448
	TTCTATGCTCTGCATCTGAAGGGTATTATGTGGAATACTCAC TGTTCTTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAAC TACACTTTTCTTCCATACATTCTCTCTCAAGGTT	2449
	AAGTTTTT <u>G</u> AAAAACACT	2450
	AGTGTTTTCAAAAACCTT	2451
Haemophilia B Trp42Term TGG-TAG	CAAAACACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTT TATAGACTGAATTTT <u>G</u> GAAGCAGTATGTTGGTAAGCAATTCAT TTTATCCTCTAGCTAATATATGAAACATATGAG	2452
	CTCATATGTTTCATATATTAGCTAGAGGATAAAATGAATTGCTT ACCAACATACTGCTTCCAA <u>A</u> AATTCAAGTCTATAAAGAATAAAAG AAGACAAATTAACGGTAATATCTAAAGTGTTTTG	2453
	TGAATTTT <u>G</u> GAAGCAGT	2454
	ACTGCTTCCAA <u>A</u> AATTCA	2455

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia B Lys43Glu gAAG-GAG	AAACACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTTTA TAGACTGAATTTTGGAGCAGTATGTTGGTAAGCAATTCATTT TATCCTCTAGCTAATATATGAAACATATGAGAA	2456
	TTCTCATATGTTTCATATATTAGCTAGAGGATAAAATGAATTGC TTACCAACATACTGCTTCCAAAATTCAGTCTATAAAGAATAAAA GAAGACAAATTAACGGTAATATCTAAAGTGTTT	2457
	AATTTTGGAGCAGTAT	2458
	ATACTGCTTCCAAAATT	2459
Haemophilia B Gln44Term gCAG-TAG	CACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTTTATAG ACTGAATTTTGGAGCAGTATGTTGGTAAGCAATTCATTTTAT CCTCTAGCTAATATATGAAACATATGAGAATTA	2460
	TAATTCTCATATGTTTCATATATTAGCTAGAGGATAAAATGAAT TGCTTACCAACATACTGCTTCCAAAATTCAGTCTATAAAGAAT AAAAGAAGACAAATTAACGGTAATATCTAAAGTG	2461
	TTTGGAGCAGTATGTT	2462
	AACATACTGCTTCCAAA	2463
Haemophilia B Asp49Gly GAT-GGT	CCGGGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAAC CTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTA AATGGCGGCAGTTGCAAGGATGACATTAATTCCTA	2464
	TAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATG GATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAA ATTGAATTGGCACGTAAACTGCTTAGAATGCCCGG	2465
	AGATGGAGATCAGTGTG	2466
	CACACTGATCTCCATCT	2467
Haemophilia B Gln50His CAGt-CAC	GCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTAT CTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATG GCGGCAGTTGCAAGGATGACATTAATTCCTATGAA	2468
	TTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAA CATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTA AGAAATTGAATTGGCACGTAAACTGCTTAGAATGC	2469
	GGAGATCAGTGTGAGTC	2470
	GACTCACACTGATCTCC	2471
Haemophilia B Gln50Pro CAG-CCG	GGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTA TCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAAT GGCGGCAGTTGCAAGGATGACATTAATTCCTATGA	2472
	TCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAAC ATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAA GAAATTGAATTGGCACGTAAACTGCTTAGAATGCC	2473
	TGGAGATCAGTGTGAGT	2474
	ACTCACACTGATCTCCA	2475
Haemophilia B Gln50Term gCAG-TAG	GGGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCT ATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAA TGGCGGCAGTTGCAAGGATGACATTAATTCCTATG	2476

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
tCAG-TAG	CATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACA TGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAG AAATTGAATTGGCACGTAAACTGCTTAGAATGCCC	2477
	ATGGAGATCAGTGTGAG	2478
	CTCACACTGATCTCCAT	2479
Haemophilia B Cys51Arg gTGT-CGT	CATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCT CAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGG CGGCAGTTGCAAGGATGACATTAATTCCTATGAAT	2480
	ATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAA ACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTT AAGAAATTGAATTGGCACGTAAACTGCTTAGAATG	2481
	GAGATCAGTGTGAGTCC	2482
	GGACTCACACTGATCTC	2483
Haemophilia B Cys51Ser gTGT-AGT	CATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCT CAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGG CGGCAGTTGCAAGGATGACATTAATTCCTATGAAT	2484
	ATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAA ACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTT AAGAAATTGAATTGGCACGTAAACTGCTTAGAATG	2485
	GAGATCAGTGTGAGTCC	2486
	GGACTCACACTGATCTC	2487
Haemophilia B Cys51Trp TGTg-TGG	TTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCA AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGT	2488
	ACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTT AAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGG TTAAGAAATTGAATTGGCACGTAAACTGCTTAGAA	2489
	GATCAGTGTGAGTCCAA	2490
	TTGGACTCACACTGATC	2491
Haemophilia B Glu52Term tGAG-TAG	TCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAA AGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGG CAGTTGCAAGGATGACATTAATTCCTATGAATGTT	2492
	AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAG GTTAAGAAATTGAATTGGCACGTAAACTGCTTAGA	2493
	ATCAGTGTGAGTCCAAT	2494
	ATTGGACTCACACTGAT	2495
Haemophilia B Pro55Ala tCCA-GCA	TTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAG ATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCA AGGATGACATTAATTCCTATGAATGTTGGTGTCCCT	2496
	AGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACT GCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCT TTGAGATAGGTTAAGAAATTGAATTGGCACGTAAA	2497
	AGTCCAATCCATGTTTA	2498

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAAACATGGATTGGACT	2499
Haemophilia B Pro55Arg CCA-CGA	TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGA TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAA GGATGACATTAATTCCTATGAATGTTGGTGTCCCTT	2500
	AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAAC TGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATC TTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2501
	GTCCAATCCATGTTTAA	2502
	TTAAACATGGATTGGAC	2503
Haemophilia B Pro55Gln CCA-CAA	TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGA TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAA GGATGACATTAATTCCTATGAATGTTGGTGTCCCTT	2504
	AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAAC TGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATC TTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2505
	GTCCAATCCATGTTTAA	2506
	TTAAACATGGATTGGAC	2507
Haemophilia B Pro55Leu CCA-CTA	TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGA TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAA GGATGACATTAATTCCTATGAATGTTGGTGTCCCTT	2508
	AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAAC TGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATC TTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2509
	GTCCAATCCATGTTTAA	2510
	TTAAACATGGATTGGAC	2511
Haemophilia B Pro55Ser tCCA-TCA	TTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAG ATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCA AGGATGACATTAATTCCTATGAATGTTGGTGTCCCTT	2512
	AGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACT GCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCT TTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2513
	AGTCCAATCCATGTTTAA	2514
	TAAACATGGATTGGACT	2515
Haemophilia B Cys56Arg aTGT-CGT	ACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATC AGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGG ATGACATTAATTCCTATGAATGTTGGTGTCCCTTTG	2516
	CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCA ACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGT	2517
	CCAATCCATGTTTAAAT	2518
	ATTTAAACATGGATTGG	2519
Haemophilia B Cys56Ser aTGT-AGT	ACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATC AGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGG ATGACATTAATTCCTATGAATGTTGGTGTCCCTTTG	2520

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCA ACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGT	2521
	CCAATCCATGTTTAAAT	2522
	ATTTAAACATGGATTGG	2523
Haemophilia B Cys56Ser TGT-TCT	CGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCA GTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGA TGACATTAATTCCTATGAATGTTGGTGTCCCTTTGG	2524
	CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGC AACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACG	2525
	CAATCCATGTTTAAATG	2526
	CATTTAAACATGGATTG	2527
Haemophilia B Cys56Tyr TGT-TAT	CGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCA GTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGA TGACATTAATTCCTATGAATGTTGGTGTCCCTTTGG	2528
	CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGC AACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACG	2529
	CAATCCATGTTTAAATG	2530
	CATTTAAACATGGATTG	2531
Haemophilia B Asn58Lys AATg-AAG	ATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAG TCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAA	2532
	TTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCA TCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACT GATCTCCATCTTTGAGATAGGTTAAGAAATTGAAT	2533
	TGTTTAAATGGCGGCAG	2534
Haemophilia B Gly59Asp GGC-GAC	CTGCCGCCATTTAAACA	2535
	TCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTC CAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAT TCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGG	2536
	CCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGT CATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACA CTGATCTCCATCTTTGAGATAGGTTAAGAAATTGA	2537
	TTTAAATGGCGGCAGTT	2538
Haemophilia B Gly59Val GGC-GTC	AACTGCCGCCATTTAAA	2539
	TCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTC CAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAT TCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGG	2540
	CCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGT CATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACA CTGATCTCCATCTTTGAGATAGGTTAAGAAATTGA	2541
	TTTAAATGGCGGCAGTT	2542

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AACTGCCGCCATTATAA	2543
Haemophilia B Gly59Ser tGGC-AGC	TTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTATTCCCTATGAATGTTGGTGTCCCTTTGGATTTGAAG	2544
	CTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTATAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAA	2545
	GTTTAAATGGCGGCAGT	2546
	ACTGCCGCCATTATAAC	2547
Haemophilia B Gly60Ser cGGC-AGC	AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAATCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAA	2548
	TTCTTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTATAACATGGATTGGACTCACTGATCTCCATCTTTGAGATAGGTTAAGAAATT	2549
	TAAATGGCGGCAGTTGC	2550
	GCAACTGCCGCCATTATA	2551
Haemophilia B Gly60Cys cGGC-TGC	AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAATCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAA	2552
	TTCTTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTATAACATGGATTGGACTCACTGATCTCCATCTTTGAGATAGGTTAAGAAATT	2553
	TAAATGGCGGCAGTTGC	2554
	GCAACTGCCGCCATTATA	2555
Haemophilia B Gly60Asp GGC-GAC	ATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAATCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAA	2556
	TTCTTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTATAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAAT	2557
	AAATGGCGGCAGTTGCA	2558
	TGCAACTGCCGCCATTATA	2559
Haemophilia B Gly60Arg cGGC-CGC	AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAATCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAA	2560
	TTCTTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTATAACATGGATTGGACTCACTGATCTCCATCTTTGAGATAGGTTAAGAAATT	2561
	TAAATGGCGGCAGTTGC	2562
	GCAACTGCCGCCATTATA	2563

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia B Cys62Tyr TGC-TAC	TAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTG	2564
	CAGTTCTTTCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGAATCACACTGATCTCCATCTTTGAGATAGGTTA	2565
	CGGCAGTTGCAAGGATG	2566
	CATCCTTGCAACTGCCG	2567
Haemophilia B Cys62Ser TGC-TCC	TAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTG	2568
	CAGTTCTTTCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGAATCACACTGATCTCCATCTTTGAGATAGGTTA	2569
	CGGCAGTTGCAAGGATG	2570
	CATCCTTGCAACTGCCG	2571
Haemophilia B Cys62Term TGC-TGA	AACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGT	2572
	ACAGTTCTTTCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGT	2573
	GGCAGTTGCAAGGATGA	2574
	TCATCCTTGCAACTGCC	2575
Haemophilia B Asp64Glu GATg-GAG	TCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTA	2576
	TAATTCACAGTTCTTTCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGA	2577
	TGCAAGGATGACATTAA	2578
	TTAATGTCATCCTTGCA	2579
Haemophilia B Asp64Gly GAT-GGT	ATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATT	2580
	AATTCACAGTTCTTTCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGAT	2581
	TTGCAAGGATGACATTAA	2582
	TAATGTCATCCTTGCAA	2583
Haemophilia B Asp64Asn gGAT-AAT	TATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAAT	2584

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTC ATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACAT GGATTGGACTCACACTGATCTCCATCTTTGAGATA	2585
	GTTGCAAGGATGACATT	2586
	AATGTCATCCTTGCAAC	2587
Haemophilia B Ile66Ser ATT-AGT	AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCC CTTTGGATTGAAGGAAAGAACTGTGAATTAGGTAA	2588
	TTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACC AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTT	2589
	GGATGACATTAATTCCT	2590
	AGGAATTAATGTCATCC	2591
Haemophilia B Ile66Thr ATT-ACT	AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCC CTTTGGATTGAAGGAAAGAACTGTGAATTAGGTAA	2592
	TTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACC AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTT	2593
	GGATGACATTAATTCCT	2594
	AGGAATTAATGTCATCC	2595
Haemophilia B Asn67Lys AATt-AAA	TGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAG TTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTT GGATTGAAGGAAAGAACTGTGAATTAGGTAAGTAA	2596
	TTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGA CACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGC CATTTAAACATGGATTGGACTCACACTGATCTCCA	2597
	GACATTAATTCCTATGA	2598
	TCATAGGAATTAATGTC	2599
Haemophilia B Tyr69Cys TAT-TGT	ATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCA AGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATT TGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATT	2600
	AATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAA GGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTG CCGCCATTTAAACATGGATTGGACTCACACTGAT	2601
	TAATTCCTATGAATGTT	2602
	AACATTCATAGGAATTA	2603
Haemophilia B Cys71Term TGTt-TGA	TGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGA CATTAAATTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGA AAGAACTGTGAATTAGGTAAGTAACTATTTTTTGA	2604
	TTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAA ATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTT GCAACTGCCGCCATTTAAACATGGATTGGACTCA	2605
	TATGAATGTTGGTGTCC	2606

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGACACCA <u>A</u> CATTCATA	2607
Haemophilia B Cys71Ser TGT-TCT	GTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG ACATTAATTCCTATGAAT <u>G</u> TTGGTGTCCCTTTGGATTTGAAGG AAAGAACTGTGAATTAGGTAAGTAACTATTTTTTTGA	2608
	TCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAA TCCAAAGGGACACCA <u>A</u> CATTCATAGGAATTAATGTCATCCTTG CAACTGCCGCCATTTAAACATGGATTGGACTCAC	2609
	CTATGAAT <u>G</u> TTGGTGTG	2610
	GACACCA <u>A</u> CATTCATAG	2611
Haemophilia B Cys71Tyr TGT-TAT	GTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG ACATTAATTCCTATGAAT <u>G</u> TTGGTGTCCCTTTGGATTTGAAGG AAAGAACTGTGAATTAGGTAAGTAACTATTTTTTTGA	2612
	TCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAA TCCAAAGGGACACCA <u>A</u> CATTCATAGGAATTAATGTCATCCTTG CAACTGCCGCCATTTAAACATGGATTGGACTCAC	2613
	CTATGAAT <u>G</u> TTGGTGTG	2614
	GACACCA <u>A</u> CATTCATAG	2615
Haemophilia B Cys71Ser aTGT-AGT	TGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGAT GACATTAATTCCTATGAAT <u>T</u> GTTGGTGTCCCTTTGGATTTGAAG GAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTTG	2616
	CAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAAT CCAAAGGGACACCA <u>A</u> ATTCATAGGAATTAATGTCATCCTTGC AACTGCCGCCATTTAAACATGGATTGGACTCACA	2617
	CCTATGAAT <u>T</u> GTTGGTGT	2618
	ACACCA <u>A</u> CATTCATAGG	2619
Haemophilia B Trp72Arg tTGG-AGG	GAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGAC ATTAATTCCTATGAATG <u>T</u> GGTGTCCCTTTGGATTTGAAGGAA AGAACTGTGAATTAGGTAAGTAACTATTTTTTTGAAT	2620
	ATTCAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCA AATCCAAAGGGACACCA <u>A</u> CATTCATAGGAATTAATGTCATCCT TGCAACTGCCGCCATTTAAACATGGATTGGACTC	2621
	ATGAATG <u>T</u> GGTGTCCC	2622
	GGGACACCA <u>A</u> CATTCAT	2623
Haemophilia B Trp72Term TGGt-TGA	GTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACAT TAATTCCTATGAATGTT <u>G</u> GTGTCCCTTTGGATTTGAAGGAAAG AACTGTGAATTAGGTAAGTAACTATTTTTTTGAATAC	2624
	GTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTT CAAATCCAAAGGGACAC <u>C</u> CAATTCATAGGAATTAATGTCATC CTTGCAACTGCCGCCATTTAAACATGGATTGGAC	2625
	GAATGTTG <u>G</u> GTGTCCCTT	2626
	AAGGGACAC <u>C</u> CAATTC	2627
Haemophilia B Cys73Tyr TGT-TAT	CCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCTATGAATGTTGGT <u>G</u> TCCCTTTGGATTTGAAGGAAAGAA CTGTGAATTAGGTAAGTAACTATTTTTTTGAATACTC	2628

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCC TTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCA TCCTTGCAACTGCCGCCATTTAAACATGGATTGG	2629
	ATGTTGGTGTCCCTTTG	2630
	CAAAGGGACACCAACAT	2631
Haemophilia B Cys73Arg gTGT-CGT	TCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCTATGAATGTTGGTGTCCCTTTGGATTGGAAGGAAAGAA CTGTGAATTAGGTAAGTAACTATTTTTTGAATACT	2632
	AGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCT TCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCAT CCTTGCAACTGCCGCCATTTAAACATGGATTGGA	2633
	AATGTTGGTGTCCCTTT	2634
	AAAGGGACACCAACATT	2635
Haemophilia B Cys73Phe TGT-TTT	CCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCTATGAATGTTGGTGTCCCTTTGGATTGGAAGGAAAGAA CTGTGAATTAGGTAAGTAACTATTTTTTGAATACTC	2636
	GAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCC TTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCA TCCTTGCAACTGCCGCCATTTAAACATGGATTGG	2637
	ATGTTGGTGTCCCTTTG	2638
	CAAAGGGACACCAACAT	2639
Haemophilia B Cys73Term TGTc-TGA	CAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAT TCCTATGAATGTTGGTGTCCCTTTGGATTGGAAGGAAAGAACT GTGAATTAGGTAAGTAACTATTTTTTGAATACTCA	2640
	TGAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTC CTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTC ATCCTTGCAACTGCCGCCATTTAAACATGGATTG	2641
	TGTTGGTGTCCCTTTGG	2642
	CCAAAGGGACACCAACA	2643
Haemophilia B Gly76Val GGA-GTA	GTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGA ATGTTGGTGTCCCTTTGGATTGGAAGGAAAGAACTGTGAATTA GGTAAGTAACTATTTTTTGAATACTCATGGTTCAA	2644
	TTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACA GTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAA TTAATGTCATCCTTGCAACTGCCGCCATTTAAAC	2645
	TCCCTTTGGATTGGAAG	2646
	CTTCAAATCCAAAGGGA	2647
Haemophilia B Gly76Arg tGGA-AGA	TGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATG AATGTTGGTGTCCCTTTGGATTGGAAGGAAAGAACTGTGAATT AGGTAAGTAACTATTTTTTGAATACTCATGGTTCA	2648
	TGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACA GTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAA TTAATGTCATCCTTGCAACTGCCGCCATTTAAACA	2649
	GTCCCTTTGGATTGAA	2650

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTCAAATCCAAAGGGAC	2651
Haemophilia B Phe77Cys TTT-TGT	TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATG TTGGTGTCCCTTTGGATTGAAGGAAAGAACTGTGAATTAGGT AAGTAACTATTTTTGAATACTCATGGTTCAAAGT	2652
	ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTC ACAGTTCTTTCCCTTCAATCCAAAGGGACACCAACATTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTA	2653
	CTTTGGATTGAAGGAA	2654
	TTCTTCAATCCAAAG	2655
Haemophilia B Phe77Ser TTT-TCT	TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATG TTGGTGTCCCTTTGGATTGAAGGAAAGAACTGTGAATTAGGT AAGTAACTATTTTTGAATACTCATGGTTCAAAGT	2656
	ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTC ACAGTTCTTTCCCTTCAATCCAAAGGGACACCAACATTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTA	2657
	CTTTGGATTGAAGGAA	2658
	TTCTTCAATCCAAAG	2659
Haemophilia B Phe77Tyr TTT-TAT	TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATG TTGGTGTCCCTTTGGATTGAAGGAAAGAACTGTGAATTAGGT AAGTAACTATTTTTGAATACTCATGGTTCAAAGT	2660
	ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTC ACAGTTCTTTCCCTTCAATCCAAAGGGACACCAACATTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTA	2661
	CTTTGGATTGAAGGAA	2662
	TTCTTCAATCCAAAG	2663
Haemophilia B Glu78Lys tGAA-AAA	AATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTT GGTGTCCCTTTGGATTGAAGGAAAGAACTGTGAATTAGGTA AGTAACTATTTTTGAATACTCATGGTTCAAAGTTT	2664
	AAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAAT TCACAGTTCTTTCCCTTCAAATCCAAAGGGACACCAACATTCAT AGGAATTAATGTCATCCTTGCAACTGCCGCCATT	2665
	TTGGATTGAAGGAAAG	2666
	CTTTCCTTCAAATCCAA	2667
Haemophilia B Gly79Val GGA-GTA	GCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGT GTCCCTTTGGATTGAAGGAAAGAACTGTGAATTAGGTAAGTA ACTATTTTTGAATACTCATGGTTCAAAGTTTCCCT	2668
	AGGGAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTAC CTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACA TTCATAGGAATTAATGTCATCCTTGCAACTGCCGC	2669
	ATTTGAAGGAAAGAACT	2670
	AGTTCTTTCCTTCAAAT	2671
Haemophilia B Gly79Arg GGA-AGA	GGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGG TGTCCCTTTGGATTGAAGGAAAGAACTGTGAATTAGGTAAGT AACTATTTTTGAATACTCATGGTTCAAAGTTTCCC	2672

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
aGGA-AGA	GGGAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACC TAATTCACAGTTCTTTCTTCAAATCCAAAGGGACACCAACAT TCATAGGAATTAATGTCATCCTTGCAACTGCCGCC	2673
	GATTTGAAGGAAAGAAC	2674
	GTTCTTTCTTCAAATC	2675
Haemophilia B Gly79Glu GGA-GAA	GCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGT GTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTA ACTATTTTTGAATACTCATGGTTCAAAGTTTCCCT	2676
	AGGGAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTAC CTAATTCACAGTTCTTTCTTCAAATCCAAAGGGACACCAACA TTCATAGGAATTAATGTCATCCTTGCAACTGCCGC	2677
	ATTTGAAGGAAAGAAC	2678
	AGTTCTTTCTTCAAAT	2679
Haemophilia B Cys88Ser TGT-TCT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT CTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGC AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT	2680
	ACCACCTTGTTATCAGCACTATTTTTACAAAAGTCTCGCATC TGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAA	2681
	TGTAACATGTAACATTA	2682
	TAATGTTACATGTTACA	2683
Haemophilia B Cys88Phe TGT-TTT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT CTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGC AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT	2684
	ACCACCTTGTTATCAGCACTATTTTTACAAAAGTCTCGCATC TGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAA	2685
	TGTAACATGTAACATTA	2686
	TAATGTTACATGTTACA	2687
Haemophilia B Cys88Arg aTGT-CGT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT TCTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGG	2688
	CCACCTTGTTATCAGCACTATTTTTACAAAAGTCTCGCATCT GCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAAA	2689
	ATGTAACATGTAACATT	2690
	AATGTTACATGTTACAT	2691
Haemophilia B Cys88Tyr TGT-TAT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT CTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGC AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT	2692
	ACCACCTTGTTATCAGCACTATTTTTACAAAAGTCTCGCATC TGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAA	2693
	TGTAACATGTAACATTA	2694

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAATGTTAC <u>A</u> TGTTACA	2695
Haemophilia B Ile90Thr ATT-ACT	ATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTA GATGTAACATGTAACATTAAGAATGGCAGATGCGAGCAGTTTT GTAAAAATAGTGCTGATAACAAGGTGGTTTGCTC	2696
	GAGCAAACCACCTTGTTATCAGCACTATTTTTACAAAACCTGCT CGCATCTGCCATTCTTA <u>A</u> TGTTACATGTTACATCTAAAAGAAG CAAAATAGACAGTAACAGCATCATTTAACATGCAT	2697
	ATGTAACATTAAGAATG	2698
	CATTCTTA <u>A</u> TGTTACAT	2699
Haemophilia B Asn92His gAAT-CAT	TGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGT AACATGTAACATTAAGAATGGCAGATGCGAGCAGTTTTGTAAA AATAGTGCTGATAACAAGGTGGTTTGCTCCTGTA	2700
	TACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTACAAAA CTGCTCGCATCTGCCAT <u>I</u> CTTAATGTTACATGTTACATCTAAA AGAAGCAAAATAGACAGTAACAGCATCATTTAACA	2701
	ACATTAAGA <u>A</u> ATGGCAGA	2702
	TCTGCCATT <u>C</u> TTAATGT	2703
Haemophilia B Asn92Lys AATg-AAA	TTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAA CATGTAACATTAAGAAT <u>T</u> GGCAGATGCGAGCAGTTTTGTAAAAA TAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT	2704
	AGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTACAA AACTGCTCGCATCTGCC <u>A</u> TTCTTAATGTTACATGTTACATCTA AAAGAAGCAAAATAGACAGTAACAGCATCATTTAA	2705
	ATTAAGAAT <u>T</u> GGCAGATG	2706
	CATCTGCC <u>A</u> TTCTTAAT	2707
Haemophilia B Gly93Asp GGC-GAC	AAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACA TGTAACATTAAGAATG <u>G</u> CAGATGCGAGCAGTTTTGTAAAAATA GTGCTGATAACAAGGTGGTTTGCTCCTGTACTGA	2708
	TCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTAC AAACTGCTCGCATCTG <u>C</u> CATTCTTAATGTTACATGTTACATC TAAAAGAAGCAAAATAGACAGTAACAGCATCATTT	2709
	TAAGAATG <u>G</u> CAGATGCG	2710
	CGCATCTG <u>C</u> CATTCTTA	2711
Haemophilia B Gly93Ser tGGC-AGC	TAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAAC ATGTAACATTAAGAATG <u>G</u> CAGATGCGAGCAGTTTTGTAAAAAT AGTGCTGATAACAAGGTGGTTTGCTCCTGTACTG	2712
	CAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTACA AAACTGCTCGCATCTG <u>C</u> CATTCTTAATGTTACATGTTACATCT AAAAGAAGCAAAATAGACAGTAACAGCATCATTTA	2713
	TTAAGAATG <u>G</u> CAGATGC	2714
	GCATCTG <u>C</u> CATTCTTAA	2715
Haemophilia B Arg94Ser AGAt-AGT	GATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTA ACATTAAGAATGGCAG <u>A</u> TGCGAGCAGTTTTGTAAAAATAGTG CTGATAACAAGGTGGTTTGCTCCTGTACTGAGGGA	2716

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTT TTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTACATGTTA CATCTAAAAGAAGCAAAATAGACAGTAACAGCATC	2717
	AATGGCAGATGCGAGCA	2718
	TGCTCGCATCTGCCATT	2719
Haemophilia B Cys95Tyr TGC-TAC	TGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAAC ATTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCT GATAACAAGGTGGTTTGCTCCTGTACTGAGGGATA	2720
	TATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTAT TTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTACATGTT ACATCTAAAAGAAGCAAAATAGACAGTAACAGCA	2721
	TGGCAGATGCGAGCAGT	2722
	ACTGCTCGCATCTGCCA	2723
Haemophilia B Cys95Trp TGCg-TGG	GCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACA TTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTG ATAACAAGGTGGTTTGCTCCTGTACTGAGGGATAT	2724
	ATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTA TTTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTACATGT TACATCTAAAAGAAGCAAAATAGACAGTAACAGC	2725
	GGCAGATGCGAGCAGTT	2726
	AACTGCTCGCATCTGCC	2727
Haemophilia B Cys95Term TGCg-TGA	GCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACA TTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTG ATAACAAGGTGGTTTGCTCCTGTACTGAGGGATAT	2728
	ATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTA TTTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTACATGT TACATCTAAAAGAAGCAAAATAGACAGTAACAGC	2729
	GGCAGATGCGAGCAGTT	2730
	AACTGCTCGCATCTGCC	2731
Haemophilia B Gln97Pro CAG-CCG	TACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAG AATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAAC AAGGTGGTTTGCTCCTGTACTGAGGGATATCGACT	2732
	AGTCGATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCA GCACTATTTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTT ACATGTTACATCTAAAAGAAGCAAAATAGACAGTA	2733
	ATGCGAGCAGTTTTGTA	2734
	TACAAAACCTGCTCGCAT	2735
Haemophilia B Gln97Glu gCAG-GAG	TACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAG GAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAAC CAAGGTGGTTTGCTCCTGTACTGAGGGATATCGAC	2736
	GTCGATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAG CACTATTTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTA CATGTTACATCTAAAAGAAGCAAAATAGACAGTAA	2737
	GATGCGAGCAGTTTTGT	2738

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACAAA <u>A</u> CTGCTCGCATC	2739
Haemophilia B Cys99Arg tTGT-CGT	TCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGG CAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGT GGTTTGCTCCTGTACTGAGGGATATCGACTTGCAG	2740
	CTGCAAGTCGATATCCCTCAGTACAGGAGCAAACACCTTGT TATCAGCACTATTTTTACAAA <u>A</u> CTGCTCGCATCTGCCATTCTTA ATGTTACATGTTACATCTAAAAGAAGCAAATAGA	2741
	AGCAGTTTTGTAAAAAT	2742
	ATTTTACAAA <u>A</u> CTGCT	2743
Haemophilia B Cys99Tyr TGT-TAT	CTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGGC AGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTG GTTTGCTCCTGTACTGAGGGATATCGACTTGCAGA	2744
	TCTGCAAGTCGATATCCCTCAGTACAGGAGCAAACACCTTG TTATCAGCACTATTTTTACAAA <u>A</u> CTGCTCGCATCTGCCATTCTT AATGTTACATGTTACATCTAAAAGAAGCAAATAGA	2745
	GCAGTTTTGTAAAAATA	2746
	TATTTTACAAA <u>A</u> CTGC	2747
Warfarin sensitivity Ala(-10)Thr cGCC-ACC	TTTTTGCTAAAACTAAAGAATTATTCTTTACATTTTCAGTTTTT CTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGA GGTATAATTCAGGTAAATTGGAAGAGTTTGTTT	2748
	GAACAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCG ATTCAGAATTTTGTTGGCGTTTTTCATGATCAAGAAAACTGAA ATGTAAAAGAATAATTCTTTAGTTTTAGCAAAAAA	2749
	ATGAAAACGCCAACAAA	2750
	TTTGTTGGCGTTTTTCAT	2751
Warfarin sensitivity Ala(-10)Val GCC-GTC	TTTTTGCTAAAACTAAAGAATTATTCTTTACATTTTCAGTTTTT TTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGA GGTATAATTCAGGTAAATTGGAAGAGTTTGTTTCA	2752
	TGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCC GATTTCAGAATTTTGTTGGCGTTTTTCATGATCAAGAAAACTGA AATGTAAAAGAATAATTCTTTAGTTTTAGCAAAAAA	2753
	TGAAAACGCCAACAAA	2754
	TTTTGTTGGCGTTTTTCA	2755
Haemophilia B Gly(-26)Val GGA-GTA	TGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCCTCA TCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTAC AGGTTTGTTTCCTTTTTTAAATACATTGAGTATGC	2756
	GCATACTCAATGTATTTTAAAAAGGAAACAAACCTGTACATT CAGCACTGAGTAGATATCTAAAAGGCAGATGGTGATGAGGC CTGGTGATTCTGCCATGATCATGTTACGCGCTGCA	2757
	CCTTTTAGGATATCTAC	2758
	GATGATATCTAAAAGG	2759
Haemophilia B Leu(-27)Term TTΔ-TΔΔ	TTATGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCC TCATCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATG TACAGGTTTGTTTCCTTTTTTAAATACATTGAGTA	2760

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
TTA-TAA	TACTCAATGTATTTTAAAAAAGGAAACAAACCTGTACATTCAG CACTGAGTAGATATCCTAAAAGGCAGATGGTGATGAGGCCTG GTGATTCTGCCATGATCATGTTACGCGCTGCATAA	2761
	CTGCCTTTTAGGATATC	2762
	GATATCCTAAAAGGCAG	2763
Haemophilia B Ile(-30)Asn ATC-AAC	TAGCAAAGGTTATGCAGCGCGTGAACATGATCATGGCAGAAT CACCAGGCCTCATCACCATCTGCCTTTTAGGATATCTACTCAG TGCTGAATGTACAGGTTTGTTCCTTTTTTAAAATA	2764
	TATTTTAAAAAAGGAAACAAACCTGTACATTCAGCACTGAGTA GATATCCTAAAAGGCAGATGGTGATGAGGCCTGGTGATTCTG CCATGATCATGTTACGCGCTGCATAACCTTTGCTA	2765
	CATCACCATCTGCCTTT	2766
	AAAGGCAGATGGTGATG	2767
Haemophilia B Ile(-40)Phe gATC-TTC	ACTAATCGACCTTACCACTTTCACAATCTGCTAGCAAAGGTTA TGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCCTCA TCACCATCTGCCTTTTAGGATATCTACTCAGTGCTG	2768
	CAGCACTGAGTAGATATCCTAAAAGGCAGATGGTGATGAGGC CTGGTGATTCTGCCATGATCATGTTACGCGCTGCATAACCTT TGCTAGCAGATTGTGAAAGTGGTAAGGTCGATTAGT	2769
	TGAACATGATCATGGCA	2770
	TGCCATGATCATGTTCA	2771
Haemophilia B Arg(-44)His CGC-CAC	ACTTTGGTACAACCTAATCGACCTTACCACTTTCACAATCTGCT AGCAAAGGTTATGCAGCGCGTGAACATGATCATGGCAGAATC ACCAGGCCTCATCACCATCTGCCTTTTAGGATATCT	2772
	AGATATCCTAAAAGGCAGATGGTGATGAGGCCTGGTGATTCT GCCATGATCATGTTACGCGCTGCATAACCTTTGCTAGCAGA TTGTGAAAGTGGTAAGGTCGATTAGTTGTACCAAAGT	2773
	TATGCAGCGCGTGAACA	2774
	TGTTACGCGCTGCATA	2775

EXAMPLE 16

Alpha thalassemia - Hemoglobin alpha locus 1

[0228] The thalassemia syndromes are a heterogeneous group of inherited anemias characterized by defects in the synthesis of one or more globin chain subunits. For example, beta-thalassemia discussed in Example 6, is caused by a decrease in beta-chain production relative to alpha-chain production; the converse is the case for alpha-thalassemia. The attached table discloses the correcting oligonucleotide base sequences for the hemoglobin alpha locus 1 oligonucleotides of the invention.

Table 18

HBA1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia alpha Met(-1)Val cATG-GTG	CCCTGGCGCGCTCGCGGCCCGGCACTCTTCTGGTCCCCACA GACTCAGAGAGAACCCACC <u>A</u> TGGTGCTGTCTCCTGCCGACAA GACCAACGTCAAGGCCCGCTGGGGTAAGGTCGGCGCGC	2776
	GCGCGCCGACCTTACCCAGGGCGCCTTGACGTTGGTCTTG TCGGCAGGAGACAGCACC <u>A</u> TGGTGGGTTCTCTCTGAGTCTGT GGGGACCAGAAGAGTGCCGGGCCGCGAGCGCGCCAGGG	2777
	AACCCACC <u>A</u> TGGTGCTG	2778
	CAGCACC <u>A</u> TGGTGGGTT	2779
Haemoglobin variant Ala12Asp GCC-GAC	CACAGACTCAGAGAGAACCCACCATGGTGCTGTCTCCTGCCG ACAAGACCAACGTCAAGG <u>C</u> CGCCTGGGGTAAGGTCGGCGCG CACGCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTG	2780
	CACCTCTCCAGGGCCTCCGCACCATACTCGCCAGCGTGCGC GCCGACCTTACCCAGGG <u>C</u> GCTTGACGTTGGTCTTGTCGG CAGGAGACAGCACCATGGTGGGTTCTCTCTGAGTCTGTG	2781
	CGTCAAGG <u>C</u> CGCCTGGG	2782
	CCCAGGG <u>C</u> GCTTGACG	2783
Haemoglobin variant Gly15Asp GGT-GAT	AGAGAGAACCCACCATGGTGCTGTCTCCTGCCGACAAGACCA ACGTCAAGGCCCGCTGGG <u>G</u> TAAGGTCGGCGCGCACGCTGG CGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCT	2784
	AGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCGCC AGCGTGCGCGCCGACCTT <u>A</u> CCCCAGGCGGCCTTGACGTTGG TCTTGTCGGCAGGAGACAGCACCATGGTGGGTTCTCTCT	2785
	CGCCTGGG <u>G</u> TAAGGTCG	2786
	CGACCTT <u>A</u> CCCCAGGCG	2787
Haemoglobin variant Tyr24Cys TAT-TGT	CTGCCGACAAGACCAACGTCAAGGCCCGCTGGGGTAAGGTC GGCGCGCACGCTGGCGAGT <u>A</u> TGGTGCGGAGGCCCTGGAGA GGTGAGGCTCCCTCCCCTGCTCCGACCCGGGCTCCTCGCC	2788
	GGCGAGGAGCCCGGGTCGGAGCAGGGGAGGGAGCCTCACC TCTCCAGGGCCTCCGCACC <u>A</u> CTCGCCAGCGTGCGCGCCG ACCTTACCCAGGCGGCCTTGACGTTGGTCTTGTCGGCAG	2789
	TGGCGAGT <u>A</u> TGGTGCGG	2790
	CCGCACC <u>A</u> CTCGCCA	2791
Haemoglobin variant Glu27Asp GAGg-GAT	GACCAACGTCAAGGCCCGCTGGGGTAAGGTCGGCGCGCAC GCTGGCGAGTATGGTGCGGAG <u>G</u> CCCTGGAGAGGTGAGGCT CCCTCCCCTGCTCCGACCCGGGCTCCTCGCCCCGCCGGACC	2792
	GGTCCGGGCGGGCGAGGAGCCCGGGTCGGAGCAGGGGAG GGAGCCTCACCTCTCCAGGG <u>C</u> TCCGCACCATACTCGCCAG CGTGCGCGCCGACCTTACCCAGGGCGGCCTTGACGTTGGTC	2793
	GGTGCGGAG <u>G</u> CCCTGGA	2794
	TCCAGGG <u>C</u> TCCGCACC	2795

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemoglobin variant Asn68Lys AACg-AAG	GAGCCACGGCTCTGCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAACGCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG	2796
	CGCGTGCAGGTGCTCAGGGCGGACAGCGCGTTGGGCATGT CGTCCACGTGCGCCACGGCGTTGGTCAGCGCGTCGGCCACC TTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC	2797
	CTGACCAACGCCGTGGC	2798
	GCCACGGCGTTGGTCAG	2799
Haemoglobin variant Asp74Gly GAC-GGC	AGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGACC AACGCCGTGGCGCACGTGGACGACATGCCCAACGCGCTGTC CGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGGA	2800
	TCCACCCGAAGCTTGTGCGCGTGCAGGTCGCTCAGGGCGGA CAGCGCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGG TCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCT	2801
	GCACGTGGACGACATGC	2802
	GCATGTCGTCCACGTGC	2803
Haemoglobin variant Asp74His gGAC-CAC	CAGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGAC CAACGCCGTGGCGCACGTGGACGACATGCCCAACGCGCTGT CCGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGG	2804
	CCACCCGAAGCTTGTGCGCGTGCAGGTCGCTCAGGGCGGAC AGCGCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGT CAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCTG	2805
	CGCACGTGGACGACATG	2806
	CATGTCGTCCACGTGCG	2807
Haemoglobin variant Asn78His cAAC-CAC	CACGGCAAGAAGGTGGCCGACGCGCTGACCAACGCCGTGG CGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGAGC GACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAACT	2808
	AGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTCG CTCAGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGC CACGGCGTTGGTCAGCGCGTCGGCCACCTTCTTGCCGTG	2809
	ACATGCCCACGCGCTG	2810
	CAGCGCGTTGGGCATGT	2811
Haemoglobin variant His87Tyr gCAC-TAC	ACCAACGCCGTGGCGCACGTGGACGACATGCCCAACGCGCT GTCCGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGG ACCCGGTCAACTTCAAGGTGAGCGGCGGGCCGGGAGCGA	2812
	TCGCTCCCGGCCCCGCGCTCACCTTGAAGTTGACCGGGTCC ACCCGAAGCTTGTGCGCGTGCAGGTCGCTCAGGGCGGACAG CGCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGT	2813
	GCGACCTGCACGCGCAC	2814
	GTGCGCGTGCAGGTCGC	2815

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemoglobin variant Lys90Asn AAGc-AAC	GGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGA GCGACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAAC TTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTCGAG	2816
	CTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGT TGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTGCTC AGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCC	2817
	GCGCACAAGCTTCGGGT	2818
	ACCCGAAGCTTGTGCGC	2819
Haemoglobin variant Lys90Thr AAG-ACG	TGGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTG AGCGACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAA CTTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTCGA	2820
	TCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGTT GACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTGCTCA GGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCCA	2821
	CGCGCACAAGCTTCGGG	2822
	CCCGAAGCTTGTGCGCG	2823
Haemoglobin variant Arg92Gln CGG-CAG	ACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGAGCGAC CTGCACGCGCACAAGCTTCCGGGTGGACCCGGTCAACTTCAA GGTGAGCGGCGGGCCGGGAGCGATCTGGGTGAGGGGGCG	2824
	CGCCCCTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTT GAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGT CGCTCAGGGCGGACAGCGCGTTGGGCATGTCGTCCACGT	2825
	CAAGCTTCCGGGTGGACC	2826
	GGTCCACCCGAAGCTTG	2827
Haemoglobin variant Asp94Gly GAC-GGC	ACGACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCAC GCGCACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGAG CGGCGGGCCGGGAGCGATCTGGGTGAGGGGGCGAGATGG	2828
	CCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCCGCT CACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGT GCAGGTGCTCAGGGCGGACAGCGCGTTGGGCATGTCGT	2829
	TCGGGTGGACCCGGTCA	2830
	TGACCGGGTCCACCCGA	2831
Haemoglobin variant Pro95Arg CCG-CGG	ACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG CACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGAGCGG CGGGCCGGGAGCGATCTGGGTGAGGGGGCGAGATGGCGC	2832
	GCGCCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCC GCTCACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCG CGTGCAGGTGCTCAGGGCGGACAGCGCGTTGGGCATGT	2833
	GGTGGACCCGGTCAACT	2834
	AGTTGACCGGGTCCACC	2835

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemoglobin variant Ser102Arg AGCc-AGA	CGGCGGCTGCGGGCCTGGGCCCTCGGCCCCACTGACCCTC TTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTG GCCGCCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCAC	2836
	GTGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGGCC AGGGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCAGAGAA GAGGGTCAGTGGGGCCGAGGGCCCAGGCCCGCAGCCGCCG	2837
	CTCCTAAGCCACTGCCT	2838
	AGGCAGTGGCTTAGGAG	2839
Haemoglobin variant Glu116Lys cGAG-AAG	TTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTG GCCGCCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGC CTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGC	2840
	GCACGGTGCTCACAGAAGCCAGGAACCTGTCCAGGGAGGCG TGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGGCA GGGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCAGAGAA	2841
	TCCCCGCCGAGTTCACC	2842
	GGTGAACCTCGGCGGGGA	2843
Haemoglobin variant Ala120Glu GCG-GAG	TCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGCCACCTC CCCGCCGAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAA GTTCTTGCTTCTGTGAGCACCGTGTGACCTCCAAATA	2844
	TATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAGGAACCTG TCCAGGGAGGCGTGACCCGCAGGGGTGAACTCGGCGGGGA GGTGGGCGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGA	2845
	CACCCCTGCGGTGCACG	2846
	CGTGCACCCGCAGGGGTG	2847
Thalassaemia alpha Leu129Pro CTG-CCG	TGGCCGCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCAC GCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGTG ACCTCCAAATACCGTTAAGCTGGAGCCTCGGTGGCCAT	2848
	ATGGCCACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGC ACGGTGCTCACAGAAGCCAGGAACCTGTCCAGGGAGGCGTG CACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGGCA	2849
	CAAGTTCCTGGCTTCTG	2850
	CAGAAGCCAGGAACCTG	2851
Haemoglobin variant Arg141Leu CGT-CTT	TGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCG TGCTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTGGCCA TGCTTCTTGCCCTTGGGCCTCCCCCAGCCCTCCT	2852
	AGGAGGGGCTGGGGGGAGGCCCAAGGGGCAAGAAGCATGG CCACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCACG GTGCTCACAGAAGCCAGGAACCTGTCCAGGGAGGCGTGCA	2853
	CAAATACCGTTAAGCTG	2854
	CAGCTTAACGGTATTTG	2855

EXAMPLE 17

Alpha-thalassemia - Hemoglobin alpha locus 2

[0229] The attached table discloses the correcting oligonucleotide base sequences for the hemoglobin alpha locus 2 oligonucleotides of the invention.

Table 19

HBA2 Mutations and Genome-Correcting Oligos

5

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia alpha Met(-1)Thr ATG-ACG	CCTGGCGCGCTCGCGGGCCGGCACTCTTCTGGTCCCCACAG ACTCAGAGAGAACCCACCATGGTGCTGTCTCCTGCCGACAAG ACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCA	2856
	TGCGCGCCGACCTTACCCCAGGCGGCCTTGACGTTGGTCTT GTCGGCAGGAGACAGCACCATGGTGCGGTTCTCTCTGAGTCT GTGGGGACCAGAAGAGTGCCGGCCCGCAGCGCGCCAGG	2857
	ACCCACCATGGTGCTGT	2858
	ACAGCACCATGGTGCGG	2859
Haemoglobin variant Ala12Asp GCC-GAC	CACAGACTCAGAGAGAACCCACCATGGTGCTGTCTCCTGCCG ACAAGACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCG CACGCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTG	2860
	CACCTCTCCAGGGCCTCCGCACCATACTCGCCAGCGTGCGC GCCGACCTTACCCCAGGCGGCCTTGACGTTGGTCTTGTGCG CAGGAGACAGCACCATGGTGCGGTTCTCTCTGAGTCTGTG	2861
	CGTCAAGGCCGCCTGGG	2862
	CCCAGGCGGCCTTGACG	2863
Haemoglobin variant Lys16Glu TAAG-GAG	AGAGAACCCACCATGGTGCTGTCTCCTGCCGACAAGACCAAC GTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCACGCTGGCG AGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCTCC	2864
	GGAGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCG CCAGCGTGCGCGCCGACCTTACCCCAGGCGGCCTTGACGTT GGTCTTGTGCGCAGGAGACAGCACCATGGTGCGGTTCTCT	2865
	CCTGGGGTAAGGTCGGC	2866
	GCCGACCTTACCCCAGG	2867
Haemoglobin variant His20Gln CACg-CAA	GGTGCTGTCTCCTGCCGACAAGACCAACGTCAAGGCCGCCT GGGGTAAGGTCGGCGCGCACGCTGGCGAGTATGGTGCGGA GGCCCTGGAGAGGTGAGGCTCCCTCCCCTGCTCCGACCCG	2868
	CGGGTCGGAGCAGGGGAGGAGCCTCACCTCTCCAGGGCC TCCGCACCATACTCGCCAGCGTGCGCGCCGACCTTACCCA GGCGGCCTTGACGTTGGTCTTGTGCGCAGGAGACAGCACC	2869
	GGCGCGCACGCTGGCGA	2870
	TCGCCAGCGTGCGCGCC	2871
Haemoglobin variant Glu27Asp GAGg-GAC	GACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCAC GCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCT CCCTCCCCTGCTCCGACCCGGGCTCCTCGCCCGCCCGGACC	2872

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGTCCGGGCGGGCGAGGAGCCCGGGTCCGAGCAGGGGAG GGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCGCCAG CGTGCGCGCCGACCTTACCCAGGCGGCCTTGACGTTGGTC	2873
	GGTGCGGAGGCCCTGGA	2874
	TCCAGGGCCTCCGCACC	2875
Thalassaemia alpha Leu29Pro CTG-CCG	ACGTCAAGGCCGCTGGGGTAAGGTCGGCGCGCACGCTGG CGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCTCC CCTGCTCCGACCCGGGCTCCTCGCCCGCCCGACCCACAG	2876
	CTGTGGGTCCGGGCGGGCGAGGAGCCCGGGTCCGAGCAGG GGAGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCG CCAGCGTGCGCGCCGACCTTACCCAGGCGGCCTTGACGT	2877
	GGAGGCCCTGGAGAGGT	2878
	ACCTCTCCAGGGCCTCC	2879
Haemoglobin variant Asp47His cGAC-CAC	GCTTCTCCCCGCAGGATGTTCTGTCTTCCCCACCACCAAG ACCTACTTCCCGCACTTCGACCTGAGCCACGGCTCTGCCCAG GTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGA	2880
	TCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCTGG GCAGAGCCGTGGCTCAGGTGGAAGTGCGGGAAGTAGGTCTT GGTGGTGGGGAAGGACAGGAACATCCTGCGGGGAGAAGC	2881
	CGCACTTCGACCTGAGC	2882
	GCTCAGGTGGAAGTGCG	2883
Haemoglobin variant Leu48Arg CTG-CGG	CTCCCCGCAGGATGTTCTGTCTTCCCCACCACCAAGACCT ACTTCCCGCACTTCGACCTGAGCCACGGCTCTGCCCAGGTTA AGGGCCACGGCAAGAAGGTGGCCGACGCGCTGACCAA	2884
	TTGGTCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACC TGGGCAGAGCCGTGGCTCAGGTGGAAGTGCGGGAAGTAGGT CTTGGTGGTGGGGAAGGACAGGAACATCCTGCGGGGAG	2885
	CTTCGACCTGAGCCACG	2886
	CGTGGCTCAGGTGGAAG	2887
Haemoglobin variant Gln54Glu cCAG-GAG	CTGTCCTTCCCCACCACCAAGACCTACTTCCCGCACTTCGAC CTGAGCCACGGCTCTGCCAGGTTAAGGGCCACGGCAAGAA GGTGGCCGACGCGCTGACCAACGCCGTGGCGCACGTGG	2888
	CCACGTGCGCCACGGCGTTGGTCAGCGCGTCGGCCACCTTC TTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTCAGGTC GAAGTGCGGGAAGTAGGTCTTGGTGGTGGGGAAGGACAG	2889
	GCTCTGCCAGGTTAAG	2890
	CTTAACCTGGGCAGAGC	2891
Haemoglobin variant Gly59Asp GGC-GAC	CCAAGACCTACTTCCCGCACTTCGACCTGAGCCACGGCTCTG CCCAGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTG ACCAACGCCGTGGCGCACGTGGACGACATGCCCAACGC	2892

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGTCAG CGCGTCGGCCACCTTCTTG <u>C</u> CGTGGCCCTTAACCTGGGCAG AGCCGTGGCTCAGGTCGAAGTGCGGGAAGTAGGTCTTGG	2893
	GGGCCACG <u>G</u> CAAGAAGG	2894
	CCTTCTTG <u>C</u> CGTGGCCC	2895
Haemoglobin variant Asn68Lys AACg-AAG	GAGCCACGGCTCTGCCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAA <u>C</u> GCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG	2896
	CGCGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGT CGTCCACGTGCGCCACGGC <u>G</u> TTGGTCAGCGCGTCGGCCACC TTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC	2897
	CTGACCAA <u>C</u> GCCGTGGC	2898
	GCCACGGC <u>G</u> TTGGTCAG	2899
Haemoglobin variant Asn68Lys AACg-AAA	GAGCCACGGCTCTGCCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAA <u>C</u> GCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG	2900
	CGCGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGT CGTCCACGTGCGCCACGGC <u>G</u> TTGGTCAGCGCGTCGGCCACC TTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC	2901
	CTGACCAA <u>C</u> GCCGTGGC	2902
	GCCACGGC <u>G</u> TTGGTCAG	2903
Haemoglobin variant Asn78Lys AACg-AAA	CGGCAAGAAGGTGGCCGACGCGCTGACCAACGCCGTGGCG CACGTGGACGACATGCCCAA <u>C</u> GCGCTGTCCGCCCTGAGCGA CCTGCACGCGCACAAGCTTCGGGTGACCCGGTCAACTTC	2904
	GAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGT CGCTCAGGGCGGACAGCGC <u>G</u> TTGGGCATGTCGTCCACGTGC GCCACGGCGTTGGTCAGCGCGTCGGCCACCTTCTTGCCG	2905
	ATGCCCAA <u>C</u> GCGCTGTC	2906
	GACAGCGC <u>G</u> TTGGGCAT	2907
Haemoglobin variant Asp85Val GAC-GTC	CGCTGACCAACGCCGTGGCGCACGTGGACGACATGCCCAAC GCGCTGTCCGCCCTGAGCGA <u>A</u> CCTGCACGCGCACAAGCTTCG GGTGGACCCGGTCAACTTCAAGGTGAGCGGCGGGCCGGG	2908
	CCCGGCCCGCCGCTCACCTTGAAGTTGACCGGGTCCACCCG AAGCTTGTGCGCGTGCAGG <u>T</u> CGCTCAGGGCGGACAGCGCGT TGGGCATGTCGTCCACGTGCGCCACGGCGTTGGTCAGCG	2909
	CCTGAGCGA <u>A</u> CCTGCACG	2910
	CGTGCAGG <u>T</u> CGCTCAGG	2911
Haemoglobin variant Lys90Asn AAGc-AAT	GGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGA GCGACCTGCACGCGCACAAG <u>C</u> TTCCGGTGACCCGGTCAAC TTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTGAG	2912

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGT TGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTGCGTC AGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCC	2913
	GCGCACAAGCTTCGGGT	2914
	ACCCGAAGCTTGTGCGC	2915
Haemoglobin variant Asp94His gGAC-CAC	GACGACATGCCAACGCGCTGTCCGCCCTGAGCGACCTGCA CGCGCACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGA GCGGCGGGGCCGGGAGCGATCTGGGTGAGGGGCGAGATG	2916
	CATCTCGCCCTCGACCCAGATCGCTCCCGGCCCGCCGCTC ACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTG CAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGTCGTC	2917
	TTCGGGTGGACCCGGTC	2918
	GACCGGGTCCACCCGAA	2919
Haemoglobin variant Pro95Leu CCG-CTG	ACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG CACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGAGCGG CGGGCCGGGAGCGATCTGGGTGAGGGGCGAGATGGCGC	2920
	GCGCCATCTCGCCCTCGACCCAGATCGCTCCCGGCCCGCC GCTCACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCG CGTGCAAGTCGCTCAGGGCGGACAGCGCGTTGGGCATGT	2921
	GGTGGACCCGGTCAACT	2922
	AGTTGACCGGGTCCACC	2923
Haemoglobin variant Ser102Arg aAGC-CGC	TAGCGCAGGCGGCGGCTGCGGGCCTGGGCGCACTGACCC TCTTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCC TGCCCGCCACCTCCCCGCCGAGTTCACCCCTGCGGTGC	2924
	GCACCGCAGGGGTGAAGTTCGGCGGGGAGGTGGGCGGCCAG GGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCAGAGAAGA GGGTCAGTGCGGCCAGGCCCGCAGCCGCCGCTGCGCTA	2925
	AGCTCCTAAGCCACTGC	2926
	GCAGTGGCTTAGGAGCT	2927
Haemoglobin H disease Cys104Tyr TGC-TAC	GGCGGCGGCTGCGGGCCTGGGCCGCACTGACCCTCTTCTCT GCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGC CCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGCCTC	2928
	GAGGCGTGACCCGAGGGGTGAAGTTCGGCGGGGAGGTGGG CGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCA GAGAAGAGGGTCAGTGCGGCCAGGCCCGCAGCCGCCGCC	2929
	AAGCCACTGCCTGCTGG	2930
	CCAGCAGGCAGTGGCTT	2931
Haemoglobin variant Ala111Val GCC-GTC	CCGCACTGACCCTCTTCTCTGCACAGCTCCTAAGCCACTGCC TGCTGGTGACCCTGGCCGCCACCTCCCCGCCGAGTTCACC CCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGGCTTC	2932

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAAGCCAGGAACTTGTCCAGGGAGGCGTGCACCGCAGGGGT GAACTCGGCGGGGAGGTGGGCGGGCCAGGGTCACCAGCAGG CAGTGGCTTAGGAGCTGTGCAGAGAAGAGGGTCAGTGC GG	2933
	CCTGGCCGCCCACCTCC	2934
	GGAGGTGGCGGGCCAGG	2935
Haemoglobin variant Ala120Glu GCG-GAG	TCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGCCACCTC CCCGCCGAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAA GTTCTTGCTTCTGTGAGCACCGTGTGACCTCCAAATA	2936
	TATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAGGAACTTG TCCAGGGAGGCGTGCACCGCAGGGGTGAACTCGGCGGGGA GGTGGGCGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGA	2937
	CACCCCTGCGGTGCACG	2938
	CGTGCACCGCAGGGGTG	2939
Haemoglobin variant His122Gln CACg-CAG	CCACTGCCTGCTGGTGACCCTGGCCGCCACCTCCCCGCCG AGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTG GCTTCTGTGAGCACCGTGTGACCTCCAAATACCGTTAA	2940
	TTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAG GAACTTGTCCAGGGAGGCGTGCACCGCAGGGGTGAACTCGG CGGGGAGGTGGGCGGCCAGGGTCACCAGCAGGCAGTGG	2941
	GCGGTGCACGCCTCCCT	2942
	AGGGAGGCGTGCACCGC	2943
Haemoglobin variant Ala123Ser cGCC-TCC	CACTGCCTGCTGGTGACCCTGGCCGCCACCTCCCCGCCGA GTTACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGG CTTCTGTGAGCACCGTGTGACCTCCAAATACCGTTAAG	2944
	CTTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCA GGA ACTTGTCCAGGGAGGCGTGCACCGCAGGGGTGAACTCG GCGGGGAGGTGGGCGGCCAGGGTCACCAGCAGGCAGTGTG	2945
	CGGTGCACGCCTCCCTG	2946
	CAGGGAGGCGTGCACCG	2947
Thalassaemia alpha Leu125Pro CTG-CCG	TGCTGGTGACCCTGGCCGCCACCTCCCCGCCGAGTTCACC CCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTG AGCACCGTGTGACCTCCAAATACCGTTAAGCTGGAGC	2948
	GCTCCAGCTTAACGGTATTTGGAGGTCAGCACGGTGCTCACA GAAGCCAGGAACTTGTCCAGGGAGGCGTGCACCGCAGGGGT GAACTCGGCGGGGAGGTGGGCGGCCAGGGTCACCAGCA	2949
	CGCCTCCCTGGACAAGT	2950
	ACTTGTCCAGGGAGGCG	2951
Haemoglobin variant Ser131Pro tTCT-CCT	GCCCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGCCTC CCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGTGACCTC CAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTTCTC	2952
	GAGGAACGGCTACCGAGGCTCCAGCTTAACGGTATTTGGAG GTCAGCACGGTGCTCACAGAGCCAGGAACTTGTCCAGGGA GGCGTGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGC	2953

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCCTGGCTTCTGTGAGC	2954
	GCTCACAG <u>A</u> AGCCAGGA	2955
Haemoglobin variant Leu136Met gCTG-ATG	GAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCT GGCTTCTGTGAGCACCGTG <u>C</u> TGACCTCCAAATACCGTTAAGC TGGAGCCTCGGTAGCCGTTCTCCTGCCCGCTGGGCCT	2956
	AGGCCCAGCGGGCAGGAGGAACGGCTACCGAGGCTCCAGC TTAACGGTATTTGGAGGTCAG <u>C</u> CACGGTGCTCACAGAAGCCAG GAACTTGTCCAGGGAGGCGTGACCGCAGGGGTGAACTC	2957
	GCACCGTG <u>C</u> TGACCTCC	2958
	GGAGGTCAG <u>C</u> CACGGTGC	2959
Haemoglobin variant Leu136Pro CTG-CCG	AGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTG GCTTCTGTGAGCACCGTG <u>C</u> TGACCTCCAAATACCGTTAAGCT GGAGCCTCGGTAGCCGTTCTCCTGCCCGCTGGGCCTC	2960
	GAGGCCCAGCGGGCAGGAGGAACGGCTACCGAGGCTCCAG CTTAACGGTATTTGGAGGTCAG <u>C</u> CACGGTGCTCACAGAAGCCA GGAACCTGTCCAGGGAGGCGTGACCGCAGGGGTGAACT	2961
	CACCGTG <u>C</u> TGACCTCCA	2962
	TGGAGGTCAG <u>C</u> CACGGTG	2963
Haemoglobin variant Arg141Cys cCGT-TGT	GTGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACC GTGCTGACCTCCAAATAC <u>C</u> GTTAAGCTGGAGCCTCGGTAGCC GTTCTCCTGCCCCGCTGGGCCTCCCAACGGGGCCCTCC	2964
	GGAGGGCCCGTTGGGAGGCCCAGCGGGCAGGAGGAACGGC TACCGAGGCTCCAGCTTAAC <u>G</u> GTATTTGGAGGTCAGCACGGT GCTCACAGAAGCCAGGAACCTTGTCCAGGGAGGCGTGAC	2965
	CCAAATAC <u>C</u> GTTAAGCT	2966
	AGCTTAAC <u>G</u> GTATTTGG	2967
Haemoglobin variant Term142Gln tTAA-CAA	CACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTG CTGACCTCCAAATACCGT <u>T</u> AAGCTGGAGCCTCGGTAGCCGTT CCTCCTGCCCGCTGGGCCTCCCAACGGGGCCCTCCTCC	2968
	GGAGGAGGGCCCGTTGGGAGGCCCAGCGGGCAGGAGGAAC GGCTACCGAGGCTCCAGCTT <u>A</u> ACGGTATTTGGAGGTCAGCA CGGTGCTCACAGAAGCCAGGAACCTTGTCCAGGGAGGCGTG	2969
	AATACCGT <u>T</u> AAGCTGGA	2970
	TCCAGCTT <u>A</u> ACGGTATT	2971
Haemoglobin variant Term142Lys tTAA-AAA	CACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTG CTGACCTCCAAATACCGT <u>T</u> AAGCTGGAGCCTCGGTAGCCGTT CCTCCTGCCCGCTGGGCCTCCCAACGGGGCCCTCCTCC	2972
	GGAGGAGGGCCCGTTGGGAGGCCCAGCGGGCAGGAGGAAC GGCTACCGAGGCTCCAGCTT <u>A</u> ACGGTATTTGGAGGTCAGCA CGGTGCTCACAGAAGCCAGGAACCTTGTCCAGGGAGGCGTG	2973
	AATACCGT <u>T</u> AAGCTGGA	2974
	TCCAGCTT <u>A</u> ACGGTATT	2975

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemoglobin variant Term142Tyr TAAg-TAT	CGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGCT GACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTTCC TCCTGCCCCGCTGGGCCTCCCAACGGGCCCTCCTCCCC	2976
	GGGGAGGAGGGCCCGTTGGGAGGCCAGCGGGCAGGAGGA ACGGCTACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGC ACGGTGCTCACAGAAGCCAGGAACCTTGTCAGGGAGGCG	2977
	TACCGTTAAGCTGGAGC	2978
	GCTCCAGCTTAACGGTA	2979

EXAMPLE 18

Human mismatch repair - MLH1

[0230] The human MLH1 gene is homologous to the bacterial *mutL* gene, which is involved in mismatch repair. Mutations in the MLH1 gene have been identified in many individuals with hereditary nonpolyposis colorectal cancer (HNPCC). Mutations in the MLH1 gene are also implicated in predisposition to a variety of cancers associated with, for example, Muir-Torre syndrome and Turcot syndrome. The attached table discloses the correcting oligonucleotide base sequences for the MLH1 oligonucleotides of the invention.

Table 20

MLH1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Met1Arg ATG-AGG	TTGGCTGAAGGCACTTCCGTTGAGCATCTAGACGTTTCCTTG GCTCTTCTGGCGCCAAAATGTCGTTTCGTGGCAGGGGTTATTC GGCGGCTGGACGAGACAGTGGTGAACCGCATCGCGGC	2980
	GCCGCGATGCGGTTCACTGTCTCGTCCAGCCGCCGAAT AACCCCTGCCACGAACGACATTTTGGCGCCAGAAGAGCCAA GGAAACGTCTAGATGCTCAACGGAAGTGCCTTCAGCCAA	2981
	CGCCAAAATGTCGTTTCG	2982
	CGAACGACATTTTGGCG	2983
Non-polyposis colorectal cancer Met1Lys ATG-AAG	TTGGCTGAAGGCACTTCCGTTGAGCATCTAGACGTTTCCTTG GCTCTTCTGGCGCCAAAATGTCGTTTCGTGGCAGGGGTTATTC GGCGGCTGGACGAGACAGTGGTGAACCGCATCGCGGC	2984
	GCCGCGATGCGGTTCACTGTCTCGTCCAGCCGCCGAAT AACCCCTGCCACGAACGACATTTTGGCGCCAGAAGAGCCAA GGAAACGTCTAGATGCTCAACGGAAGTGCCTTCAGCCAA	2985
	CGCCAAAATGTCGTTTCG	2986

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGAACGAC <u>A</u> TTTTGGCG	2987
Non-polyposis colorectal cancer Met35Arg ATG-AGG	TGGTGAACCGCATCGCGGCGGGGGAAGTTATCCAGCGGCCA GCTAATGCTATCAAAGAGAT <u>G</u> ATTGAGAACTGGTACGGAGGG AGTCGAGCCGGGCTCACTTAAGGGCTACGACTTAACGG	2988
	CCGTTAAGTCGTAGCCCTTAAGTGAGCCCGGCTCGACTCCCT CCGTACCAGTTCTCAATC <u>A</u> TCTCTTTGATAGCATTAGCTGGCC GCTGGATAACTCCCCCGCCGCGATGCGGTTACCA	2989
	CAAAGAGATGATTGAGA	2990
	TCTCAATC <u>A</u> TCTCTTTG	2991
Non-polyposis colorectal cancer Ser44Phe TCC-TTC	TAGAGTAGTTGCAGACTGATAAATTATTTTCTGTTTGATTGGC AGTTTAGATGCAAAAT <u>C</u> CACAAGTATTCAAGTGATTGTTAAAG AGGGAGGCCTGAAGTTGATTGAGATCCAAGACAA	2992
	TTGTCTTGGATCTGAATCAACTTCAGGCCTCCCTCTTTAACAA TCACTTGAATACTTGTG <u>G</u> ATTTTGCATCTAACTGGCAAATCA AACAGAAAATAATTTATCAGTCTGCAACTACTCTA	2993
	TGCAAAAT <u>C</u> CACAAGTA	2994
	TACTTGTG <u>G</u> ATTTTGCA	2995
Non-polyposis colorectal cancer Gln62Lys CAA-AAA	GCAAAATCCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGC CTGAAGTTGATTGAGATC <u>C</u> AAGACAATGGCACCGGGATCAGG GTAAGTAAAACCTCAAAGTAGCAGGATGTTTGTGCGC	2996
	GCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGAT CCCGGTGCCATTGTCTT <u>G</u> GATCTGAATCAACTTCAGGCCTCC CTCTTTAACAATCACTTGAATACTTGTGGATTTTGC	2997
	TTCAGATC <u>C</u> AAGACAAT	2998
	ATTGTCTT <u>G</u> GATCTGAA	2999
Non-polyposis colorectal cancer Gln62Term CAA-TAA	GCAAAATCCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGC CTGAAGTTGATTGAGATC <u>C</u> AAGACAATGGCACCGGGATCAGG GTAAGTAAAACCTCAAAGTAGCAGGATGTTTGTGCGC	3000
	GCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGAT CCCGGTGCCATTGTCTT <u>G</u> GATCTGAATCAACTTCAGGCCTCC CTCTTTAACAATCACTTGAATACTTGTGGATTTTGC	3001
	TTCAGATC <u>C</u> AAGACAAT	3002
	ATTGTCTT <u>G</u> GATCTGAA	3003
Non-polyposis colorectal cancer Asn64Ser AAT-AGT	CCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGT TGATTGAGATCCAAGACA <u>A</u> TGGCACCGGGATCAGGGTAAGTA AAACCTCAAAGTAGCAGGATGTTTGTGCGCTTCATGG	3004
	CCATGAAGCGCACAAACATCCTGCTACTTTGAGGTTTTACTTA CCCTGATCCCGGTGCCA <u>T</u> TGTCTTGGATCTGAATCAACTTCA GGCCTCCCTCTTTAACAATCACTTGAATACTTGTGG	3005
	CCAAGACA <u>A</u> TGGCACCG	3006
	CGGTGCCA <u>T</u> TGTCTTGG	3007

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polypoidis colorectal cancer Gly67Arg GGG-AGG	ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTGAG ATCCAAGACAATGGCACC <u>GGG</u> GATCAGGGTAAGTAAACCTCA AAGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA	3008
	TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGT TTTACTTACCCTGATCC <u>CGG</u> TGCCATTGTCTTGGATCTGAATC AACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT	3009
	ATGGCACCC <u>GGG</u> GATCAGG	3010
	CCTGATCC <u>CGG</u> TGCCAT	3011
Non-polypoidis colorectal cancer Gly67Arg GGG-CGG	ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTGAG ATCCAAGACAATGGCACC <u>GGG</u> GATCAGGGTAAGTAAACCTCA AAGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA	3012
	TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGT TTTACTTACCCTGATCC <u>CGG</u> TGCCATTGTCTTGGATCTGAATC AACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT	3013
	ATGGCACCC <u>GGG</u> GATCAGG	3014
	CCTGATCC <u>CGG</u> TGCCAT	3015
Non-polypoidis colorectal cancer Gly67Trp GGG-TGG	ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTGAG ATCCAAGACAATGGCACC <u>GGG</u> GATCAGGGTAAGTAAACCTCA AAGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA	3016
	TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGT TTTACTTACCCTGATCC <u>CGG</u> TGCCATTGTCTTGGATCTGAATC AACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT	3017
	ATGGCACCC <u>GGG</u> GATCAGG	3018
	CCTGATCC <u>CGG</u> TGCCAT	3019
Non-polypoidis colorectal cancer Cys77Arg TGT-CGT	GTAACATGATTATTTACTCATCTTTTTGGTATCTAACAGAAAGA AGATCTGGATATTGTAT <u>TGT</u> GAAAGGTTCACTACTAGTAAACTG CAGTCCTTTGAGGATTTAGCCAGTATTTCTACCT	3020
	AGGTAGAAATACTGGCTAAATCCTCAAAGGACTGCAGTTTACT AGTAGTGAACCTTTTAC <u>A</u> TACAATATCCAGATCTTCTTTCTGTT AGATACCAAAAAGATGAGTAAATAATCATGTTAC	3021
	ATATTGTAT <u>TGT</u> GAAAGG	3022
	CCTTTTAC <u>A</u> TACAATAT	3023
Non-polypoidis colorectal cancer Cys77Tyr TGT-TAT	TAACATGATTATTTACTCATCTTTTTGGTATCTAACAGAAAGAA GATCTGGATATTGTAT <u>TGT</u> GAAAGGTTCACTACTAGTAAACTGC AGTCCTTTGAGGATTTAGCCAGTATTTCTACCTA	3024
	TAGGTAGAAATACTGGCTAAATCCTCAAAGGACTGCAGTTTAC TAGTAGTGAACCTTTTAC <u>A</u> TACAATATCCAGATCTTCTTTCTGT TAGATACCAAAAAGATGAGTAAATAATCATGTTA	3025
	TATTGTAT <u>TGT</u> GAAAGG	3026
	ACCTTTTAC <u>A</u> TACAATA	3027

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Ser93Gly AGT-GGT	CTGGATATTGTATGTGAAAGGTTCACTACTAGTAAACTGCAGT CCTTTGAGGATTTAGCCAGTATTTCTACCTATGGCTTTCGAGG TGAGGTAAGCTAAAGATTCAAGAAATGTGTAAAAT	3028
	ATTTTACACATTTCTTGAATCTTTAGCTTACCTCACCTCGAAAG CCATAGGTAGAAATACTGGCTAAATCCTCAAAGGACTGCAGT TTACTAGTAGTGAACCTTTCACATACAATATCCAG	3029
	ATTTAGCCAGTATTTCT	3030
	AGAAATACTGGCTAAAT	3031
Non-polyposis colorectal cancer Arg100Term CGA-TGA	TTCCTACTAGTAAACTGCAGTCCTTTGAGGATTTAGCCAGTA TTTCTACCTATGGCTTTCGAGGTGAGGTAAGCTAAAGATTCAA GAAATGTGTAAAATATCCTCCTGTGATGACATTGT	3032
	ACAATGTCATCACAGGAGGATATTTTACACATTTCTTGAATCTT TAGCTTACCTCACCTCGAAAGCCATAGGTAGAAATACTGGCT AAATCCTCAAAGGACTGCAGTTTACTAGTAGTGAA	3033
	ATGGCTTTCGAGGTGAG	3034
	CTCACCTCGAAAGCCAT	3035
Non-polyposis colorectal cancer Ile107Arg ATA-AGA	ACCCAGCAGTGAGTTTTCTTTCAGTCTATTTTCTTTCTTCCT TAGGCTTTGGCCAGCATAAGCCATGTGGCTCATGTTACTATTA CAACGAAAACAGCTGATGGAAAGTGTGCATACAG	3036
	CTGTATGCACACTTTCCATCAGCTGTTTTCGTTGTAATAGTAA CATGAGCCACATGGCTTATGCTGGCCAAAGCCTAAGGAAGAA AAGAAAATAGACTGAAAGAAAACTCACTGCTGGGT	3037
	GGCCAGCATAAGCCATG	3038
	CATGGCTTATGCTGGCC	3039
Non-polyposis colorectal cancer Thr117Arg ACG-AGG	TTTCTTTTCTTCCTTAGGCTTTGGCCAGCATAAGCCATGTGGC TCATGTTACTATTACAACGAAAACAGCTGATGGAAAGTGTGCA TACAGGTATAGTGCTGACTTCTTTTACTCATATAT	3040
	ATATATGAGTAAAAGAAGTCAGCACTATACCTGTATGCACACT TTCCATCAGCTGTTTTCGTTGTAATAGTAACATGAGCCACATG GCTTATGCTGGCCAAAGCCTAAGGAAGAAAAGAAA	3041
	TATTACAACGAAAACAG	3042
	CTGTTTTCGTTGTAATA	3043
Non-polyposis colorectal cancer Thr117Met ACG-ATG	TTTCTTTTCTTCCTTAGGCTTTGGCCAGCATAAGCCATGTGGC TCATGTTACTATTACAACGAAAACAGCTGATGGAAAGTGTGCA TACAGGTATAGTGCTGACTTCTTTTACTCATATAT	3044
	ATATATGAGTAAAAGAAGTCAGCACTATACCTGTATGCACACT TTCCATCAGCTGTTTTCGTTGTAATAGTAACATGAGCCACATG GCTTATGCTGGCCAAAGCCTAAGGAAGAAAAGAAA	3045
	TATTACAACGAAAACAG	3046
	CTGTTTTCGTTGTAATA	3047

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Gly133Term GGA-TGA	TCTATCTCTCTACTGGATATTAATTTGTTATATTTCTCATTAGA GCAAGTTACTCAGATGGAAACTGAAAGCCCCTCCTAAACCA TGTGCTGGCAATCAAGGGACCCAGATCACGGTAA	3048
	TTACCGTGATCTGGGTCCCTTGATTGCCAGCACATGGTTTAG GAGGGGCTTTTCAGTTTTCCATCTGAGTAACTTGCTCTAATGAG AAAATATAACAAATTAATATCCAGTAGAGAGATAGA	3049
	ACTCAGATGGAAACTG	3050
	CAGTTTTCCATCTGAGT	3051
Non-polyposis colorectal cancer Val185Gly GTA-GGA	TAGTGTGTGTTTTGGCAACTCTTTCTTACTCTTTGTTTTTC TTTTCCAGGTATTCAGTACACAATGCAGGCATTAGTTTCTCAG TTAAAAAGTAAGTTCTTGGTTTATGGGGGATGG	3052
	CCATCCCCCATAAACCAAGAACTTACTTTTTTAAGTGAAGAAC TAATGCCTGCATTGTGTACTGAATACCTGGAAAAGAAAAACAA AAGAGTAAGAAAAGAGTTGCCAAAAACACACACTA	3053
	GTATTCAGTACACAATG	3054
	CATTGTGTACTGAATAC	3055
Non-polyposis colorectal cancer Ser193Pro TCA-CCA	TTTCTTACTCTTTTGTCTTTCTTTTCCAGGTATTCAGTACACAA TGCAGGCATTAGTTTCTCAGTTAAAAAGTAAGTTCTTGGTTT ATGGGGGATGGTTTTGTCTTATGAAAAGAAAAAA	3056
	TTTTTTCTTTTCATAAAACAAAACCATCCCCCATAAACCAAGAA CTTACTTTTTTAACTGAGAAACTAATGCCTGCATTGTGTACTG AATACCTGGAAAAGAAAACAAAAGAGTAAGAAA	3057
	TTAGTTTCTCAGTTAAA	3058
	TTTAACTGAGAAACTAA	3059
Non-polyposis colorectal cancer Val213Met GTG-ATG	TTTGTTTATCAGCAAGGAGAGACAGTAGCTGATGTTAGGACA CTACCCAATGCCTCAACCGTGGACAATATTCGCTCCATCTTTG GAAATGCTGTTAGTCGGTATGTCGATAACCTATATA	3060
	TATATAGGTTATCGACATACCGACTAACAGCATTTCCAAAGAT GGAGCGAATATTGTCCACGGTTGAGGCATTGGGTAGTGTCTC AACATCAGCTACTGTCTCTCCTTGCTGATAAACAAA	3061
	CCTCAACCGTGGACAAT	3062
	ATTGTCCACGGTTGAGG	3063
Non-polyposis colorectal cancer Arg217Cys CGC-TGC	CAAGGAGAGACAGTAGCTGATGTTAGGACACTACCCAATGCC TCAACCGTGGACAATATTGCTCCATCTTTGGAAATGCTGTTA GTCGGTATGTCGATAACCTATATAAAAAAATCTTTT	3064
	AAAAGATTTTTTTATATAGGTTATCGACATACCGACTAACAGC ATTTCCAAAGATGGAGCGAATATTGTCCACGGTTGAGGCATT GGGTAGTGTCTAACATCAGCTACTGTCTCTCCTTG	3065
	ACAATATTGCTCCATC	3066
	GATGGAGCGAATATTGT	3067

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Ile219Val ATC-GTC	GAGACAGTAGCTGATGTTAGGACACTACCCAATGCCTCAACC GTGGACAATATTCGCTCC <u>A</u> TCTTTGGAAATGCTGTTAGTCGGT ATGTCGATAACCTATATAAAAAAATCTTTTACATTT	3068
	AAATGTAAAAGATTTTTTTATATAGGTTATCGACATACCGACTA ACAGCATTTCCAAAGATGGAGCGAATATTGTCCACGGTTGAG GCATTGGGTAGTGTCTTAACATCAGCTACTGTCTC	3069
	TTCGCTCC <u>A</u> TCTTTGGA	3070
	TCCAAAGATGGAGCGAA	3071
Non-polyposis colorectal cancer Gly244Asp GGT-GAT	CTAATAGAGAACTGATAGAAATTGGATGTGAGGATAAAACCCT AGCCTTCAAATGAATG <u>G</u> TTACATATCCAATGCAAACACTACTCA GTGAAGAAGTGCATCTTCTTACTCTTCATCAACCG	3072
	CGGTTGATGAAGAGTAAGAAGATGCACTTCTTCACTGAGTAG TTTGCATTGGATATGTAACCATTCATTTTGAAGGCTAGGGTTT TATCCTCACATCCAATTTCTATCAGTTCTCTATTAG	3073
	AATGAATG <u>G</u> TTACATAT	3074
	ATATGTAACCATTCATT	3075
Non-polyposis colorectal cancer Ser252Term TCA-TAA	GATGTGAGGATAAAACCCTAGCCTTCAAATGAATGGTTACAT ATCCAATGCAAACACTACTCAGTGAAGAAGTGCATCTTCTTACTC TTCATCAACCGTAAGTTAAAAAGAACCACATGGGA	3076
	TCCCATGTGGTTCTTTTTAACTTACGGTTGATGAAGAGTAAGA AGATGCACTTCTTCACTGAGTAGTTTGCATTGGATATGTAACC ATTCATTTTGAAGGCTAGGGTTTTATCCTCACATC	3077
	AAACTACTCAGTGAAGA	3078
	TCTTCACTGAGTAGTTT	3079
Non-polyposis colorectal cancer Glu268Gly GAA-GGA	CACCCCTCAGGACAGTTTTGAACTGGTTGCTTTCTTTTATTG TTTAGATCGTCTGGTAGAATCAACTTCCTTGAGAAAAGCCATA GAAACAGTGTATGCAGCCTATTTGCCCAAAACAC	3080
	GTGTTTTTGGGCAAATAGGCTGCATACACTGTTTCTATGGCTT TTCTCAAGGAAGTTGATTCTACCAGACGATCTAAACAATAAAA AGAAAGCAACCAGTTCAAACACTGTCCTGAGGGGTG	3081
	TCTGGTAGAATCAACTT	3082
	AAGTTGATTCTACCAGA	3083
Non-polyposis colorectal cancer Ser269Term TCA-TGA	CCCTCAGGACAGTTTTGAACTGGTTGCTTTCTTTTATTGTTTA GATCGTCTGGTAGAATCAACTTCCTTGAGAAAAGCCATAGAAA CAGTGTATGCAGCCTATTTGCCCAAAACACACA	3084
	TGTGTGTTTTTGGGCAAATAGGCTGCATACACTGTTTCTATGG CTTTTCTCAAGGAAGTTGATTCTACCAGACGATCTAAACAATA AAAAGAAAGCAACCAGTTCAAACACTGTCCTGAGGGG	3085
	GGTAGAATCAACTTCCT	3086
	AGGAAGTTGATTCTACC	3087

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Glu297Term GAA-TAA	CTTTTCTCCCCCTCCCACTATCTAAGGTAATTGTTCTCTCTTA TTTCCTGACAGTTTATGAAATCAGTCCCCAGAATGTGGATGTT AATGTGCACCCACAAAGCATGAAGTTCACCTCC	3088
	GGAAGTGAAGTTCATGCTTTGTGGGGTGCACATTAACATCCA CATTCTGGGGACTGATTTCTAAACTGTCAGGAAAATAAGAGA GAACAATTACCTTAGATAGTGGGAGGGGGAGAAAAAG	3089
	ACAGTTTAGAAATCAGT	3090
	ACTGATTTCTAAACTGT	3091
Non-polyposis colorectal cancer Gln301Term CAG-TAG	CTCCCACTATCTAAGGTAATTGTTCTCTCTTATTTTCTGACAG TTTAGAAATCAGTCCCCAGAATGTGGATGTTAATGTGCACCCC ACAAAGCATGAAGTTCACCTCCTGCACGAGGAGA	3092
	TCTCCTCGTGCAGGAAGTGAAGTTCATGCTTTGTGGGGTGC CATTAAACATCCACATTCTGGGGACTGATTTCTAAACTGTCAGG AAAATAAGAGAGAACAATTACCTTAGATAGTGGGAG	3093
	TCAGTCCCCAGAATGTG	3094
	CACATTCTGGGGACTGA	3095
Non-polyposis colorectal cancer Val326Ala GTG-GCG	ATGTGCACCCACAAAGCATGAAGTTCACCTCCTGCACGAGG AGAGCATCCTGGAGCGGGTGCAGCAGCACATCGAGAGCAAG CTCCTGGGCTCCAATTCCTCCAGGATGTACTTCACCCA	3096
	TGGGTGAAGTACATCCTGGAGGAATTGGAGCCCAGGAGCTT GCTCTCGATGTGCTGCTGCACCCGCTCCAGGATGCTCTCCTC GTGCAGGAAGTGAAGTTCATGCTTTGTGGGGTGCACAT	3097
	GGAGCGGGTGCAGCAGC	3098
	GCTGCTGCACCCGCTCC	3099
Non-polyposis colorectal cancer His329Pro CAC-CCC	CCACAAAGCATGAAGTTCACCTCCTGCACGAGGAGAGCATCC TGGAGCGGGTGCAGCAGCACATCGAGAGCAAGCTCCTGGGC TCCAATTCCTCCAGGATGTACTTCACCCAGGTCAGGGC	3100
	GCCCTGACCTGGGTGAAGTACATCCTGGAGGAATTGGAGCC CAGGAGCTTGCTCTCGATGTGCTGCTGCACCCGCTCCAGGAT GCTCTCCTCGTGCAGGAAGTGAAGTTCATGCTTTGTGG	3101
	GCAGCAGCACATCGAGA	3102
	TCTCGATGTGCTGCTGC	3103
Non-polyposis colorectal cancer Val384Asp GTT-GAT	CAAGTCTGACCTCGTCTTCTACTTCTGGAAGTAGTGATAAGGT CTATGCCACACAGATGGTTCGTACAGATTCCCGGGAACAGAA GCTTGATGCATTTCTGCAGCCTCTGAGCAAACCCCT	3104
	AGGGGTTTGCTCAGAGGCTGCAGAAATGCATCAAGCTTCTGT TCCCGGGAATCTGTACGAACCATCTGGTGGGCATAGACCTTA TCACTACTTCCAGAAAGTAGAAGACGAGGTCAGACTTG	3105
	CCAGATGGTTCGTACAG	3106
	CTGTACGAACCATCTGG	3107

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Ala441Thr GCT-ACT	AGTGGCAGGGCTAGGCAGCAAGATGAGGAGATGCTTGAAC CCCAGCCCCTGCTGAAGTG <u>G</u> CTGCCAAAAATCAGAGCTTGA GGGGGATACAACAAAGGGGACTTCAGAAATGTCAGAGA	3108
	TCTCTGACATTTCTGAAGTCCCCTTTGTTGTATCCCCCTCAA GCTCTGATTTTTGGCAG <u>C</u> CACTTCAGCAGGGGCTGGGAGTTC AAGCATCTCCTCATCTTGCTGCCTAGCCCTGCCACT	3109
	CTGAAGTG <u>G</u> CTGCCAAA	3110
	TTTGGCAG <u>C</u> CACTTCAG	3111
Non-polyposis colorectal cancer Arg487Term CGA-TGA	CTTCATTGCAGAAAGAGACATCGGGAAGATTCTGATGTGGAA ATGGTGGAAGATGATTCC <u>C</u> GAAAGGAAATGACTGCAGCTTGT ACCCCCCGGAGAAGGATCATTAACTCACTAGTGTTT	3112
	AAACACTAGTGAGGTTAATGATCCTTCTCCGGGGGGTACAAG CTGCAGTCATTTCTTT <u>C</u> GGAATCATCTTCCACCATTTCAC ATCAGAATCTTCCCGATGTCTTTCTGCAATGAAG	3113
	ATGATTCC <u>C</u> GAAAGGAA	3114
	TTCCTTT <u>C</u> GGAATCAT	3115
Non-polyposis colorectal cancer Ala492Thr GCA-ACA	AGACATCGGGAAGATTCTGATGTGGAAATGGTGGAAGATGAT TCCCGAAAGGAAATGACT <u>G</u> CAGCTTGTACCCCCCGGAGAAG GATCATTAACTCACTAGTGTTTTGAGTCTCCAGGAAG	3116
	CTTCCTGGGAGACTCAAAACACTAGTGAGGTTAATGATCCTTCT CCGGGGGGTACAAGCTG <u>C</u> AGTCATTTCTTTCCGGGAATCATC TTCCACCATTTCACATCAGAATCTTCCCGATGTCT	3117
	AAATGACT <u>G</u> CAGCTTGT	3118
	ACAAGCTG <u>C</u> AGTCATT	3119
Non-polyposis colorectal cancer Val506Ala GTT-GCT	CCCGAAAGGAAATGACTGCAGCTTGTACCCCCCGGAGAAGG ATCATTAACTCACTAGTG <u>T</u> TTTGAGTCTCCAGGAAGAAATTA ATGAGCAGGGACATGAGGGTACGTAAACGCTGTGGCC	3120
	GGCCACAGCGTTTACGTACCCTCATGTCCCTGCTCATTATTT CTTCCTGGGAGACTCAAA <u>A</u> CACTAGTGAGGTTAATGATCCTTCT CCGGGGGGTACAAGCTGCAGTCATTTCTTTCCGGG	3121
	CACTAGTG <u>T</u> TTTGAGTC	3122
	GACTCAAA <u>A</u> CACTAGTG	3123
Non-polyposis colorectal cancer Gln542Leu CAG-CTG	GGGAGATGTTGCATAACCACTCCTTCGTGGGCTGTGTGAATC CTCAGTGGGCCTTGGCAC <u>A</u> GCATCAAACCAAGTTATACCTTC TCAACACCACCAAGCTTAGGTAAATCAGCTGAGTGTG	3124
	CACACTCAGCTGATTTACCTAAGCTTGGTGGTGTGAGAAGG TATACTTGTTTTGATGCT <u>T</u> GTGCCAAGGCCCACTGAGGATTC ACACAGCCCACGAAGGAGTGGTTATGCAACATCTCCC	3125
	CTTGGCAC <u>A</u> GCATCAAA	3126
	TTTGATGCT <u>T</u> GTGCCAAG	3127

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Leu549Pro CTT-CCT	CCTTCGTGGGCTGTGTGAATCCTCAGTGGGCCTTGGCACAG CATCAAACCAAGTTATACCTTCTCAACACCACCAAGCTTAGGT AAATCAGCTGAGTGTGTGAACAAGCAGAGCTACTACA	3128
	TGTAGTAGCTCTGCTTGTTACACACTCAGCTGATTTACCTAA GCTTGGTGGTGTGAGAAGGTATAACTTGGTTTGATGCTGTG CCAAGGCCCACTGAGGATTCACACAGCCCACGAAGG	3129
	GTTATACCTTCTCAACA	3130
	TGTTGAGAAGGTATAAC	3131
Non-polyposis colorectal cancer Asn551Thr AAC-ACC	TGGGCTGTGTGAATCCTCAGTGGGCCTTGGCACAGCATCAA CCAAGTTATACCTTCTCAACACCACCAAGCTTAGGTAAATCAG CTGAGTGTGTGAACAAGCAGAGCTACTACAACAATG	3132
	CATTGTTGTAGTAGCTCTGCTTGTTACACACTCAGCTGATTT ACCTAAGCTTGGTGGTGTGAGAAGGTATAACTTGGTTTGAT GCTGTGCCAAGGCCCACTGAGGATTCACACAGCCCA	3133
	CCTTCTCAACACCACCA	3134
	TGGTGGTGTGAGAAGG	3135
Non-polyposis colorectal cancer Gln562Term CAG-TAG	ATGAATTCAGCTTTTCCTTAAAGTCACTTCATTTTTATTTTCAG TGAAGAACTGTTCTACCAGATACTCATTTATGATTTTGCCAATT TTGGTGTTCAGGTTATCGGTAAGTTTAGATC	3136
	GATCTAACTTACCGATAACCTGAGAACACCAAAATTGGCAAA ATCATAAATGAGTATCTGGTAGAACAGTTCTTCACTGAAAATA AAAATGAAGTGACTTTAAGGAAAAGCTGAATTCAT	3137
	TGTTCTACCAGATACTC	3138
	GAGTATCTGGTAGAACA	3139
Non-polyposis colorectal cancer Ile565Phe ATT-TTT	GCTTTTCCTTAAAGTCACTTCATTTTTATTTTCAGTGAAGAACT GTTCTACCAGATACTCATTTATGATTTTGCCAATTTGGTGTTCT TCAGGTTATCGGTAAGTTTAGATCCTTTTCACT	3140
	AGTGAAAAGGATCTAACTTACCGATAACCTGAGAACACCAAA ATTGGCAAAATCATAAATGAGTATCTGGTAGAACAGTTCTTCA CTGAAAATAAAATGAAGTGACTTTAAGGAAAAGC	3141
	AGATACTCATTTATGAT	3142
	ATCATAAATGAGTATCT	3143
Non-polyposis colorectal cancer Leu574Pro CTC-CCC	TTTTCAGTGAAGAACTGTTCTACCAGATACTCATTTATGATTTT GCCAATTTTGGTGTTCTCAGGTTATCGGTAAGTTTAGATCCTT TTCACCTCTGAAATTTCAACTGATCGTTTCTGAA	3144
	TTCAGAAACGATCAGTTGAAATTTCAGAAGTGAAAAGGATCTA AACTTACCGATAACCTGAGAACACCAAAATTGGCAAAATCATA AATGAGTATCTGGTAGAACAGTTCTTCACTGAAAA	3145
	TGGTGTTCAGAGTTAT	3146
	ATAACCTGAGAACACCA	3147

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Leu582Val CTC-GTC	TGGATGCTCCGTTAAAGCTTGCTCCTTCATGTTCTTGCTTCTT CCTAGGAGCCAGCACCGCTCTTTGACCTTGCCATGCTTGCCT TAGATAGTCCAGAGAGTGGCTGGACAGAGGAAGATG	3148
	CATCTTCCTCTGTCCAGCCACTCTCTGGACTATCTAAGGCAA GCATGGCAAGGTCAAAGAAGCGGTGCTGGCTCCTAGGAAGAA GCAAGAACATGAAGGAGCAAGCTTTAACGGAGCATCCA	3149
	CAGCACCGCTCTTTGAC	3150
	GTCAAAGAAGCGGTGCTG	3151
Non-polyposis colorectal cancer Leu607His CTT-CAT	TGCTTGCCTTAGATAGTCCAGAGAGTGGCTGGACAGAGGAAG ATGGTCCCAAAGAAGGACTTGCTGAATACATTGTTGAGTTTCT GAAGAAGAAGGCTGAGATGCTTGCAGACTATTTCTC	3152
	GAGAAATAGTCTGCAAGCATCTCAGCCTTCTTCTTCAGAACT CAACAATGTATTAGCAAGTCCTTCTTTGGGACCATCTTCCTC TGTCAGCCACTCTCTGGACTATCTAAGGCAAGCA	3153
	AGAAGGACTTGCTGAAT	3154
	ATTCAGCAAGTCCTTCT	3155
Non-polyposis colorectal cancer Lys618Term AAG-TAG	ACAGAGGAAGATGGTCCCAAAGAAGGACTTGCTGAATACATT GTTGAGTTTCTGAAGAAGAAGGCTGAGATGCTTGCAGACTAT TTCTCTTTGGAAATTGATGAGGTGTGACAGCCATTCT	3156
	AGAATGGCTGTCACACCTCATCAATTTCCAAAGAGAAATAGTC TGCAAGCATCTCAGCCTTCTTCTTCAGAACTCAACAATGTAT TCAGCAAGTCCTTCTTTGGGACCATCTTCCTCTGT	3157
	TGAAGAAGAAGGCTGAG	3158
	CTCAGCCTTCTTCTTCA	3159
Non-polyposis colorectal cancer Lys618Thr AAG-ACG	CAGAGGAAGATGGTCCCAAAGAAGGACTTGCTGAATACATTG TTGAGTTTCTGAAGAAGAAGGCTGAGATGCTTGCAGACTATTT CTCTTTGGAAATTGATGAGGTGTGACAGCCATTCTT	3160
	AAGAATGGCTGTCACACCTCATCAATTTCCAAAGAGAAATAGT CTGCAAGCATCTCAGCCTTCTTCTTCAGAACTCAACAATGTA TTCAGCAAGTCCTTCTTTGGGACCATCTTCCTCTG	3161
	GAAGAAGAAGGCTGAGA	3162
	TCTCAGCCTTCTTCTTC	3163
Non-polyposis colorectal cancer Arg659Leu CGA-CTA	TACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGAC TGCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATCA AGCAGATACTAAGCATTTCCGTACATGCATGTGTGC	3164
	GCACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCAC TGACCTCAGTGGCTAGTGAAGAATGAAGATAGGCAGTCCCT CCAAAGGGGGCACATAGTTGTCAATCAGAAGGGGTA	3165
	CATTCTTCGACTAGCCA	3166
	TGGCTAGTGAAGAATG	3167

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Arg659Pro CGA-CCA	TACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGAC TGCCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATCA AGCAGATACTAAGCATTTCGGTACATGCATGTGTGC	3168
	GCACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCAC TGACCTCAGTGGCTAGTCGAAGAATGAAGATAGGCAGTCCCT CCAAAGGGGGGCACATAGTTGTCAATCAGAAGGGGTA	3169
	CATTCTTCGACTAGCCA	3170
	TGGCTAGTCGAAGAATG	3171
Non-polyposis colorectal cancer Arg659Term CGA-TGA	TTACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGA CTGCCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATC AAGCAGATACTAAGCATTTCGGTACATGCATGTGTG	3172
	CACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCACT GACCTCAGTGGCTAGTCCGAAGAATGAAGATAGGCAGTCCCTC CAAAGGGGGGCACATAGTTGTCAATCAGAAGGGGTAA	3173
	TCATTCTTCGACTAGCC	3174
	GGCTAGTCGAAGAATGA	3175
Non-polyposis colorectal cancer Ala681Thr GCT-ACT	TTGGACCAGGTGAATTGGGACGAAGAAAAGGAATGTTTTGAA AGCCTCAGTAAAGAATGCCTATGTTCTATTCCATCCGGAAG CAGTACATATCTGAGGAGTCGACCCTCTCAGGCCAGC	3176
	GCTGGCCTGAGAGGGTGCAGTCTCAGATATGTACTGCTTCC GGATGGAATAGAACATAGCGCATTCTTTACTGAGGCTTTCAA ACATTCTTTTCTTCGTCCCAATTCACCTGGTCCAA	3177
	AAGAATGCCTATGTTC	3178
	GAACATAGCGCATTCTT	3179
Non-polyposis colorectal cancer Trp712Term TGG-TAG	AGGCTTATGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTG GCTCCATTCCAACTCCTGGAAGTGGACTGTGGAACACATTG TCTATAAAGCCTTGCCTCACACATTCTGCCTCCTAA	3180
	TAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATAGACAATG TGTTCCACAGTCCACTTCCAGGAGTTTGAATGGAGCCAGGC ACTTCACTCTGGAACACATTAGATGTCATAAGCCT	3181
	AAACTCCTGGAAGTGGA	3182
	TCCACTTCCAGGAGTTT	3183
Non-polyposis colorectal cancer Trp714Term TGG-TAG	ATGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCAT TCCAACTCCTGGAAGTGGACTGTGGAACACATTGTCTATAAA GCCTTGCCTCACACATTCTGCCTCCTAAACATTT	3184
	AAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATAG ACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGAATGGAG CCAGGCACTTCACTCTGGAAAACACATTAGATGTCAT	3185
	CTGGAAGTGGACTGTGG	3186
	CCACAGTCCACTTCCAG	3187

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Trp714Term TGG-TGA	TGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCATT CCAACTCCTGGAAGTGGACTGTGGAACACATTGTCTATAAA GCCTTGCGCTCACACATTCTGCCTCCTAAACATTTTC	3188
	GAAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATA GACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGGAATGGA GCCAGGCACTTCACTCTGGAAAACACATTAGATGTCA	3189
	TGGAAGTGGACTGTGGA	3190
	TCCACAGTCCACTTCCA	3191
Non-polyposis colorectal cancer Val716Met GTG-ATG	ATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCATTCCAA ACTCCTGGAAGTGGACTGTGGAACACATTGTCTATAAAGCCT TGCGCTCACACATTCTGCCTCCTAAACATTTTCACAG	3192
	CTGTGAAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTT TATAGACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGGAAT GGAGCCAGGCACTTCACTCTGGAAAACACATTAGAT	3193
	AGTGGACTGTGGAACAC	3194
	GTGTTCCACAGTCCACT	3195
Non-polyposis colorectal cancer Tyr721Term TAT-TAA	GAGTGAAGTGCCTGGCTCCATTCCAACTCCTGGAAGTGGAC TGTGGAACACATTGTCTATAAAGCCTTGCGCTCACACATTCTG CCTCCTAAACATTTACAGAAGATGGAAATATCCTG	3196
	CAGGATATTTCCATCTTCTGTGAAATGTTTAGGAGGCAGAATG TGTGAGCGCAAGGCTTTATAGACAATGTGTTCCACAGTCCAC TTCCAGGAGTTTGGAATGGAGCCAGGCACTTCACTC	3197
	ATTGTCTATAAAGCCTT	3198
	AAGGCTTTATAGACAAT	3199
Non-polyposis colorectal cancer Lys751Arg AAA-AGA	CTAAACATTTACAGAAGATGGAAATATCCTGCAGCTTGCTAA CCTGCCTGATCTATACAAGTCTTTGAGAGGTGTTAAATATGG TTATTTATGCACTGTGGGATGTGTTCTTCTTTCTC	3200
	GAGAAAGAAGAACACATCCACAGTGCATAAATAACCATATTT AACACCTCTCAAAGACTTTGTATAGATCAGGCAGGTTAGCAA GCTGCAGGATATTTCCATCTTCTGTGAAATGTTTAG	3201
	TCTATACAAGTCTTTG	3202
	CAAAGACTTTGTATAGA	3203
Non-polyposis colorectal cancer Arg755Trp AGG-TGG	ACAGAAGATGGAAATATCCTGCAGCTTGCTAACCTGCCTGAT CTATACAAAGTCTTTGAGAGGTGTTAAATATGGTTATTTATGC ACTGTGGGATGTGTTCTTCTTTCTCTGTATTCCGAT	3204
	ATCGGAATACAGAGAAAGAAGAACACATCCACAGTGCATAA ATAACCATATTTAACACCTCTCAAAGACTTTGTATAGATCAGG CAGGTTAGCAAGCTGCAGGATATTTCCATCTTCTGT	3205
	TCTTTGAGAGGTGTTAA	3206
	TTAACACCTCTCAAAGA	3207

EXAMPLE 19

Human mismatch repair - MSH2

[0231] The human MSH2 gene is homologous to the bacterial *mutS* gene, which is involved in mismatch repair. Mutations in the MSH2 gene have been identified in a variety of cancers, including, for example, ovarian tumors, colorectal cancer, endometrial cancer, uterine cancer. The attached table discloses the correcting oligonucleotide base sequences for the MSH2 oligonucleotides of the invention.

Table 21

MSH2 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non polyposis colorectal cancer Gln252Term CAG-TAG	TTTTCCACAAAAGACATTTATCAGGACCTCAACCGGTTGTTGA AAGGCCAAAAGGGAGAGCAGATGAATAGTGCTGTATTGCCAG AAATGGAGAATCAGGTACATGGATTATAAATGTGAA	3208
	TTCACATTTATAATCCATGTACCTGATTCTCCATTTCTGGCAAT ACAGCACTATTCATCTGCTCTCCCTTTTGCCTTTCAACAACC GGTTGAGGTCCTGATAAATGTCTTTTGTGGAAAA	3209
	AGGGAGAGCAGATGAAT	3210
	ATTCATCTGCTCTCCCT	3211
Non polyposis colorectal cancer Gln288Term CAG-TAG	TCATCACTGTCTGCGGTAATCAAGTTTTTAGAACTCTTATCAG ATGATTCCAACCTTTGGACAGTTTGAAGTACTACTTTTGACTT CAGCCAGTATATGAAATTGGATATTGCAGCAGTCA	3212
	TGACTGCTGCAATATCCAATTTTCACTACTGGCTGAAGTCAAA AGTAGTCAGTTCAAAGTGTCCAAAGTTGGAATCATCTGATAAG AGTTCTAAAACTTGATTACCGCAGACAGTGATGA	3213
	ACTTTGGACAGTTTGAA	3214
	TTCAAAGTGTCCAAAGT	3215
Non polyposis colorectal cancer Ala305Thr GCA-ACA	AACCTTTGGACAGTTTGAAGTACTACTTTTGACTTCAGCCAGT ATATGAAATTGGATATTGCAGCAGTCAGAGCCCTTAACCTTTT TCAGGTAAAAAAAAAAAAAAAAAAAAAAAAAAGG	3216
	CCTTTTTTTTTTTTTTTTTTTTTTTTTTTTACCTGAAAAAGGTTAA GGGCTCTGACTGCTGCAATATCCAATTTTCACTACTGGCTGAA GTCAAAGTAGTCAGTTCAAAGTGTCCAAAGTT	3217
	TGGATATTGCAGCAGTC	3218
	GACTGCTGCAATATCCA	3219
Non polyposis colorectal cancer Gly322Asp GGC-GAC	AGCTTGCCATTCTTTCTATTTTATTTTTGTTTACTAGGGTTCT GTTGAAGATACCACTGGCTCTCAGTCTCTGGCTGCCTTGCTG AATAAGTGTAACCCCTCAAGGACAAAGACTTGT	3220
	ACAAGTCTTTGTCTTGAGGGGTTTTACTTATTTCAGCAAGG CAGCCAGAGACTGAGAGCCAGTGGTATCTTCAACAGAACCT AGTAAACAAAAATAAAATAGAAAGAATGGCAAGCT	3221
	TACCACTGGCTCTCAGT	3222
	ACTGAGAGCCAGTGGTA	3223

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non polyposis colorectal cancer Ser323Cys TCT-TGT	TTGCCATTCTTTCTATTTTATTTTTGTTTACTAGGGTTCTGTT GAAGATACCACTGGCTCTCAGTCTCTGGCTGCCTTGCTGAAT AAGTGTAACCCCTCAAGGACAAAGACTTGTTAA	3224
	TTAACAAGTCTTTGTCCTTGAGGGGTTTTACACTTATTCAGCA AGGCAGCCAGAGACTGAGAGCCAGTGGTATCTTCAACAGAAC CCTAGTAAACAAAAAATAAAATAGAAAGAATGGCAA	3225
	CACTGGCTCTCAGTCTC	3226
	GAGACTGAGAGCCAGTG	3227
Non polyposis colorectal cancer Arg383Term CGA-TGA	GTGGAAGCTTTTGTAGAAGATGCAGAATTGAGGCAGACTTTA CAAGAAGATTTACTTCGTGATTCCAGATCTTAACCGACTTG CCAAGAAGTTTCAAAGACAAGCAGCAAACCTTACAAG	3228
	CTTGTAAGTTTGCTGCTTGCTTTGAACTTCTTGCGCAAGTCG GTTAAGATCTGGGAATCGACGAAGTAAATCTTCTGTAAAGTC TGCCTCAATTCTGCATCTTCTACAAAAGCTTCCAC	3229
	TACTTCGTGATTCCCA	3230
	TGGGAATCGACGAAGTA	3231
Non polyposis colorectal cancer Gln397Term CAA-TAA	CAAGAAGATTTACTTCGTGATTCCAGATCTTAACCGACTTG CCAAGAAGTTTCAAAGACAAGCAGCAAACCTTACAAGATTGTTA CCGACTCTATCAGGGTATAAATCAACTACCTAATG	3232
	CATTAGGTAGTTGATTTATACCCTGATAGAGTCGGTAACAATC TTGTAAGTTTGCTGCTTGCTTTGAACTTCTTGCGCAAGTCGG TTAAGATCTGGGAATCGACGAAGTAAATCTTCTTG	3233
	TTCAAAGACAAGCAGCA	3234
	TGCTGCTTGCTTTGAA	3235
Non polyposis colorectal cancer Arg406Term CGA-TGA	GATCTTAACCGACTTGCCAAGAAGTTTCAAAGACAAGCAGCA AACTTACAAGATTGTTACCGACTCTATCAGGGTATAAATCAAC TACCTAATGTTATACAGGCTCTGGAAAAACATGAAG	3236
	CTTCATGTTTTTCCAGAGCCTGTATAACATTAGGTAGTTGATTT ATACCCTGATAGAGTCGGTAACAATCTTGTAAAGTTTGCTGCTT GTCTTTGAACTTCTTGCGCAAGTCGGTTAAGATC	3237
	ATTGTTACCGACTCTAT	3238
	ATAGAGTCGGTAACAAT	3239
Non polyposis colorectal cancer Gln419Term CAG-TAG	GCAAACCTACAAGATTGTTACCGACTCTATCAGGGTATAAATC AACTACCTAATGTTATACAGGCTCTGGAAAAACATGAAGGTAA CAAGTGATTTTGTGTTTTGTTTTCTTCAACTCA	3240
	TGAGTTGAAGGAAAACAAAAAACAATCACTTGTTACCTTC ATGTTTTTCCAGAGCCTGTATAACATTAGGTAGTTGATTTATAC CCTGATAGAGTCGGTAACAATCTTGTAAAGTTTGC	3241
	ATGTTATACAGGCTCTG	3242
	CAGAGCCTGTATAACAT	3243
Non polyposis colorectal cancer Gln429Term	TATTCTGTAAATGAGATCTTTTTATTTGTTTGTGTTTACTACTTT CTTTTAGGAAAACACCAGAAATTATTGTTGGCAGTTTTTGTGA CTCCTCTTACTGATCTTCGTTCTGACTTCTCCA	3244

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
CAG-TAG	TGGAGAAGTCAGAACGAAGATCAGTAAGAGGAGTCACAAAAA CTGCCAACAAATAATTTCTG <u>G</u> TGTTTTCTAAAGAAAGTAGTA AAACAAACAAATAAAAAGATCTCATTTTACAGAATA	3245
	GAAAACACCAGAAATTA	3246
	TAATTTCTG <u>G</u> TGTTTTC	3247
Non polyposis colorectal cancer Leu458Term TTA-TGA	CTCCTCTTACTGATCTTCGTTCTGACTTCTCCAAGTTTCAGGA AATGATAGAAACAACCTT <u>T</u> AGATATGGATCAGGTATGCAATATA CTTTTTAATTTAAGCAGTAGTTATTTTTAAAAAGC	3248
	GCTTTTTAAAAATAACTACTGCTTAAATTA AAAAGTATATTGCA TACCTGATCCATATCTA <u>A</u> AGTTGTTTCTATCATTTCTGAAACT TGGAGAAGTCAGAACGAAGATCAGTAAGAGGAG	3249
	AACAACCTT <u>T</u> AGATATGG	3250
	CCATATCTA <u>A</u> AGTTGTT	3251
Non polyposis colorectal cancer Gln518Term CAG-TAG	TTTCTTCTTGATTATCAAGGCTTGACCCTGGCAAACAGATTA AACTGGATTCCAGTGCA <u>C</u> AGTTTGGATATTACTTTCTGTAAAC CTGTAAGGAAGAAAAAGTCCTTCGTAACAATAAAA	3252
	TTTTATTGTTACGAAGGACTTTTTCTTCCTTACAGGTTACACGA AAGTAATATCCAACT <u>G</u> TGCACTGGAATCCAGTTTAATCTGTT TGCCAGGGTCCAAGCCTTGATAATCAAGAAGAAA	3253
	CCAGTGCA <u>C</u> AGTTTGA	3254
	TCCAACT <u>G</u> TGCACTGG	3255
Non polyposis colorectal cancer Arg524Pro CGT-CCT	GCTTGGACCCTGGCAAACAGATTAACTGGATTCCAGTGCAAC AGTTTGGATATTACTTTCTG <u>T</u> GTAACCTGTAAGGAAGAAAAAGT CCTTCGTAACAATAAAAACTTTAGTACTGTAGATAT	3256
	ATATCTACAGTACTAAAGTTTTTATTGTTACGAAGGACTTTTTTC TTCCTTACAGGTTACAC <u>G</u> AAAGTAATATCCAACTGTGCACTG GAATCCAGTTTAATCTGTTTGCCAGGGTCCAAGC	3257
	TTACTTTCTG <u>T</u> GTAACCT	3258
	AGGTTACAC <u>G</u> AAAGTAA	3259
Non polyposis colorectal cancer Glu562Val GAG-GTG	TTAATATTTTTAATAAAACTGTTATTTGATTTGCAGCAAATTG ACTTCTTTAAATGAAG <u>A</u> GTATACCAAAAATAAAACAGAATATG AAGAAGCCCAGGATGCCATTGTTAAAGAAATTGT	3260
	ACAATTTCTTTAACAATGGCATCCTGGGCTTCTTCATATTCTGT TTTATTTTTGGTATAC <u>T</u> CTTCATTAAAGAAGTCAATTTGCTGC AAATCGAAATAACAGTTTTATTA AAAATATTAA	3261
	AAATGAAG <u>A</u> GTATACCA	3262
	TGGTATAC <u>T</u> CTTCATT	3263
Glioma Glu580Term GAA-TAA	AATGAAGAGTATACCAAAAATAAAACAGAATATGAAGAAGCCC AGGATGCCATTGTTAAAG <u>A</u> AAATTGTCAATATTTCTTCAGGTAA ACTTAATAGAACTAATAATGTTCTGAATGTCACCT	3264

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGGTGACATTCAGAACATTATTAGTTCTATTAAGTTTACCTGAA GAAATATTGACAATTTCTTTAACAATGGCATCCTGGGCTTCTT CATATTCTGTTTTATTTTGGTATACTCTTCATT	3265
	TTGTTAAAGAAATTGTC	3266
	GACAATTTCTTTAACAA	3267
Non polyposis colorectal cancer Gln601Term CAG-TAG	TGTTTTATTTTTATACAGGCTATGTAGAACCAATGCAGACACT CAATGATGTGTTAGCTCAGCTAGATGCTGTTGTCAGCTTTGCT CACGTGTCAAATGGAGCACCTGTTCCATATGTAC	3268
	GTACATATGGAACAGGTGCTCCATTTGACACGTGAGCAAAGC TGACAACAGCATCTAGCTGAGCTAACACATCATTGAGTGTCT GCATTGGTTCTACATAGCCTGTATAAAAAATAAAACA	3269
	TGTTAGCTCAGCTAGAT	3270
	ATCTAGCTGAGCTAACA	3271
Non polyposis colorectal cancer Tyr619Term TAT-TAG	AGCTCAGCTAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAAT GGAGCACCTGTTCCATATGTACGACCAGCCATTTTGGAGAAA GGACAAGGAAGAATTATATTAAGCATCCAGGCAT	3272
	ATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTTCTCCA AAATGGCTGGTCGTACATATGGAACAGGTGCTCCATTTGACA CGTGAGCAAAGCTGACAACAGCATCTAGCTGAGCT	3273
	GTTCCATATGTACGACC	3274
	GGTCGTACATATGGAAC	3275
Non polyposis colorectal cancer Arg621Term CGA-TGA	CAGCTAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAATGGA GCACCTGTTCCATATGTACGACCAGCCATTTTGGAGAAAGGA CAAGGAAGAATTATATTAAGCATCCAGGCATGCTT	3276
	AAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTTT TCCAAAATGGCTGGTCGTACATATGGAACAGGTGCTCCATTT GACACGTGAGCAAAGCTGACAACAGCATCTAGCTG	3277
	CATATGTACGACCAGCC	3278
	GGCTGGTCGTACATATG	3279
Non polyposis colorectal cancer Pro622Leu CCA-CTA	TAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAATGGAGCAC CTGTTCCATATGTACGACCAGCCATTTTGGAGAAAGGACAAG GAAGAATTATATTAAGCATCCAGGCATGCTTGTGT	3280
	ACACAAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTC CTTTCTCCAAAATGGCTGGTCGTACATATGGAACAGGTGCTC CATTTGACACGTGAGCAAAGCTGACAACAGCATCTA	3281
	TGTACGACCAGCCATTT	3282
	AAATGGCTGGTCGTACA	3283
Non polyposis colorectal cancer Ala636Pro	CCTGTTCCATATGTACGACCAGCCATTTTGGAGAAAGGACAA GGAAGAATTATATTAAGCATCCAGGCATGCTTGTGTTGAAG TTCAAGATGAAATTGCATTTATTCCTAATGACGTAT	3284

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
GCA-CCA	ATACGTCATTAGGAATAAATGCAATTTTCATCTTGAACCTTCAACA CAAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCCTT CTCCAAAATGGCTGGTCGTACATATGGAACAGG	3285
	TATTTAAAGCATCCAGG	3286
	CCTGGATGCTTTTAATA	3287
Non polyposis colorectal cancer His639Arg CAT-CGT	ATGTACGACCAGCCATTTTGGAGAAAGGACAAGGAAGAATTA TATTTAAAGCATCCAGGCATGCTTGTGTTGAAGTTCAAGATGA AATTGCATTTATTCCTAATGACGTATACTTTGAAAA	3288
	TTTTCAAAGTATACGTCATTAGGAATAAATGCAATTTTCATCTTG AACTTCAACACAAGCATGCCTGGATGCTTTTAATATAATTCTT CCTTGTCCCTTCTCCAAAATGGCTGGTCGTACAT	3289
	ATCCAGGCATGCTTGTG	3290
	CACAAGCATGCCTGGAT	3291
Non polyposis colorectal cancer His639Tyr CAT-TAT	TATGTACGACCAGCCATTTTGGAGAAAGGACAAGGAAGAATT ATATTTAAAGCATCCAGGCATGCTTGTGTTGAAGTTCAAGATG AAATTGCATTTATTCCTAATGACGTATACTTTGAAA	3292
	TTTCAAAGTATACGTCATTAGGAATAAATGCAATTTTCATCTTGA ACTTCAACACAAGCATGCCTGGATGCTTTTAATATAATTCTTC CTTGTCCCTTCTCCAAAATGGCTGGTCGTACATA	3293
	CATCCAGGCATGCTTGT	3294
	ACAAGCATGCCTGGATG	3295
Non polyposis colorectal cancer Glu647Lys GAA-AAA	AAAGGACAAGGAAGAATTATATTTAAAGCATCCAGGCATGCTT GTGTTGAAGTTCAAGATGAAATTGCATTTATTCCTAATGACGT ATACTTTGAAAAAGATAAACAGATGTTCCACATCA	3296
	TGATGTGGAACATCTGTTTATCTTTTCAAAGTATACGTCATTA GGAATAAATGCAATTTTCATCTTGAACCTTCAACACAAGCATGCC TGGATGCTTTTAATATAATTCTTCCTTGTCCCTT	3297
	TTCAAGATGAAATTGCA	3298
	TGCAATTTTCATCTTGAA	3299
Non polyposis colorectal cancer Tyr656Term TAC-TAG	ATCCAGGCATGCTTGTGTTGAAGTTCAAGATGAAATTGCATTT ATTCCTAATGACGTATACCTTTGAAAAAGATAAACAGATGTTCC ACATCATTACTGGTAAAAAACCTGGTTTTTGGGCT	3300
	AGCCCAAAAACCAGGTTTTTTACCAGTAATGATGTGGAACATC TGTTTATCTTTTTCAAAGTATACGTCATTAGGAATAAATGCAAT TTCATCTTGAACCTTCAACACAAGCATGCCTGGAT	3301
	GACGTATACCTTTGAAAA	3302
	TTTTCAAAGTATACGTC	3303
Non polyposis colorectal cancer Gly674Asp GGT-GAT	GAAAGAAGTTTAAATCTTGCTTTCTGATATAATTTGTTTTGTA GGCCCCAATATGGGAGGTAAATCAACATATATTCGACAACT GGGGTGATAGTACTCATGGCCCAAATTGGGTGTTT	3304
	AAACACCCAATTTGGGCCATGAGTACTATCACCCAGTTTGTG GAATATATGTTGATTTACCTCCCATATTGGGGCCTACAAAACA AATTATATCAGAAAGCAAGATTTTAACTTCTTTC	3305

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TATGGGAGGTAAATCAA	3306
	TTGATTTACCTCCATA	3307
Non polyposis colorectal cancer Arg680Term CGA-TGA	TTGCTTTCTGATATAATTTGTTTTGTAGGCCCAATATGGGAG GTAAATCAACATATATTGACAAACTGGGGTGATAGTACTCAT GGCCCAAATTGGGTGTTTTGTGCCATGTGAGTCAG	3308
	CTGACTCACATGGCACAAAACACCCAATTTGGGCCATGAGTA CTATCACCCCAGTTTGTCTGAATATATGTTGATTTACCTCCCAT ATTGGGGCCTACAAAACAAATTATATCAGAAAGCAA	3309
	CATATATTGACAAACT	3310
	AGTTTGTCTGAATATATG	3311
Non polyposis colorectal cancer Gly692Arg GGG-CGG	ATGGGAGGTAAATCAACATATATTGACAAACTGGGGTGATA GTACTCATGGCCCAAATTGGGTGTTTTGTGCCATGTGAGTCA GCAGAAGTGTCATTGTGGACTGCATCTTAGCCCGAG	3312
	CTCGGGCTAAGATGCAGTCCACAATGGACACTTCTGCTGACT CACATGGCACAAAACACCCAATTTGGGCCATGAGTACTATCA CCCAGTTTGTCTGAATATATGTTGATTTACCTCCCAT	3313
	CCCAAATTGGGTGTTTT	3314
	AAAACACCCAATTTGGG	3315
Non polyposis colorectal cancer Cys697Arg TGT-CGT	ACATATATTGACAAACTGGGGTGATAGTACTCATGGCCCAA ATTGGGTGTTTTGTGCCATGTGAGTCAGCAGAAGTGTCATT GTGGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACA	3316
	TGTCACCAGCCCCTACTCGGGCTAAGATGCAGTCCACAATGG ACACTTCTGCTGACTCACATGGCACAAAACACCCAATTTGGG CCATGAGTACTATCACCCAGTTTGTCTGAATATATGT	3317
	TTGTGCCATGTGAGTCA	3318
	TGACTCACATGGCACAA	3319
Non polyposis colorectal cancer Cys697Phe TGT-TTT	CATATATTGACAAACTGGGGTGATAGTACTCATGGCCCAAAT TGGGTGTTTTGTGCCATGTGAGTCAGCAGAAGTGTCATTGT GGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACAG	3320
	CTGTACCAGCCCCTACTCGGGCTAAGATGCAGTCCACAATG GACACTTCTGCTGACTCACATGGCACAAAACACCCAATTTGG GCCATGAGTACTATCACCCAGTTTGTCTGAATATATG	3321
	TGTGCCATGTGAGTCAG	3322
	CTGACTCACATGGCACAA	3323
Non polyposis colorectal cancer Gln718Term CAA-TAA	GAGTCAGCAGAAGTGTCATTGTGGACTGCATCTTAGCCCGA GTAGGGGCTGGTGACAGTCAATTGAAAGGAGTCTCCACGTTT ATGGCTGAAATGTTGGAACTGCTTCTATCCTCAGGT	3324
	ACCTGAGGATAGAAGCAGTTTCCAACATTTAGCCATGAACG TGGAGACTCCTTTCAATTGACTGTCACCAGCCCCTACTCGGG CTAAGATGCAGTCCACAATGGACACTTCTGCTGACTC	3325
	GTGACAGTCAATTGAAA	3326
	TTTCAATTGACTGTCAC	3327

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non polyposis colorectal cancer Leu811Term TTA-TGA	CCAATCAGATACCAACTGTTAATAATCTACATGTCACAGCACT CACCAGTGAAGAGACCTTAACTATGCTTTATCAGGTGAAGAAA GGTATGTACTATTGGAGTACTCTAAATTCAGAACT	3328
	AGTTCTGAATTTAGAGTACTCCAATAGTACATACCTTTCTTCAC CTGATAAAGCATAGTTAAGGTCTCTTCAGTGGTGAGTGCTGT GACATGTAGATTATTAACAGTTGGTATCTGATTGG	3329
	AGAGACCTTAACTATGC	3330
	GCATAGTTAAGGTCTCT	3331
Non polyposis colorectal cancer Ala834Thr GCT-ACT	TTCCCCAAATTTCTTATAGGTGTCTGTGATCAAAGTTTTGGGA TTCATGTTGCAGAGCTTGCTAATTTCCCTAAGCATGTAATAGA GTGTGCTAAACAGAAAGCCCTGGAAGTTGAGGAGT	3332
	ACTCCTCAAGTTCCAGGGCTTTCTGTTTAGCACACTCTATTAC ATGCTTAGGGAAATTAGCAAGCTCTGCAACATGAATCCCCAAA CTTTGATCACAGACACCTATAAGAAATTTGGGGAA	3333
	CAGAGCTTGCTAATTC	3334
	GAAATTAGCAAGCTCTG	3335
Non polyposis colorectal cancer Gln861Term CAA-TAA	ATAGAGTGTGCTAAACAGAAAGCCCTGGAAGTTGAGGAGTTT CAGTATATTGGAGAATCGCAAGGATATGATATCATGGAACCA GCAGCAAAGAAGTGCTATCTGGAAAGAGAGGTTTGTC	3336
	GACAAACCTCTCTTTCCAGATAGCACTTCTTTGCTGCTGGTTC CATGATATCATATCCTTGCGATTCTCCAATATACTGAAACTCC TCAAGTTCCAGGGCTTTCTGTTTAGCACACTCTAT	3337
	GAGAATCGCAAGGATAT	3338
	ATATCCTTGCGATTCTC	3339
Non polyposis colorectal cancer Thr905Arg ACA-AGA	AGGAGTTCCTGTCCAAGGTGAAACAAATGCCCTTTACTGAAAT GTCAGAAGAAAACATCAACAATAAAGTTAAACAGCTAAAAGCT GAAGTAATAGCAAAGAATAATAGCTTTGTAAATGA	3340
	TCATTTACAAAGCTATTATTCTTTGCTATTACTTCAGCTTTTAG CTGTTTTAACTTTATTGTGATGTTTTCTTCTGACATTCAGTAA AGGGCATTGTGTTTACCTTGGACAGGAACCTCT	3341
	AAACATCACAATAAAGT	3342
	ACTTTATTGTGATGTTT	3343

EXAMPLE 20

Human mismatch repair - MSH6

[0232] The human MSH6 gene is homologous to the bacterial *mutS* gene, which is involved in mismatch repair. Mutations in the MSH6 gene have been identified in a variety of cancers, including particularly hereditary nonpolyposis colorectal cancer. The attached table discloses the correcting oligonucleotide base sequences for the MSH6 oligonucleotides of the invention.

Table 22

MSH6 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Ser144Ile AGC-ATC	GGAAATCAGTCCGTGTTTCATGTACAGTTTTTTGATGACAGCCC AACAAGGGGCTGGGTTAGCAAAGGCTTTTAAAGCCATATAC AGGTAAGAGTCACTACTGCCATGTGTGTGTGTTTGT	3344
	ACAAACACACACACATGGCAGTAGTACTCTTACCTGTATATG GCTTTAAAGCCTTTTGCTAACCCAGCCCCCTTGTTGGGCTGT CATCAAAAACTGTACATGAACACGGACTGATTTCC	3345
	CTGGGTTAGCAAAGGC	3346
	GCCTTTTGCTAACCCAG	3347
Endometrial cancer Ser156Term TCA-TGA	CGTGAGCCTCTGCACCCGGCCCTTATTGTTTATAAATACATTT CTTTCTAGGTTCAAATCAAAGGAAGCCCAGAAGGGAGGTCA TTTTTACAGTGCAAAGCCTGAAATACTGAGAGCAAT	3348
	ATTGCTCTCAGTATTTTCAAGGCTTTGCACTGTAAAAATGACCTC CCTTCTGGGCTTCCTTTGATTTTGAACCTAGAAAGAAATGTAT TTATAACAATAAGGGCCGGGTGCAGAGGCTCACG	3349
	TTCAAATCAAAGGAAG	3350
	CTTCCTTTGATTTTGAA	3351
Early onset colorectal cancer Tyr214Term TAC-TAG	TTCCAAATTTTGATTTGTTTTAAATACTCTTTCCTTGCCTGGC AGGTAGGCACAACCTACGTAACAGATAAGAGTGAAGAAGATA ATGAAATTGAGAGTGAAGAGGAAGTACAGCCTAAG	3352
	CTTAGGCTGTACTTCCTCTTCACTCTCAATTTTATTATCTTCTT CACTCTTATCTGTTACGTAAGTTGTGCCTACCTGCCAGGCAA GGAAAGAGTATTTAAAAACAAATCAAATTTTGAA	3353
	ACAACTTACGTAACAGA	3354
	TCTGTTACGTAAGTTGT	3355
Endometrial cancer Arg248Term CGA-TGA	GAAGAGGAAGTACAGCCTAAGACACAAGGATCTAGGCGAAGT AGCCGCCAAATAAAAAACGAAGGGTCATATCAGATTCTGAG AGTGACATTGGTGGCTCTGATGTGGAATTTAAGCCAG	3356
	CTGGCTTAAATTCCACATCAGAGCCACCAATGTCACCTCTCAGA ATCTGATATGACCCTTCGTTTTTTTATTTGGCGGCTACTTCGC CTAGATCCTTGTGTCTTAGGCTGTACTTCCTCTTC	3357
	TAAAAAACGAAGGGTC	3358
	GACCCTTCGTTTTTTTA	3359
Colorectal cancer Ser285Ile AGT-ATT	TTAAGCCAGACACTAAGGAGGAAGGAAGCAGTGATGAAATAA GCAGTGGAGTGGGGGATAGTGAGAGTGAAGGCCTGAACAGC CCTGTCAAAGTTGCTCGAAAGCGGAAGAGAATGGTGAC	3360
	GTCACCATTCTCTCCGCTTTCGAGCAACTTTGACAGGGCTG TTCAGGCCTTCACTCTCACTATCCCCCACTCCACTGCTTATTT CATCACTGCTTCCTTCCTTAGTGTCTGGCTTAA	3361

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGGGGATAGTGAGAGTG	3362
	CACTCTCACTATCCCCC	3363
Colorectal cancer Gly566Arg GGA-AGA	GAGGAAGATTCTTCTGGCCATACTCGTG CATATGGTGTGTGC TTTGTTGATACTTCACTGGGAAAGTTTTTCATAGGTCAGTTTTTC AGATGATCGCCATTGTTTCGAGATTTAGGACTCTAG	3364
	CTAGAGTCCTAAATCTCGAACAATGGCGATCATCTGAAAAGTGC ACCTATGAAAAACTTTCCAGTGAAGTATCAACAAAGCACACA CCATATGCACGAGTATGGCCAGAAGAATCTTCCTC	3365
	CTTCACTGGGAAAGTTT	3366
	AAACTTTCCAGTGAAG	3367
Non-polypoid colorectal cancer Gln698Glu CAG-GAG	GAATTGGCCCTCTCTGCTCTAGGTGGTGTGTCTTCTACCTCA AAAAATGCCTTATTGATCAGGAGCTTTTATCAATGGCTAATTTT GAAGAATATATTCCCTTGGATTCTGACACAGTCA	3368
	TGACTGTGTGAGAATCCAAGGGAATATATTCTTCAAAATTAGC CATTGATAAAAGCTCCTGATCAATAAGGCATTTTTTGAGGTAG AAGACACAACCACCTAGAGCAGAGAGGGCCAATTC	3369
	TTATTGATCAGGAGCTT	3370
	AAGCTCCTGATCAATAA	3371
Endometrial cancer Gln731Term CAA-TAA	CCCTTGGATTCTGACACAGTCAGCACTACAAGATCTGGTGCT ATCTTCACCAAAGCCTATCAACGAATGGTGCTAGATGCAGTG ACATTAAACAACCTGGAGATTTTTCTGAATGGAACAA	3372
	TTGTTCCATTGAGAAAAATCTCCAAGTTGTTTAAATGTCACTGC ATCTAGCACCATTGCTTGATAGGCTTTGGTGAAGATAGCACC AGATCTTGTAGTGCTGACTGTGTGAGAATCCAAGGG	3373
	AAGCCTATCAACGAATG	3374
	CATTCGTTGATAGGCTT	3375
Colorectal cancer Val800Leu GTT-CTT	GCCCCACTCTGTAACCATTATGCTATTAATGATCGTCTAGATG CCATAGAAGACCTCATGGTTGTGCCTGACAAAATCTCCGAAG TTGTAGAGCTTCTAAAGAAGCTTCCAGATCTTGAGA	3376
	TCTCAAGATCTGGAAGCTTCTTTAGAAGCTCTACAACCTTCGGA GATTTTGTGAGGCACAAACCATGAGGTCTTCTATGGCATCTAGA CGATCATTAAATAGCATAATGGTTACAGAGTGGGGC	3377
	ACCTCATGGTTGTGCCT	3378
	AGGCACAACCATGAGGT	3379
Colorectal cancer Asp803Gly GAC-GGC	GTAACCATTATGCTATTAATGATCGTCTAGATGCCATAGAAGA CCTCATGGTTGTGCCTGACAAAATCTCCGAAGTTGTAGAGCT TCTAAAGAAGCTTCCAGATCTTGAGAGGCTACTCAG	3380

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTGAGTAGCCTCTCAAGATCTGGAAGCTTCTTTAGAAGCTCTA CAACTTCGGAGATTTTGTCAGGCACAACCATGAGGTCTTCTAT GGCATCTAGACGATCATTAAATAGCATAATGGTTAC	3381
	TGTGCCTGACAAAATCT	3382
	AGATTTTGTCAGGCACA	3383
Non-polyposis colorectal cancer Tyr850Cys TAC-TGC	CTCCCCTGAAGAGTCAGAACCACCCAGACAGCAGGGCTATAA TGTATGAAGAACTACATACAGCAAGAAGAAGATTATTGATTT TCTTTCTGCTCTGGAAGGATTCAAAGTAATGTGTAA	3384
	TTACACATTACTTTGAATCCTTCCAGAGCAGAAAGAAAATCAA TAATCTTCTTCTTGCTGTATGTAGTTTCTTCATACATTATAGCC CTGCTGTCTGGGTGGTTCTGACTCTTCAGGGGAG	3385
	AACTACATACAGCAAGA	3386
	TCTTGCTGTATGTAGTT	3387
Colorectal cancer Pro1087Thr CCC-ACC	TATAGTCGAGGGGGTGATGGTCCTATGTGTGCGCCAGTAATT CTGTTGCCGGAAGATACCCCCCCCTTCTTAGAGCTTAAAGGA TCACGCCATCCTTGCATTACGAAGACTTTTTTTGGAG	3388
	CTCCAAAAAAGTCTTCGTAATGCAAGGATGGCGTGATCCTTT AAGCTCTAAGAAGGGGGGGGTATCTTCCGGCAACAGAATTAC TGGGCGACACATAGGACCATCACCCCTCGACTATA	3389
	AAGATACCCCCCCCTTC	3390
	GAAGGGGGGGGTATCTT	3391
Non-polyposis colorectal cancer Gln1258Term CAA-TAA	ACTATAAATGTCGTACATTATTTTCAACTCACTACCATTCATT AGTAGAAGATTATTCTCAAAATGTTGCTGTGCGCCTAGGACAT ATGGTATGTGCAAATTGTTTTTTCCACAAATTC	3392
	GAATTTGTGAAAAAACAATTTGCACATACCATATGTCCTAG GCGCACAGCAACATTTTGAGAATAATCTTCTACTAATGAATGG TAGTGAGTTGAAAATAATGTACGACATTTTATAGT	3393
	ATTATTCTCAAAATGTT	3394
	AACATTTTGAGAATAAT	3395

EXAMPLE 21

Hyperlipidemia - APOE

[0233] Hyperlipidemia is the abnormal elevation of plasma cholesterol and/or triglyceride levels and it is one of the most common diseases. The human apolipoprotein E protein is involved in the transport of endogenous lipids and appears to be crucial for both the direct removal of cholesterol-rich LDL from plasma and conversion of IDL particles to LDL particles. Individuals who either lack apolipoprotein E or who are homozygous for particular alleles of apoE may have have a condition

known as dysbetalipoproteinemia, which is characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis.

[0234] In a comprehensive review of apoE variants, de Knijff et al., *Hum. Mutat.* 4:178-194 (1994) found that 30 variants had been characterized, including the most common variant, apoE3. To that time, 14 apoE variants had been found to be associated with familial dysbetalipoproteinemia. The attached table discloses the correcting oligonucleotide base sequences for the APOE oligonucleotides of the invention.

Table 23

ApoE Mutations And Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Apolipoprotein E Glu13Lys cGAG-AAG	TTGTTCCACACAGGATGCCAGGCCAAGGTGGAGCAAGCGGT GGAGACAGAGCCGGAGCCC <u>G</u> AGCTGCGCCAGCAGACCGAG TGGCAGAGCGGCCAGCGCTGGGAAGTGGCACTGGGTGCT	3396
	AGCGACCCAGTGCCAGTTCCAGCGCTGGCCGCTCTGCCAC TCGGTCTGCTGGCGCAGCT <u>C</u> GGGCTCCGGCTCTGTCTCCAC CGCTTGCTCCACCTTGCCCTGGCATCCTGTGTGGAACAA	3397
	CGGAGCCC <u>G</u> AGCTGCGC	3398
	GCGCAGCT <u>C</u> GGGCTCCG	3399
Apolipoprotein E Trp20Term TGGc-TGA	CAAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAG CTGCGCCAGCAGACCGAGTG <u>G</u> CAGAGCGGCCAGCGCTGGG AACTGGCACTGGGTGCTTTTGGGATTACCTGCGCTGGGTG	3400
	CACCCAGCGCAGGTAATCCCAAAGCGACCCAGTGCCAGTT CCCAGCGCTGGCCGCTCTG <u>C</u> CACTCGGTCTGCTGGCGCAGC TCGGGCTCCGGCTCTGTCTCCACCGCTTGCTCCACCTTG	3401
	ACCGAGTG <u>G</u> CAGAGCGG	3402
	CCGCTCTG <u>C</u> CACTCGGT	3403
Apolipoprotein E Leu28Pro CTG-CCG	CAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGCCA GAGCGGCCAGCGCTGGGAAC <u>T</u> GGCACTGGGTGCTTTTGGG ATTACCTGCGCTGGGTGCAGACACTGTCTGAGCAGGTGCA	3404
	TGCACCTGCTCAGACAGTGTCTGCACCCAGCGCAGGTAATCC CAAAAGCGACCCAGTGCC <u>A</u> GTTCCAGCGCTGGCCGCTCTG CCACTCGGTCTGCTGGCGCAGCTCGGGCTCCGGCTCTG	3405
	CTGGGAAC <u>T</u> GGCACTGG	3406
	CCAGTGCC <u>A</u> GTTCCAG	3407
Apolipoprotein E Cys112Arg gTGC-CGC	CGGCTGTCCAAGGAGCTGCAGGCGGCGCAGGCCCGGCTGG GCGCGGACATGGAGGACGTG <u>T</u> GCGGCCGCCTGGTGCAGTA CCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAG G	3408

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCTCGGTGCTCTGGCCGAGCATGGCCTGCACCTCGCCGCGG TACTGCACCAGGCGGCCGCACACGTCCTCCATGTCCGCGCC CAGCCGGGCCTGCGCCGCCTGCAGCTCCTTGACAGCCG	3409
	AGGACGTGTGCGGCCGC	3410
	GCGGCCGCACACGTCCT	3411
Apolipoprotein E Gly127Asp GGC-GAC	ACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGC GGGTGCGCCTCGCCTCCACCTGCGCAAGCTGCGTAAGCG	3412
	CGCTTACGCAGCTTGCAGGTGGGAGGCGAGGCGCACCC GCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCACCTCG CCGCGGTACTGCACCAGGCGGCCGCACACGTCCTCCATGT	3413
	CATGCTCGGCCAGAGCA	3414
	TGCTCTGGCCGAGCATG	3415
Apolipoprotein E Arg136Cys gCGC-TGC	GTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGA GCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCACCTGCG CAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGC	3416
	GCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTTG CGCAGGTGGGAGGCGAGGCGCACCCGCAGCTCCTCGGTGC TCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCAC	3417
	TGCGGGTGCGCCTCGCC	3418
	GGCGAGGCGCACCCGCA	3419
Apolipoprotein E Arg136His CGC-CAC	TGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGC ACCGAGGAGCTGCGGGTGCGCCTCGCCTCCACCTGCGCAA GCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCA	3420
	TGCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTT GCGCAGGTGGGAGGCGAGGCGCACCCGCAGCTCCTCGGTG CTCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCA	3421
	GCGGGTGCGCCTCGCCT	3422
	AGGCGAGGCGCACCCGC	3423
Apolipoprotein E Arg136Ser gCGC-AGC	GTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGA GCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCACCTGCG CAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGC	3424
	GCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTTG CGCAGGTGGGAGGCGAGGCGCACCCGCAGCTCCTCGGTGC TCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCAC	3425
	TGCGGGTGCGCCTCGCC	3426
	GGCGAGGCGCACCCGCA	3427
Apolipoprotein E Arg142Cys gCGC-TGC	GTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGG TGCGCCTCGCCTCCACCTGCGCAAGCTGCGTAAGCGGCTC CTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGT	3428

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACACTGCCAGGCGCTTCTGCAGGTCATCGGCATCGCGGAGG AGCCGCTTACGCAGCTTGCGCAGGTGGGAGGCGAGGCGCA CCCGCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCAC	3429
	CCCACCTGCGCAAGCTG	3430
	CAGCTTGCGCAGGTGGG	3431
Apolipoprotein E Arg142Leu CGC-CTC	TGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGT GCGCCTCGCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCC TCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGT	3432
	TACACTGCCAGGCGCTTCTGCAGGTCATCGGCATCGCGGAG GAGCCGCTTACGCAGCTTGCGCAGGTGGGAGGCGAGGCGC ACCCGCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCA	3433
	CCACCTGCGCAAGCTGC	3434
	GCAGCTTGCGCAGGTGG	3435
Apolipoprotein E Arg145Cys gCGT-TGT	ATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGC GCCTCG CCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGAT GCCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCG	3436
	CGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCGGCA TCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGAGG CGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAGCAT	3437
	GCAAGCTGCGTAAGCGG	3438
	CCGCTTACGCAGCTTG	3439
Apolipoprotein E Arg145Pro CGT-CCT	TGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGC GCCTCGC CTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATG CCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGG	3440
	CCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCGGC ATCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGAGG CGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAGCA	3441
	CAAGCTGCGTAAGCGGC	3442
	GCCGCTTACGCAGCTTG	3443
Apolipoprotein E Lys146Gln tAAG-CAG	CTCGGCCAGAGCACCGAGGAGCTGCGGGTGC GCCTCGCCT CCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCC GATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGGGG	3444
	CCCCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCG GCATCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGA GGCGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAG	3445
	AGCTGCGTAAGCGGCTC	3446
	GAGCCGCTTACGCAGCT	3447
Apolipoprotein E Lys146Glu tAAG-GAG	CTCGGCCAGAGCACCGAGGAGCTGCGGGTGC GCCTCGCCT CCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCC GATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGGGG	3448

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCCCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCG GCATCGCGGAGGAGCCGCTTACGCAGCTTGCAGGTGGGA GGCGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAG	3449
	AGCTGCGT <u>A</u> AGCGGCTC	3450
	GAGCCGCTTACGCAGCT	3451
Apolipoprotein E Arg158Cys gCGC-TGC	GCCTCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGA TGCCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCG GGGCCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCC	3452
	GGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGCGGGCCCC GGCCTGGTACACTGCCAGGC <u>G</u> CTTCTGCAGGTCATCGGCAT CGCGGAGGAGCCGCTTACGCAGCTTGCAGGTGGGAGGC	3453
	TGCAGAAGCGCCTGGCA	3454
	TGCCAGGC <u>G</u> CTTCTGCA	3455
Apolipoprotein E Gln187Glu aCAG-GAG	CGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGC GCCTGGGGCCCCTGGTGGAA <u>C</u> AGGGCCGCGTGCGGGCCGC CACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGG G	3456
	CCCGCTCCTGTAGCGGCTGGCCGGCCAGGGAGCCCACAGT GGCGGCCCGCACGCGGCCCT <u>G</u> TTCCACCAGGGGCCCCAGG CGCTCGCGGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGC G	3457
	TGGTGGAA <u>C</u> AGGGCCGC	3458
	GCGGCCCT <u>G</u> TTCCACCA	3459
Apolipoprotein E Trp210Term TGG-TAG	TGCGGGCCGCCACTGTGGGCTCCCTGGCCGGCCAGCCGCT ACAGGAGCGGGCCCAGGCCT <u>G</u> GGGCGAGCGGCTGCGCGCG CGGATGGAGGAGATGGGCAGCCGACCCGCGACCGCCTGG A	3460
	TCCAGGCGGTGCGGGGTCCGGCTGCCATCTCCTCCATCCG CGCGCGCAGCCGCTCGCCCC <u>C</u> AGGCCTGGGCCCGCTCCTGT AGCGGCTGGCCGGCCAGGGAGCCCACAGTGGCGGCCCGCA	3461
	CCAGGCCT <u>G</u> GGGCGAGC	3462
	GCTCGCCCC <u>C</u> AGGCCTGG	3463
Apolipoprotein E Arg228Cys cCGC-TGC	CAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAGA TGGGCAGCCGACCCGCGAC <u>C</u> GCCTGGACGAGGTGAAGGA GCAGGTGGCGGAGGTGCGCGCCAAGCTGGAGGAGCAGGCC C	3464
	GGGCCTGCTCCTCCAGCTTGGCGCGCACCTCCGCCACCTGC TCCTTACCTCGTCCAGGC <u>G</u> TCGCGGGTCCGGCTGCCCAT CTCCTCCATCCGCGCGCGCAGCCGCTCGCCCCAGGCCTG	3465
	CCGCGAC <u>C</u> GCCTGGAC	3466
	GTCCAGGC <u>G</u> GTGCGGG	3467

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Apolipoprotein E Glu244Lys gGAG-AAG	CGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGG CGGAGGTGCGCGCCAAGCTG <u>G</u> AGGAGCAGGCCCAGCAGAT ACGCCTGCAGGCCGAGGCCTTCCAGGCCCGCCTCAAGAGCT	3468
	AGCTCTTGAGGCGGGCCTGGAAGGCCTCGGCCTGCAGGCGT ATCTGCTGGGCCTGCTCCT <u>C</u> CAGCTTGGCGCGCACCTCCGC CACCTGCTCCTTACCTCGTCCAGGCGGTGCGGGTCCG	3469
	CCAAGCTG <u>G</u> AGGAGCAG	3470
	CTGCTCCT <u>C</u> CAGCTTGG	3471

EXAMPLE 22

Familial hypercholesterolemia - LDLR

[0235] Familial hypercholesterolemia is characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL) and is, hence, one of the conditions producing a hyperlipoproteinemia phenotype. Familial hypercholesterolemia is an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL). Mutations in the LDL receptor (LDLR) gene cause this disorder. The attached table discloses the correcting oligonucleotide base sequences for the LDLR oligonucleotides of the invention.

Table 24

LDLR Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Glu10Term CGAG-TAG	GCGTTGAGAGACCCTTTCTCCTTTTCTCTCTCTCAGTGGGC GACAGATGCGAAAGAAAC <u>G</u> AGTTCCAGTGCCAAGACGGGAA ATGCATCTCCTACAAGTGGGTCTGCGATGGCAGCGCTG	3472
	CAGCGCTGCCATCGCAGACCCACTTGTAGGAGATGCATTTCC CGTCTTGGCACTGGAAC <u>T</u> CGTTTCTTTCGCATCTGTGCCCCA CTGAGAGAGAGGAAAAGGAGAAAGGGTCTCTCAACGC	3473
	AAAGAAAC <u>G</u> AGTTCCAG	3474
	CTGGAAC <u>T</u> CGTTTCTTT	3475
Hypercholesterolaemia Gln12Term cCAG-TAG	AGAGACCCTTTCTCCTTTTCTCTCTCTCAGTGGGCGACAGAT GCGAAAGAAACGAGTTCC <u>A</u> GTGCCAAGACGGGAAATGCATCT CCTACAAGTGGGTCTGCGATGGCAGCGCTGAGTGCC	3476
	GGCACTCAGCGCTGCCATCGCAGACCCACTTGTAGGAGATG CATTTCCCGTCTTGGCACT <u>G</u> GAACTCGTTTCTTTCGCATCTGT CGCCCACTGAGAGAGAGGAAAAGGAGAAAGGGTCTCT	3477
	ACGAGTTCC <u>A</u> GTGCCAA	3478
	TTGGCACT <u>G</u> GAACTCGT	3479

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Gln14Term cCAA-TAA	CCTTTCTCCTTTTCCTCTCTCTCAGTGGGCGACAGATGCGAAA GAAACGAGTTCCAGTGCC <u>A</u> AAGACGGGAAATGCATCTCCTACA AGTGGGTCTGCGATGGCAGCGCTGAGTGCCAGGATG	3480
	CATCCTGGCACTCAGCGCTGCCATCGCAGACCCACTTGTAGG AGATGCATTTCCCGTCTTGGCACTGGAACGTTTCTTTTCGCA TCTGTCGCCCCACTGAGAGAGAGGAAAAGGAGAAAGG	3481
	TCCAGTGCC <u>A</u> AAGACGGG	3482
	CCCGTCTTGGCACTGGA	3483
Hypercholesterolaemia Trp23Term TGG-TAG	GCGACAGATGCGAAAGAAACGAGTTCCAGTGCCAAGACGGG AAATGCATCTCCTACAAGTGGGTCTGCGATGGCAGCGCTGAG TGCCAGGATGGCTCTGATGAGTCCCAGGAGACGTGCTG	3484
	CAGCACGTCTCCTGGGACTCATCAGAGCCATCCTGGCACTCA GCGCTGCCATCGCAGACCC <u>A</u> CTTGTAGGAGATGCATTTCCCG TCTTGGCACTGGAACGTTTCTTTTCGCATCTGTCTGC	3485
	CTACAAGTGGGTCTGCG	3486
	CGCAGACCCACTTGTAG	3487
Hypercholesterolaemia Ala29Ser cGCT-TCT	AACGAGTTCCAGTGCCAAGACGGGAAATGCATCTCCTACAAG TGGGTCTGCGATGGCAGCGCTGAGTGCCAGGATGGCTCTGA TGAGTCCCAGGAGACGTGCTGTGAGTCCCCTTTGGGCA	3488
	TGCCCCAAAGGGGACTCACAGCACGTCTCCTGGGACTCATCA GAGCCATCCTGGCACTCAGCGCTGCCATCGCAGACCCACTT GTAGGAGATGCATTTCCCGTCTTGGCACTGGAACGCTT	3489
	ATGGCAGCGCTGAGTGC	3490
	GCACTCAGCGCTGCCAT	3491
Hypercholesterolaemia Cys31Tyr TGC-TAC	TCCAGTGCCAAGACGGGAAATGCATCTCCTACAAGTGGGTCT GCGATGGCAGCGCTGAGTGCCAGGATGGCTCTGATGAGTCC CAGGAGACGTGCTGTGAGTCCCCTTTGGGCATGATATG	3492
	CATATCATGCCCAAAGGGGACTCACAGCACGTCTCCTGGGAC TCATCAGAGCCATCCTGGCACTCAGCGCTGCCATCGCAGACC CACTTGTAGGAGATGCATTTCCCGTCTTGGCACTGGA	3493
	CGCTGAGTGCCAGGATG	3494
	CATCCTGGCACTCAGCG	3495
Hypercholesterolaemia Arg57Cys cCGT-TGT	AATCCTGTCTCTTCTGTAGTGTCTGTACCTGCAAATCCGGG GACTTCAGCTGTGGGGGCGCGTGTCAACCGCTGCATTCTCA GTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACAACG	3496
	CGTTGTCGCAGTCCACTTGCCATCGCACCTCCAGAACTGAG GAATGCAGCGGTTGACACGGCCCCCACAGCTGAAGTCCCCG GATTTGCAGGTGACAGACACTACAGAAGAGACAGGATT	3497
	GTGGGGGCGCGTGTCAAC	3498
	GTTGACACGGCCCCCAC	3499

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Gln64Term tCAG-TAG	TCTGTCACCTGCAAATCCGGGGACTTCAGCTGTGGGGGCCG TGTC AACCGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCA AGTGGACTGCGACAACGGCTCAGACGAGCAAGGCTGTC	3500
	GACAGCCTTGCTCGTCTGAGCCGTTGTGCGAGTCCACTTGGC CATCGCACCTCCAGAACTGAGGAATGCAGCGGTTGACACGG CCCCACAGCTGAAGTCCCCGGATTTGCAGGTGACAGA	3501
	GCATTCTCAGTTCTGG	3502
	CCAGAACTGAGGAATGC	3503
Hypercholesterolaemia Trp66Gly cTGG-GGG	ACCTGCAAATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAA CCGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGG ACTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGT	3504
	ACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTGCGAGTCCA CTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTG ACACGGCCCCCACAGCTGAAGTCCCCGGATTTGCAGGT	3505
	CTCAGTTCTGGAGGTGC	3506
	GCACCTCCAGAACTGAG	3507
Hypercholesterolaemia Trp66Term TGG-TAG	CCTGCAAATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAAC CGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGG CTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTG	3508
	CACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTGCGAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTG ACACGGCCCCCACAGCTGAAGTCCCCGGATTTGCAGG	3509
	TCAGTTCTGGAGGTGCG	3510
	CGCACCTCCAGAACTGA	3511
Hypercholesterolaemia Cys68Arg gTGC-CGC	AAATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTG CATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGA CAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCC	3512
	GGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTGCG AGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGC GGTTGACACGGCCCCCACAGCTGAAGTCCCCGGATTT	3513
	TCTGGAGGTGCGATGGC	3514
	GCCATCGCACCTCCAGA	3515
Hypercholesterolaemia Cys68Trp TGCg-TGG	ATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTGCA TTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACA ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCT	3516
	AGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTC GCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCA GCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGAT	3517
	TGGAGGTGCGATGGCCA	3518
	TGGCCATCGCACCTCCA	3519
Hypercholesterolaemia Cys68Tyr TGC-TAC	AATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTGC ATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGAC AACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCC	3520

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCTG CAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAG CGGTTGACACGGCCCCACAGCTGAAGTCCCCGGATT	3521
	CTGGAGGTGCGATGGCC	3522
	GGCCATCGCACCTCCAG	3523
Hypercholesterolaemia Asp69Asn cGAT-AAT	TCCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCAT TCCTCAGTTCTGGAGGTGCGATGGCCAAAGTGGACTGCGACA ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTG	3524
	CAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGT CGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGC AGCGGTTGACACGGCCCCACAGCTGAAGTCCCCGGA	3525
	GGAGGTGCGATGGCCAA	3526
	TTGGCCATCGCACCTCC	3527
Hypercholesterolaemia Asp69Gly GAT-GGT	CCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCATT CCTCAGTTCTGGAGGTGCGATGGCCAAAGTGGACTGCGACAA CGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTGC	3528
	GCAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTT GTCGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAAT GCAGCGGTTGACACGGCCCCACAGCTGAAGTCCCCGG	3529
	GAGGTGCGATGGCCAAAG	3530
	CTTGGCCATCGCACCTC	3531
Hypercholesterolaemia Asp69Tyr cGAT-TAT	TCCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCAT TCCTCAGTTCTGGAGGTGCGATGGCCAAAGTGGACTGCGACA ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTG	3532
	CAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGT CGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGC AGCGGTTGACACGGCCCCACAGCTGAAGTCCCCGGA	3533
	GGAGGTGCGATGGCCAA	3534
	TTGGCCATCGCACCTCC	3535
Hypercholesterolaemia Gln71Glu cCAA-GAA	GACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCATTCTCA GTTCTGGAGGTGCGATGGCCAAAGTGGACTGCGACAACGGCT CAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTGCCTTTG	3536
	CAAAGGCAGGGCCACACTTACGACAGCCTTGCTCGTCTGAG CCGTTGTCGCAGTCCACTTGGCCATCGCACCTCCAGAACTGA GGAATGCAGCGGTTGACACGGCCCCACAGCTGAAGTC	3537
	GCGATGGCCAAAGTGGAC	3538
	GTCCACTTGGCCATCGC	3539
Hypercholesterolaemia Cys74Gly cTGC-GGC	TGTGGGGGCGGTGTCAACCGCTGCATTCTCAGTTCTGGAG GTGCGATGGCCAAAGTGGACTGCGACAACGGCTCAGACGAGC AAGGCTGTCGTAAGTGTGGCCCTGCCTTTGCTATTGAGC	3540
	GCTCAATAGCAAAGGCAGGGCCACACTTACGACAGCCTTGCT CGTCTGAGCCGTTGTGCGAGTCCACTTGGCCATCGCACCTCC AGAACTGAGGAATGCAGCGGTTGACACGGCCCCCACA	3541

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AAGTGGACTGCGACAAC	3542
	GTTGTCGCAAGTCCACTT	3543
Hypercholesterolaemia Ser78Term TCA-TGA	TCAACCGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCAAG TGGACTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAG TGTGGCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCT	3544
	AGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCACACTTA CGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCCACTTGG CCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTGA	3545
	CAACGGCTCAGACGAGC	3546
	GCTCGTCTGAGCCGTTG	3547
Hypercholesterolaemia Glu80Lys cGAG-AAG	CGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGA CTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTG GCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGA	3548
	TCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCA CACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCG	3549
	GCTCAGACGAGCAAGGC	3550
	GCCTTGCTCGTCTGAGC	3551
Hypercholesterolaemia Glu80Term cGAG-TAG	CGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGA CTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTG GCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGA	3552
	TCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCA CACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCG	3553
	GCTCAGACGAGCAAGGC	3554
	GCCTTGCTCGTCTGAGC	3555
Hypercholesterolaemia Gln81Term gCAA-TAA	TGCATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGC GACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCC TGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGAGTG	3556
	CACTCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGG CCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAG TCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCA	3557
	CAGACGAGCAAGGCTGT	3558
	ACAGCCTTGCTCGTCTG	3559
Hypercholesterolaemia Cys88Arg gTGC-CGC	TGGGAGACTTCACACGGTGATGGTGGTCTCGGCCCATCCATC CCTGCAGCCCCAAGACGTGCTCCCAGGACGAGTTTCGCTG CCACGATGGGAAGTGCATCTCTCGGCAGTTCGTCTGTG	3560
	CACAGACGAACTGCCGAGAGATGCACTTCCCATCGTGGCAG CGAAACTCGTCCTGGGAGCACGTCTTGGGGGCTGCAGGGAT GGATGGGCCGAGACCACCATCACCGTGTGAAGTCTCCCA	3561
	CCAAGACGTGCTCCAG	3562
	CTGGGAGCACGTCTTG	3563

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Glu92Term cGAG-TAG	CACGGTGATGGTGGTCTCGGCCCATCCATCCCTGCAGCCCC CAAGACGTGCTCCCAGGAC <u>G</u> AGTTTCGCTGCCACGATGGGA AGTGCATCTCTCGGCAGTTTCGTCTGTGACTCAGACCGGG	3564
	CCCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTTC CCATCGTGGCAGCGAAACT <u>C</u> GTCTCTGGGAGCACGTCTTGGG GGCTGCAGGGATGGATGGGCCGAGACCACCATCACCGTG	3565
	CCCAGGAC <u>G</u> AGTTTCGC	3566
	GCGAAACT <u>C</u> GTCTCTGGG	3567
Hypercholesterolaemia Cys95Arg cTGC-CGC	GGTGGTCTCGGCCCATCCATCCCTGCAGCCCCCAAGACGTG CTCCCAGGACGAGTTTCGCT <u>T</u> GCCACGATGGGAAGTGCATCTC TCGGCAGTTTCGTCTGTGACTCAGACCGGGACTGCTTGG	3568
	CCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGCCGAGAG ATGCACTTCCCATCGTGGC <u>A</u> GCGAAACTCGTCCTGGGAGCA CGTCTTGGGGGCTGCAGGGATGGATGGGCCGAGACCACC	3569
	AGTTTCGCT <u>T</u> GCCACGAT	3570
	ATCGTGGC <u>A</u> GCGAAACT	3571
Hypercholesterolaemia Asp97Tyr cGAT-TAT	CTCGGCCCATCCATCCCTGCAGCCCCCAAGACGTGCTCCCA GGACGAGTTTCGCTGCCAC <u>G</u> ATGGGAAGTGCATCTCTCGGC AGTTTCGTCTGTGACTCAGACCGGGACTGCTTGGACGGCT	3572
	AGCCGTCCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGC CGAGAGATGCACTTCCCAT <u>C</u> GTGGCAGCGAAACTCGTCCTG GGAGCACGTCTTGGGGGCTGCAGGGATGGATGGGCCGAG	3573
	GCTGCCAC <u>G</u> ATGGGAAG	3574
	CTTCCCAT <u>C</u> GTGGCAGC	3575
Hypercholesterolaemia Trp(-12)Arg cTGG-AGG	GGGTCGGGACACTGCCTGGCAGAGGCTGCGAGCATGGGGC CCTGGGGGCTGGAAATTGCGCTGGACCGTGCCTTGCTCCTC GCCGCGGCGGGGACTGCAGGTAAGGCTTGCTCCAGGCGCC	3576
	GGCGCCTGGAGCAAGCCTTACCTGCAGTCCCCGCCGCGGCG AGGAGCAAGGCGACGGTCC <u>A</u> GCGCAATTTCCAGCCCCAGGG CCCCATGCTCGCAGCCTCTGCCAGGCAGTGTCCCGACCC	3577
	AATTGCGCTGGACCGTC	3578
	GACGGTCC <u>A</u> GCGCAATT	3579
Hypercholesterolaemia Trp(-18)Term TGGg-TGA	CAGCAGGTCGTGATCCGGGTCGGGACACTGCCTGGCAGAGG CTGCGAGCATGGGGCCCTG <u>G</u> GGCTGGAAATTGCGCTGGACC GTCGCCTTGCTCCTCGCCGCGGCGGGGACTGCAGGTAAG	3580
	CTTACCTGCAGTCCCCGCCGCGGCGAGGAGCAAGGCGACG GTCCAGCGCAATTTCCAGCC <u>C</u> CAGGGCCCCATGCTCGCAGC CTCTGCCAGGCAGTGTCCCGACCCGGATCACGACCTGCTG	3581
	GGGCCCTG <u>G</u> GGCTGGAA	3582
	TTCCAGCC <u>C</u> CAGGGCCC	3583
Hypercholesterolaemia Met(-21)Leu cATG-TTG	CAGCTAGGACACAGCAGGTCTGTGATCCGGGTCGGGACACTG CCTGGCAGAGGCTGCGAGC <u>A</u> TGGGGGCCCTGGGGCTGGAAA TTGCGCTGGACCGTGCCTTGCTCCTCGCCGCGGCGGGGA	3584

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCCCCGCCGCGGGCAGGAGCAAGGCGACGGTCCAGCGCAA TTTCCAGCCCCAGGGCCCCATGCTCGCAGCCTCTGCCAGGC AGTGTCCCGACCCGGATCACGACCTGCTGTGTCCTAGCTG	3585
	CTGCGAGCATGGGGCCC	3586
	GGGCCCCATGCTCGCAG	3587
Hypercholesterolaemia Met(-21)Val cATG-GTG	CAGCTAGGACACAGCAGGTCGTGATCCGGGTCGGGACACTG CCTGGCAGAGGCTGCGAGCATGGGGCCCTGGGGCTGGAAA TTGCGCTGGACCGTCGCCTTGCTCCTCGCCGCGGCGGGGA	3588
	TCCCCGCCGCGGGCAGGAGCAAGGCGACGGTCCAGCGCAA TTTCCAGCCCCAGGGCCCCATGCTCGCAGCCTCTGCCAGGC AGTGTCCCGACCCGGATCACGACCTGCTGTGTCCTAGCTG	3589
	CTGCGAGCATGGGGCCC	3590
	GGGCCCCATGCTCGCAG	3591
Hypercholesterolaemia Ile101Phe cATC-TTC	ATCCCTGCAGCCCCCAAGACGTGCTCCCAGGACGAGTTTCG CTGCCACGATGGGAAGTGCATCTCTCGGCAGTTCGTCTGTGA CTCAGACCGGGACTGCTTGACGGCTCAGACGAGGCCT	3592
	AGGCCTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCA CAGACGAACTGCCGAGAGATGCACTTCCCATCGTGGCAGCG AAACTCGTCCTGGGAGCACGTCTTGGGGGCTGCAGGGAT	3593
	GGAAGTGCATCTCTCGG	3594
	CCGAGAGATGCACTTCC	3595
Hypercholesterolaemia Gln104Term gCAG-TAG	GCCCCAAGACGTGCTCCCAGGACGAGTTTCGCTGCCACGA TGGAAGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCG GGAAGTCTTGACGGCTCAGACGAGGCCTCCTGCCCGG	3596
	CCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCAGTCCCGG TCTGAGTCACAGACGAACTGCCGAGAGATGCACTTCCCATCG TGGCAGCGAAACTCGTCCTGGGAGCACGTCTTGGGGGC	3597
	TCTCTCGGCAGTTCGTC	3598
	GACGAACTGCCGAGAGA	3599
Hypercholesterolaemia Cys113Arg cTGC-CGC	TTTCGCTGCCACGATGGGAAGTGCATCTCTCGGCAGTTCGTC TGTGACTCAGACCGGGACTGCTTGACGGCTCAGACGAGGC CTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTTCC	3600
	GGAAGCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGC CTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCACAGA CGAACTGCCGAGAGATGCACTTCCCATCGTGGCAGCGAAA	3601
	ACCGGGACTGCTTGAC	3602
	GTCCAAGCAGTCCCGGT	3603
Hypercholesterolaemia Glu119Lys cGAG-AAG	AAGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGGAC TGCTTGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCAC CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCT	3604
	AGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAGGTG AGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCAGTC CCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTT	3605

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCTCAGAC <u>G</u> AGGCCTCC	3606
	GGAGGCCT <u>C</u> GTCTGAGC	3607
Hypercholesterolaemia Glu119Term cGAG-TAG	AAGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGGAC TGCTTGGACGGCTCAGAC <u>G</u> AGGCCTCCTGCCCGGTGCTCAC CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCT	3608
	AGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAGGTG AGCACCGGGCAGGAGGCCT <u>C</u> GTCTGAGCCGTCCAAGCAGTC CCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTT	3609
	GCTCAGAC <u>G</u> AGGCCTCC	3610
	GGAGGCCT <u>C</u> GTCTGAGC	3611
Hypercholesterolaemia Cys122Term TGCC-TGA	TCGGCAGTTCTGTCTGTGACTCAGACCGGGACTGCTTGGACG GCTCAGACGAGGCCTCCTG <u>C</u> CCGGTGCTCACCTGTGGTCCC GCCAGCTTCCAGTGCAACAGCTCCACCTGCATCCCCAG	3612
	CTGGGGGATGCAGGTGGAGCTGTTGCACTGGAAGCTGGCGG GACCACAGGTGAGCACCGGG <u>G</u> CAGGAGGCCTCGTCTGAGCC GTCCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGCCGA	3613
	GCCTCCTG <u>C</u> CCCGGTGCT	3614
	AGCACCGGG <u>G</u> CAGGAGGC	3615
Hypercholesterolaemia Cys127Trp TGTg-TGG	TGACTCAGACCGGGACTGCTTGGACGGCTCAGACGAGGCCT CCTGCCCGGTGCTCACCTGT <u>T</u> GGTCCCGCCAGCTTCCAGTGC AACAGCTCCACCTGCATCCCCAGCTGTGGGCCTGCGAC	3616
	GTCGCAGGCCCACAGCTGGGGGATGCAGGTGGAGCTGTTGC ACTGGAAGCTGGCGGGACC <u>A</u> CAGGTGAGCACCGGGCAGGA GGCCTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCA	3617
	CTCACCTGTGGTCCCGC	3618
	GCGGGACC <u>A</u> CAGGTGAG	3619
Hypercholesterolaemia Gln133Term cCAG-TAG	TGCTTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCAC CTGTGGTCCCGCCAGCTTCC <u>A</u> GTGCAACAGCTCCACCTGCAT CCCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCG	3620
	CGCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGGATG CAGGTGGAGCTGTTGCACT <u>G</u> GAAAGCTGGCGGGACCACAGGT GAGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCA	3621
	CCAGCTTCC <u>C</u> AGTGCAAC	3622
	GTTGCACT <u>G</u> GAAAGCTGG	3623
Hypercholesterolaemia Cys134Gly gTGC-GGC	TTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCACCTG TGGTCCCGCCAGCTTCCAGT <u>G</u> GCAACAGCTCCACCTGCATCCC CCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAG	3624
	CTTCGCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGG ATGCAGGTGGAGCTGTTGC <u>A</u> CTGGAAGCTGGCGGGACCACA GGTGAGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAA	3625
	GCTTCCAGT <u>G</u> GCAACAGC	3626
	GCTGTTGC <u>A</u> CTGGAAGC	3627

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Cys139Gly cTGC-GGC	GAGGCCTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTT CCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCT GCGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGT	3628
	ACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTCGCAG GCCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA GCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGCCTC	3629
	GCTCCACCTGCATCCCC	3630
	GGGGATGCAGGTGGAGC	3631
Hypercholesterolaemia Cys139Tyr TGC-TAC	AGGCCTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTTC CAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCTG CGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGTG	3632
	CACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTCGCAG GCCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA GCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGCCT	3633
	CTCCACCTGCATCCCC	3634
	GGGGGATGCAGGTGGAG	3635
Hypercholesterolaemia Cys146Term TGCg-TGA	CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCAT CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAG ATGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTT	3636
	AAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTTC GCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGGATGC AGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAG	3637
	TGGGCCTGCGACAACGA	3638
	TCGTTGTGCGAGGCCCA	3639
Hypercholesterolaemia Asp147Asn cGAC-AAC	TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT	3640
	AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGGATG CAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA	3641
	GGGCCTGCGACAACGAC	3642
	GTCGTTGTGCGAGGCCCA	3643
Hypercholesterolaemia Asp147His cGAC-CAC	TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT	3644
	AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGGATG CAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA	3645
	GGGCCTGCGACAACGAC	3646
	GTCGTTGTGCGAGGCCCA	3647
Hypercholesterolaemia Asp147Tyr cGAC-TAC	TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT	3648

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGT <u>C</u> GCAGGCCACAGCTGGGGGATG CAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA	3649
	GGGCCTGC <u>G</u> ACAACGAC	3650
	GTCGTTGT <u>C</u> GCAGGCC	3651
Hypercholesterolaemia Cys152Arg cTGC-CGC	TTCCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCC TGCGACAACGACCCCGACT <u>T</u> GCGAAGATGGCTCGGATGAGTG GCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGG	3652
	CCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCCAC TCATCCGAGCCATCTTCGC <u>A</u> GTCGGGGTCGTTGTCGCAGGC CCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA	3653
	ACCCCGACT <u>T</u> GCGAAGAT	3654
	ATCTTCGC <u>A</u> GTCGGGGT	3655
Hypercholesterolaemia Cys152Gly cTGC-GGC	TTCCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCC TGCGACAACGACCCCGACT <u>T</u> GCGAAGATGGCTCGGATGAGTG GCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGG	3656
	CCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCCAC TCATCCGAGCCATCTTCGC <u>A</u> GTCGGGGTCGTTGTCGCAGGC CCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA	3657
	ACCCCGACT <u>T</u> GCGAAGAT	3658
	ATCTTCGC <u>A</u> GTCGGGGT	3659
Hypercholesterolaemia Cys152Trp TGCg-TGG	CCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCT GCGACAACGACCCCGACTG <u>C</u> GGAAGATGGCTCGGATGAGTGG CCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGGAC	3660
	GTCCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCC ACTCATCCGAGCCATCTTC <u>G</u> CAGTCGGGGTCGTTGTCGCAG GCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGG	3661
	CCCGACTG <u>C</u> GGAAGATGG	3662
	CCATCTTC <u>G</u> CAGTCGGG	3663
Hypercholesterolaemia Asp154Asn aGAT-AAT	TGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCTGCGA CAACGACCCCGACTGCGA <u>A</u> GATGGCTCGGATGAGTGGCCGC AGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGGACAGTA	3664
	TACTGTCCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCG GCCACTCATCCGAGCCAT <u>C</u> TTGCGAGTCGGGGTCGTTGTCG CAGGCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCA	3665
	ACTGCGA <u>A</u> GATGGCTCG	3666
	CGAGCCAT <u>C</u> TTGCGAGT	3667
Hypercholesterolaemia Ser156Leu TCG-TTG	GCTCCACCTGCATCCCCAGCTGTGGGCCTGCGACAACGAC CCCGACTGCGAAGATGGCT <u>C</u> GGATGAGTGGCCGCAGCGCTG TAGGGGTCTTTACGTGTTCCAAGGGGACAGTAGCCCTG	3668
	CAGGGGCTACTGTCCCCTTGGAACACGTAAAGACCCCTACAG CGCTGCGGCCACTCATCC <u>G</u> AGCCATCTTCGCAGTCGGGGTC GTTGTCGCAGGCCACAGCTGGGGGATGCAGGTGGAGC	3669

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGATGGCT <u>C</u> GGATGAGT	3670
	ACTCATCC <u>G</u> AGCCATCT	3671
Hypercholesterolaemia Cys163Tyr TGT-TAT	TGTGGGCCTGCGACAACGACCCCGACTGCGAAGATGGCTCG GATGAGTGGCCGACGCT <u>G</u> TAGGGGTCTTTACGTGTTCCAA GGGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTG	3672
	CAGTGGAACTCGAAGGCCGAGCAGGGGCTACTGTCCCCTTG GAACACGTAAAGACCCCTA <u>C</u> AGCGCTGCGGCCACTCATCCG AGCCATCTTCGCAGTCGGGGTCGTTGTGCGCAGGCCACACA	3673
	GCAGCGCT <u>G</u> TAGGGGTC	3674
	GACCCCTA <u>C</u> AGCGCTGC	3675
Hypercholesterolaemia Tyr167Term TACg-TAG	CAACGACCCCGACTGCGAAGATGGCTCGGATGAGTGGCCGC AGCGCTGTAGGGGTCTTTA <u>C</u> GTGTTCCAAGGGGACAGTAGC CCCTGCTCGGCCTTCGAGTTCCACTGCCTAAGTGGCGAG	3676
	CTCGCCACTTAGGCAGTGGAAGTGAAGGCCGAGCAGGGGC TACTGTCCCCTTGGAACAC <u>G</u> TAAAGACCCCTACAGCGCTGCG GCCACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTG	3677
	GGTCTTTA <u>C</u> GTGTTCCA	3678
	TGGAACAC <u>G</u> TAAAGACC	3679
Hypercholesterolaemia Gln170Term cCAA-TAA	CCCGACTGCGAAGATGGCTCGGATGAGTGGCCGCAGCGCTG TAGGGGTCTTTACGTGTT <u>C</u> AAGGGGACAGTAGCCCCTGCTC GGCCTTCGAGTTCCACTGCCTAAGTGGCGAGTGCATCC	3680
	GGATGCACTCGCCACTTAGGCAGTGGAAGTGAAGGCCGAG CAGGGGCTACTGTCCCCTT <u>G</u> GAACACGTAAAGACCCCTACAG CGCTGCGGCCACTCATCCGAGCCATCTTCGCAGTCGGG	3681
	ACGTGTT <u>C</u> AAGGGGAC	3682
	GTCCCCTT <u>G</u> GAACACGT	3683
Hypercholesterolaemia Cys176Phe TGC-TTC	CGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTT CAAGGGGACAGTAGCCCCT <u>G</u> CTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGA	3684
	TCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA GTGGAAGTGAAGGCCGAG <u>C</u> AGGGGCTACTGTCCCCTTGGA ACACGTAAAGACCCCTACAGCGCTGCGGCCACTCATCCG	3685
	TAGCCCCT <u>G</u> CTCGGCCT	3686
	AGGCCGAG <u>C</u> AGGGGCTA	3687
Hypercholesterolaemia Cys176Tyr TGC-TAC	CGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTT CAAGGGGACAGTAGCCCCT <u>G</u> CTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGA	3688
	TCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA GTGGAAGTGAAGGCCGAG <u>C</u> AGGGGCTACTGTCCCCTTGGA ACACGTAAAGACCCCTACAGCGCTGCGGCCACTCATCCG	3689
	TAGCCCCT <u>G</u> CTCGGCCT	3690
	AGGCCGAG <u>C</u> AGGGGCTA	3691

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Ser177Leu TCG-TTG	ATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAG GGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTGCCTAA GTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATGG	3692
	CCATCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAG GCAGTGGAACTCGAAGGCCGAGCAGGGGCTACTGTCCCCTT GGAACACGTAAAGACCCCTACAGCGCTGCGGCCACTCAT	3693
	CCCCTGCTCGGCCTTCG	3694
	CGAAGGCCGAGCAGGGG	3695
Hypercholesterolaemia Glu187Lys cGAG-AAG	TACGTGTTCCAAGGGGACAGTAGCCCCTGCTCGGCCTTCGA GTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGC GCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACG	3696
	CGTCAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCC AGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAACTCG AAGGCCGAGCAGGGGCTACTGTCCCCTTGGAACACGTA	3697
	TAAGTGGCGAGTGCATC	3698
	GATGCACTCGCCACTTA	3699
Hypercholesterolaemia His190Tyr cCAC-TAC	CAAGGGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATG GTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAAT	3700
	AGTTTTCTCGTCAGATTTGTCCTTGCAGTCGGGGCCACCAT CACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCAG TGGAATCGAAGGCCGAGCAGGGGCTACTGTCCCCTTG	3701
	AGTGCATCCACTCCAGC	3702
	GCTGGAGTGGATGCACT	3703
Hypercholesterolaemia Gly198Asp GGC-GAC	CCTTCGAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCA GCTGGCGCTGTGATGGTGCCCCGACTGCAAGGACAAATCT GACGAGGAAAATGCGGTATGGGCGGGGCCAGGGTGGG	3704
	CCCACCCTGGCCCCGCCCATACCGCAGTTTTCTCGTCAGAT TTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCAGCTGGA GTGGATGCACTCGCCACTTAGGCAGTGGAACTCGAAGG	3705
	TGATGGTGGCCCCGACT	3706
	AGTCGGGGCCACCATCA	3707
Hypercholesterolaemia Asp200Asn cGAC-AAC	GAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGG CGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGA GGAAAATGCGGTATGGGCGGGGCCAGGGTGGGGGCGG	3708
	CCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCTCG TCAGATTTGTCCTTGCAGTGGGGGCCACCATCACAGCGCCAG CTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAACTC	3709
	GTGGCCCCGACTGCAAG	3710
	CTTGCACTCGGGGCCAC	3711
Hypercholesterolaemia Asp200Gly GAC-GGC	AGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGC GCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAG GAAAATGCGGTATGGGCGGGGCCAGGGTGGGGGCGGG	3712

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCTC GTCAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCA GCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAAGT	3713
	TGGCCCCGACTGCAAGG	3714
	CCTTGCAGTCGGGGCCA	3715
Hypercholesterolaemia Asp200Tyr cGAC-TAC	GAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGG CGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGA GGAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGG	3716
	CCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCTCTGT CAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCAG CTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAAGTCT	3717
	GTGGCCCCGACTGCAAG	3718
	CTTGCAGTCGGGGCCAC	3719
Hypercholesterolaemia Cys201Term TGCa-TGA	CCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCT GTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAA AACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGT	3720
	ACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTT CCTCGTCAGATTTGTCCTTGCAAGTCGGGGCCACCATCACAGC GCCAGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGG	3721
	CCCGACTGCAAGGACAA	3722
	TTGTCCTTGCAAGTCGGG	3723
Hypercholesterolaemia Cys201Tyr TGC-TAC	TCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCT GTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAA AACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCG	3724
	CGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCT CTCGTCAGATTTGTCCTTGCAAGTCGGGGCCACCATCACAGCG CCAGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGA	3725
	CCCGACTGCAAGGACA	3726
	TGTCCTTGCAAGTCGGG	3727
Hypercholesterolaemia Asp203Asn gGAC-AAC	TGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGAT GGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAAGT CGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTA	3728
	TAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAG TTTTCTCGTCAGATTTGTCCTTGCAAGTCGGGGCCACCATCA CAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA	3729
	ACTGCAAGGACAAATCT	3730
	AGATTTGTCCTTGCAAGT	3731
Hypercholesterolaemia Asp203Gly GAC-GGC	GCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGAT GGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAAGT CGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTAT	3732
	ATAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCA GTTTTCTCGTCAGATTTGTCCTTGCAAGTCGGGGCCACCATC ACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGC	3733

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTGCAAGG <u>A</u> CAAATCTG	3734
	CAGATTTG <u>T</u> CCTTGCAG	3735
Hypercholesterolaemia Asp203Val GAC-GTC	GCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGAT GGTGGCCCCGACTGCAAGG <u>A</u> CAAATCTGACGAGGAAAACCTG CGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTAT	3736
	ATAGGACGCCCCGCCCCACCCTGGCCCCGCCCATACCGCA GTTTTCCTCGTCAGATTTG <u>T</u> CCTTGCAGTCGGGGCCACCATC ACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGC	3737
	CTGCAAGG <u>A</u> CAAATCTG	3738
	CAGATTTG <u>T</u> CCTTGCAG	3739
Hypercholesterolaemia Ser205Pro aTCT-CCT	AGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGG CCCCGACTGCAAGGACAAAT <u>T</u> CTGACGAGGAAAACCTGCGGTAT GGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTATCACCT	3740
	AGGTGATAGGACGCCCCGCCCCACCCTGGCCCCGCCCATAC CCGCAGTTTTCTCGTCAG <u>A</u> TTTGTCTTGCAGTCGGGGCCA CCATCACAGCGCCAGCTGGAGTGGATGCACTCGCCACT	3741
	AGGACAAAT <u>T</u> CTGACGAG	3742
	CTCGTCAG <u>A</u> TTTGTCTT	3743
Hypercholesterolaemia Asp206Glu GACg-GAG	CGAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCG ACTGCAAGGACAAATCTGAC <u>G</u> AGGAAAACCTGCGGTATGGGC GGGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCC	3744
	GGGACAGGTGATAGGACGCCCCGCCCCACCCTGGCCCCG CCCATACCGCAGTTTTCTC <u>G</u> TCAGATTTGTCTTGCAGTCG GGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTCG	3745
	AAATCTGAC <u>G</u> AGGAAAA	3746
	TTTTCTC <u>G</u> TCAGATT	3747
Hypercholesterolaemia Glu207Gln cGAG-CAG	GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGAC <u>G</u> AGGAAAACCTGCGGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT	3748
	AGGGACAGGTGATAGGACGCCCCGCCCCACCCTGGCCCC GCCATACCGCAGTTTTCTC <u>G</u> TCAGATTTGTCTTGCAGTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC	3749
	AATCTGAC <u>G</u> AGGAAAAC	3750
	GTTTTCTC <u>G</u> TCAGATT	3751
Hypercholesterolaemia Glu207Lys cGAG-AAG	GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGAC <u>G</u> AGGAAAACCTGCGGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT	3752
	AGGGACAGGTGATAGGACGCCCCGCCCCACCCTGGCCCC GCCATACCGCAGTTTTCTC <u>G</u> TCAGATTTGTCTTGCAGTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC	3753
	AATCTGAC <u>G</u> AGGAAAAC	3754

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTTTTCCT <u>C</u> GTCAGATT	3755
Hypercholesterolaemia Glu207Term cGAG-TAG	GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGAC <u>G</u> AGGAAAAGTGCAGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT	3756
	AGGGACAGGTGATAGGACGCCCCGCCCCCACCCTGGCCCC GCCCATACCGCAGTTTTCTC <u>C</u> GTCAGATTTGTCTTGCACTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC	3757
	AATCTGAC <u>G</u> AGGAAAAC	3758
	GTTTTCCT <u>C</u> GTCAGATT	3759
Hypercholesterolaemia Glu219Lys cGAA-AAA	TCTTGAGAAAATCAACACACTCTGTCCTGTTTTCCAGCTGTGG CCACCTGTGCGCCTGAC <u>G</u> AATTCCAGTGCTCTGATGGAACT GCATCCATGGCAGCCGGCAGTGTGACCGGGAATATG	3760
	CATATTCCCGGTCACACTGCCGGCTGCCATGGATGCAGTTTC CATCAGAGCACTGGAATT <u>C</u> GTCAGGGCGACAGGTGGCCACA GCTGGAAAACAGGACAGAGTGTGTTGATTTTCTCAAGA	3761
	GCCCTGAC <u>G</u> AATTCCAG	3762
	CTGGAATT <u>C</u> GTCAGGGC	3763
Hypercholesterolaemia Gln221Term cCAG-TAG	GAAAATCAACACACTCTGTCCTGTTTTCCAGCTGTGGCCACCT GTCGCCCTGACGAATT <u>C</u> AGTGCTCTGATGGAACTGCATCC ATGGCAGCCGGCAGTGTGACCGGGAATATGACTGCA	3764
	TGCAGTCATATTCCCGGTCACTGCCGGCTGCCATGGATGC AGTTTCCATCAGAGCACT <u>G</u> GAAATTCGTCAGGGCGACAGGTGG CCACAGCTGGAAAACAGGACAGAGTGTGTTGATTTTC	3765
	ACGAATT <u>C</u> AGTGCTCT	3766
	AGAGCACT <u>G</u> GAAATTCGT	3767
Hypercholesterolaemia Cys227Phe TGC-TTC	CCTGTTTTCCAGCTGTGGCCACCTGTCGCCCTGACGAATTCC AGTGCTCTGATGGAACT <u>G</u> CATCCATGGCAGCCGGCAGTGT GACCGGGAATATGACTGCAAGGACATGAGCGATGAAGT	3768
	ACTTCATCGCTCATGTCCTTGCACTCATATTCCCGGTCACT GCCGGCTGCCATGGATG <u>C</u> AGTTTCCATCAGAGCACTGGAATT CGTCAGGGCGACAGGTGGCCACAGCTGGAAAACAGG	3769
	TGGAACT <u>G</u> CATCCATG	3770
	CATGGATG <u>C</u> AGTTTCCA	3771
Hypercholesterolaemia Asp235Glu GACc-GAA	TCGCCCTGACGAATTCCAGTGCTCTGATGGAACTGCATCCA TGGCAGCCGGCAGTGTGAC <u>C</u> GGGGAATATGACTGCAAGGACA TGAGCGATGAAGTTGGCTGCGTTAATGGTGAGCGCTGG	3772
	CCAGCGCTCACCATTAAACGCAGCCAACTTCATCGCTCATGTC CTTGCACTCATATTCCCG <u>G</u> TCACACTGCCGGCTGCCATGGAT GCAGTTTCCATCAGAGCACTGGAATTCGTCAGGGCGA	3773
	CAGTGTGAC <u>C</u> GGGGAATA	3774
	TATCCCG <u>G</u> TCACACTG	3775

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Asp235Gly GAC-GGC	GTCGCCCTGACGAATTCCAGTGCTCTGATGGAACTGCATCC ATGGCAGCCGGCAGTGTG <u>A</u> CCGGGAATATGACTGCAAGGAC ATGAGCGATGAAGTTGGCTGCGTTAATGGTGAGCGCTG	3776
	CAGCGCTCACCATTAAACGCAGCCAACTTCATCGCTCATGTCC TTGCAGTCATATTCCCGGT <u>C</u> ACACTGCCGGCTGCCATGGATG CAGTTTCCATCAGAGCACTGGAATTCGTCAGGGCGAC	3777
	GCAGTGTG <u>A</u> CCGGGAAT	3778
	ATTCCCGGT <u>C</u> ACACTGC	3779
Hypercholesterolaemia Glu237Lys gGAA-AAA	CCTGACGAATTCCAGTGCTCTGATGGAACTGCATCCATGGC AGCCGGCAGTGTGACCGGG <u>G</u> AATATGACTGCAAGGACATGAG CGATGAAGTTGGCTGCGTTAATGGTGAGCGCTGGCCAT	3780
	ATGGCCAGCGCTCACCATTAAACGCAGCCAACTTCATCGCTCA TGTCCTTGCAAGTCATATT <u>C</u> CCGGTCACACTGCCGGCTGCCAT GGATGCAGTTTCCATCAGAGCACTGGAATTCGTCAGG	3781
	GTGACCGGG <u>G</u> AATATGAC	3782
	GTCATATT <u>C</u> CCGGTCAC	3783
Hypercholesterolaemia Cys240Phe TGC-TTC	TCCAGTGCTCTGATGGAACTGCATCCATGGCAGCCGGCAGT GTGACCGGGGAATATGACT <u>G</u> CAAGGACATGAGCGATGAAGTT GGCTGCGTTAATGGTGAGCGCTGGCCATCTGGTTTTCC	3784
	GGAAAACCAGATGGCCAGCGCTCACCATTAAACGCAGCCAACT TCATCGCTCATGTCTTG <u>C</u> AGTCATATTCCCGGTACACTGCC GGCTGCCATGGATGCAGTTTCCATCAGAGCACTGGA	3785
	ATATGACT <u>G</u> CAAGGACA	3786
	TGTCCTTG <u>C</u> AGTCATAT	3787
Hypercholesterolaemia Asp245Glu GATg-GAA	AACTGCATCCATGGCAGCCGGCAGTGTGACCGGGGAATATG ACTGCAAGGACATGAGCGAT <u>G</u> AAGTTGGCTGCGTTAATGGTG AGCGCTGGCCATCTGGTTTTCCATCCCCATTCTCTGT	3788
	ACAGAGAATGGGGGATGGAAAACCAGATGGCCAGCGCTCAC CATTAAACGCAGCCAACTTC <u>A</u> TCGCTCATGTCTTGCAAGTCATA TTCCCGGTACACTGCCGGCTGCCATGGATGCAGTTT	3789
	ATGAGCGATGAAGTTGG	3790
	CCAACTTC <u>A</u> TCGCTCAT	3791
Hypercholesterolaemia Cys249Tyr TGC-TAC	ATGGCAGCCGGCAGTGTGACCGGGGAATATGACTGCAAGGAC ATGAGCGATGAAGTTGGCT <u>G</u> CGTTAATGGTGAGCGCTGGCC ATCTGGTTTTCCATCCCCATTCTCTGTGCCTTGCTGCT	3792
	AGCAGCAAGGCACAGAGAATGGGGGATGGAAAACCAGATGG CCAGCGCTCACCATTAAACG <u>C</u> AGCCAACTTCATCGCTCATGTC CTTGCAAGTCATATTCCCGGTACACTGCCGGCTGCCAT	3793
	AGTTGGCT <u>G</u> CGTTAATG	3794
	CATTAAACG <u>C</u> AGCCAACT	3795
Hypercholesterolaemia Glu256Lys cGAG-AAG	AGGCTCAGACACACCTGACCTTCCTCCTCCTCTCTGGCT CTCACAGTGACACTCTG <u>C</u> GAGGGACCCAACAAGTTCAAGTGT CACAGCGGCGAATGCATCACCTGGACAAAGTCTGCA	3796

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGCAGACTTTGTCCAGGGTGATGCATTGCCCGCTGTGACACT TGAAGTTGTTGGGTCCCTCGCAGAGTGTCACTGTGAGAGCCA GAGAGAGGAAGGAGGAAGGTCAGGTGTGTCTGAGCCT	3797
	CACTCTGCCGAGGGACCC	3798
	GGGTCCCTCGCAGAGTG	3799
Hypercholesterolaemia Ser265Arg AGCg-AGA	CCTCTCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAA CAAGTTCAAGTGTACAGCGGCGAATGCATCACCTGGACAA AGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCA	3800
	TGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTC CAGGGTGATGCATTGCCGCTGTGACACTTGAAGTTGTTGGG TCCCTCGCAGAGTGTCACTGTGAGAGCCAGAGAGAGG	3801
	TGTCACAGCGGCGAATG	3802
	CATTCGCCGCTGTGACA	3803
Hypercholesterolaemia Glu267Lys cGAA-AAA	TCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAACAAG TTCAAGTGTACAGCGGCGAATGCATCACCTGGACAAAGTC TGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATG	3804
	CATCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTT TGTCAGGGTGATGCATTGCCGCTGTGACACTTGAAGTTGT TGGGTCCCTCGCAGAGTGTCACTGTGAGAGCCAGAGA	3805
	ACAGCGGCGAATGCATC	3806
	GATGCATTGCCGCTGT	3807
Hypercholesterolaemia Glu267Term cGAA-TAA	TCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAACAAG TTCAAGTGTACAGCGGCGAATGCATCACCTGGACAAAGTC TGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATG	3808
	CATCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTT TGTCAGGGTGATGCATTGCCGCTGTGACACTTGAAGTTGT TGGGTCCCTCGCAGAGTGTCACTGTGAGAGCCAGAGA	3809
	ACAGCGGCGAATGCATC	3810
	GATGCATTGCCGCTGT	3811
Hypercholesterolaemia Lys273Glu cAAA-GAA	CACTCTGCGAGGGACCCAACAAGTTCAAGTGTACAGCGG CGAATGCATCACCTGGACAAGTCTGCAACATGGCTAGAGA CTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCG	3812
	CGCACTCTTTGATGGGTTTCTGACCAAGTCCCGGCAGTCTC TAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTGCCCGC TGTGACACTTGAAGTTGTTGGGTCCCTCGCAGAGTGT	3813
	CCCTGGACAAGTCTGC	3814
	GCAGACTTTGTCCAGGG	3815
Hypercholesterolaemia Cys275Term TGCg-TGA	CGAGGGACCCAACAAGTTCAAGTGTACAGCGGCGAATGCA TCACCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGG GACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCT	3816
	AGACTCACCGCACTTTTGTGGGTTCTGACCAAGTCCCG GCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCA TTCGCCGCTGTGACACTTGAAGTTGTTGGGTCCCTCG	3817

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AAAGTCTGCAACATGGC	3818
	GCCATGTTGCAGACTTT	3819
Hypercholesterolaemia Asp280Gly GAC-GGC	AGTTCAAGTGTACAGCGGCGAATGCATCACCCCTGGACAAAG TCTGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAA CCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCT	3820
	AGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTCA TCTGACCAAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTG TCCAGGGTGATGCATTCGCCGCTGTGACACTTGA	3821
	GGCTAGAGACTGCCGGG	3822
	CCCGGCAGTCTCTAGCC	3823
Hypercholesterolaemia Cys281Tyr TGC-TAC	TCAAGTGTACAGCGGCGAATGCATCACCCCTGGACAAAGTCT GCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCC ATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGC	3824
	GCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGG TTCATCTGACCAAGTCCCGGCAGTCTCTAGCCATGTTGCAGAC TTTGTCCAGGGTGATGCATTCGCCGCTGTGACACTTGA	3825
	TAGAGACTGCCGGGACT	3826
	AGTCCCGGCAGTCTCTA	3827
Hypercholesterolaemia Asp283Asn gGAC-AAC	TGTCACAGCGGCGAATGCATCACCCCTGGACAAAGTCTGCAAC ATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAA GAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGT	3828
	ACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGA TGGGTTTCATCTGACCAAGTCCCGGCAGTCTCTAGCCATGTTGC AGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGACA	3829
	ACTGCCGGGACTGGTCA	3830
	TGACCAAGTCCCGGCAGT	3831
Hypercholesterolaemia Asp283Glu GACT-GAG	TCACAGCGGCGAATGCATCACCCCTGGACAAAGTCTGCAACAT GGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAAAG AGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTT	3832
	AAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTT GATGGGTTTCATCTGACCAAGTCCCGGCAGTCTCTAGCCATGTT GCAGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGA	3833
	TGCCGGGACTGGTCAGA	3834
	TCTGACCAAGTCCCGGCA	3835
Hypercholesterolaemia Asp283Tyr gGAC-TAC	TGTCACAGCGGCGAATGCATCACCCCTGGACAAAGTCTGCAAC ATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAA GAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGT	3836
	ACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGA TGGGTTTCATCTGACCAAGTCCCGGCAGTCTCTAGCCATGTTGC AGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGACA	3837
	ACTGCCGGGACTGGTCA	3838
	TGACCAAGTCCCGGCAGT	3839

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Trp284Term TGGt-TGA	CAGCGGCGAATGCATCACCCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTG	3840
	CACAAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTTCATCTGACCCAGTCCCAGGAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTCCGCCGCTG	3841
	CGGGACTGGTCAGATGA	3842
	TCATCTGACCCAGTCCCG	3843
Hypercholesterolaemia Ser285Leu TCA-TTA	GCGGCGAATGCATCACCCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTGGG	3844
	CCCACAAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTTCATCTGACCCAGTCCCAGGAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTCCGCCG	3845
	GGACTGGTCAGATGAAC	3846
	GTTTCATCTGACCCAGTCC	3847
Hypercholesterolaemia Lys290Arg AAA-AGA	CCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTGGGGAGCCAGGAAAGGGA	3848
	TCCCTTTCTGGCTCCCCACAAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTTCATCTGACCCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGG	3849
	ACCCATCAAAGAGTGCG	3850
	CGCACTCTTTGATGGGT	3851
Hypercholesterolaemia Cys297Phe TGC-TTC	GGGTAGGGGCCCCGAGAGTGACCCAGTCTGCATCCCCTGGCCC TGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTG	3852
	CACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTTCGTTGGTCCCTGCGCAGGGCCAGGGGATGCAGACTGGTCACTCTCGGGCCCCCTACCC	3853
	CAACGAATGCTTGGACA	3854
	TGTCCAAGCATTTCGTTG	3855
Hypercholesterolaemia Cys297Tyr TGC-TAC	GGGTAGGGGCCCCGAGAGTGACCCAGTCTGCATCCCCTGGCCC TGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTG	3856
	CACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTTCGTTGGTCCCTGCGCAGGGCCAGGGGATGCAGACTGGTCACTCTCGGGCCCCCTACCC	3857
	CAACGAATGCTTGGACA	3858
	TGTCCAAGCATTTCGTTG	3859
Hypercholesterolaemia His306Tyr cCAC-TAC	TGCATCCCCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACAGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCCTGTGCCCGACGGCTTCCAGCTGG	3860

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGCCGATC TTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCC AAGCATTTCGTTGGTCCCTGCGCAGGGCCAGGGGATGCA	3861
	GCTGTTCCACGTCTGC	3862
	GCAGACGTGGGAACAGC	3863
Hypercholesterolaemia Cys308Gly cTGC-GGC	CCCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAA CGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTA CGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCC	3864
	GGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTA GCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGT TGTGTCCAAGCATTCTTGGTCCCTGCGCAGGGCCAGGG	3865
	CCCACGTCTGCAATGAC	3866
	GTCATTGCAGACGTGGG	3867
Hypercholesterolaemia Cys308Tyr TGC-TAC	CCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAAC GGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTAC GAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCA	3868
	TGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTA GCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGT GTTGTCCAAGCATTCTTGGTCCCTGCGCAGGGCCAGG	3869
	CCACGTCTGCAATGACC	3870
	GGTCATTGCAGACGTGG	3871
Hypercholesterolaemia Gly314Ser cGGC-AGC	ACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCT TGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGAC GGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTG	3872
	CACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCG GGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGAC GTGGGAACAGCCGCCGTTGTTGTCCAAGCATTCTTGGT	3873
	TTAAGATCGGCTACGAG	3874
	CTCGTAGCCGATCTTA	3875
Hypercholesterolaemia Gly314Val GGC-GTC	CCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCT GCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGAC GGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGA	3876
	TCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCG GGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGACG TGGGAACAGCCGCCGTTGTTGTCCAAGCATTCTTGG	3877
	TAAGATCGGCTACGAGT	3878
	ACTCGTAGCCGATCTTA	3879
Hypercholesterolaemia Tyr315Term TACg-TAA	CGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCTGCAA TGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTT CCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTT	3880
	GAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCC GTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCA GACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTCTG	3881

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATCGGCTAC <u>G</u> AGTGCCT	3882
	AGGCACTC <u>G</u> TAGCCGAT	3883
Hypercholesterolaemia Cys317Gly gTGC-GGC	TGCTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCCGGG	3884
	CCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGC <u>A</u> CTCGTAGCCGATCTTAAGGTCA TTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCA	3885
	GCTACGAGTGCCTGTGC	3886
	GCACAGGC <u>A</u> CTCGTAGC	3887
Hypercholesterolaemia Cys317Ser gTGC-AGC	TGCTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCCGGG	3888
	CCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGC <u>A</u> CTCGTAGCCGATCTTAAGGTCA TTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCA	3889
	GCTACGAGTGCCTGTGC	3890
	GCACAGGC <u>A</u> CTCGTAGC	3891
Hypercholesterolaemia Pro320Arg CCC-CGC	ACAACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCC <u>C</u> GACGGCTTCCAGCTGGTGGCC CAGCGAAGATGCGAAGGTGATTTCCGGGTGGGACTGAG	3892
	CTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGGCC ACCAGCTGGAAGCCGTCG <u>G</u> GGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGT	3893
	CCTGTGCC <u>C</u> GACGGCT	3894
	AGCCGTCG <u>G</u> GGGCACAGG	3895
Hypercholesterolaemia Asp321Asn cGAC-AAC	AACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCC <u>G</u> ACGGCTTCCAGCTGGTGGCCCA GCGAAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCC	3896
	GGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCG <u>G</u> GGGGCACAGGCACTCGTAGCCG ATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTT	3897
	TGTGCCCC <u>G</u> ACGGCTTC	3898
	GAAGCCGTCG <u>G</u> GGGCACA	3899
Hypercholesterolaemia Asp321Glu GACg-GAG	CGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGAC <u>G</u> GGCTTCCAGCTGGTGGCCAGC GAAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCCCT	3900
	AGGGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCC <u>G</u> TCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCG	3901
	TGCCCCGACGGCTTCCA	3902
	TGGAAGCC <u>G</u> TCGGGGCA	3903

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Gly322Ser cGGC-AGC	GGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTAC GAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCG AAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCCCTG	3904
	CAGGGCTCAGTCCCACCCGAAATCACCTTCGCATCTTCGCT GGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTA GCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCC	3905
	GCCCCGACGGCTTCCAG	3906
	CTGGAAGCCGTCGGGGC	3907
Hypercholesterolaemia Gln324Term cCAG-TAG	TGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGC CTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCGAAGATG CGAAGGTGATTTCCGGGTGGGACTGAGCCCTGGGCCCC	3908
	GGGGCCCAGGGCTCAGTCCCACCCGAAATCACCTTCGCAT CTTCGCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCA CTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACA	3909
	ACGGCTTCCAGCTGGTG	3910
	CACCAGCTGGAAGCCGT	3911
Hypercholesterolaemia Arg329Pro CGA-CCA	ATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCT TCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCCGG GTGGGACTGAGCCCTGGGCCCCCTCTGCGCTTCCTGAC	3912
	GTCAGGAAGCGCAGAGGGGGGCCAGGGCTCAGTCCCACCC GGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGC CGTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCAT	3913
	GGCCCAGCGAAGATGCG	3914
	CGCATCTTCGCTGGGCC	3915
Hypercholesterolaemia Arg329Term gCGA-TGA	AATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGG CTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCC GGGTGGGACTGAGCCCTGGGCCCCCTCTGCGCTTCCTGA	3916
	TCAGGAAGCGCAGAGGGGGGCCAGGGCTCAGTCCCACCCG GAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCC GTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATT	3917
	TGGCCCAGCGAAGATGC	3918
	GCATCTTCGCTGGGCCA	3919
Hypercholesterolaemia Glu336Lys tGAG-AAG	TCTAGCCATTGGGGAAGAGCCTCCCCACCAAGCCTCTTTCTC TCTCTTCCAGATATCGATGAGTGTGAGGATCCCGACACCTGC AGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACAAGT	3920
	ACTTGTAGCCACCCTCCAGTTACGCAGAGCTGGCTGCAG GTGTCGGGATCCTGACACTCATCGATATCTGGAAGAGAGAGA AAGAGGCTTGGTGGGGAGGCTCTTCCCCAATGGCTAGA	3921
	ATATCGATGAGTGTCAG	3922
	CTGACACTCATCGATAT	3923
Hypercholesterolaemia Gln338Term tCAG-TAG	CATTGGGGAAGAGCCTCCCCACCAAGCCTCTTTCTCTCTT CCAGATATCGATGAGTGTGAGGATCCCGACACCTGCAGCCAG CTCTGCGTGAACCTGGAGGGTGGCTACAAGTGCCAGT	3924

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACTGGCACTTGTAGCCACCCTCCAGGTTACGCAGAGCTGG CTGCAGGTGTCGGGATCCTGACACTCATCGATATCTGGAAGA GAGAGAAAGAGGCTTGGTGGGGAGGCTCTTCCCCAATG	3925
	ATGAGTGTGAGGATCCC	3926
	GGGATCCTGACACTCAT	3927
Hypercholesterolaemia Cys343Arg cTGC-CGC	TCCCCACCAAGCCTCTTTCTCTCTTTCCAGATATCGATGAGT GTCAGGATCCCGACACCTGCAGCCAGCTCTGCGTGAACCTG GAGGGTGGCTACAAGTGCCAGTGTGAGGAAGGCTTCC	3928
	GGAAGCCTTCCTCACACTGGCACTTGTAGCCACCCTCCAGGT TCACGCAGAGCTGGCTGCAGGTGTCGGGATCCTGACACTCA TCGATATCTGGAAGAGAGAGAAAGAGGCTTGGTGGGGA	3929
	CCGACACCTGCAGCCAG	3930
	CTGGCTGCAGGTGTCGG	3931
Hypercholesterolaemia Gln345Arg CAG-CGG	CAAGCCTCTTTCTCTCTTTCCAGATATCGATGAGTGTGAGGA TCCCGACACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTG GCTACAAGTGCCAGTGTGAGGAAGGCTTCCAGCTGGA	3932
	TCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTAGCCACCC TCCAGGTTACGCAGAGCTGGCTGCAGGTGTCGGGATCCTG ACACTCATCGATATCTGGAAGAGAGAGAAAGAGGCTTG	3933
	CTGCAGCCAGCTCTGCG	3934
	CGCAGAGCTGGCTGCAG	3935
Hypercholesterolaemia Cys347Tyr TGC-TAC	TCTTTCTCTCTTTCCAGATATCGATGAGTGTGAGGATCCCGA CACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACA AGTGCCAGTGTGAGGAAGGCTTCCAGCTGGACCCCCA	3936
	TGGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTAG CCACCCTCCAGGTTACGCAGAGCTGGCTGCAGGTGTCGGG ATCCTGACACTCATCGATATCTGGAAGAGAGAGAAAGA	3937
	CCAGCTCTGCGTGAACC	3938
	GGTTCACGCAGAGCTGG	3939
Hypercholesterolaemia Cys347Arg cTGC-CGC	CTTTTCTCTCTTTCCAGATATCGATGAGTGTGAGGATCCCG ACACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTAC AAGTGCCAGTGTGAGGAAGGCTTCCAGCTGGACCCCC	3940
	GGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTAG CCACCCTCCAGGTTACGCAGAGCTGGCTGCAGGTGTCGGG ATCCTGACACTCATCGATATCTGGAAGAGAGAGAAAGAG	3941
	GCCAGCTCTGCGTGAAC	3942
	GTTACGCAGAGCTGGC	3943
Hypercholesterolaemia Gly352Asp GGT-GAT	CAGATATCGATGAGTGTGAGGATCCCGACACCTGCAGCCAGC TCTGCGTGAACCTGGAGGGTGGCTACAAGTGCCAGTGTGAG GAAGGCTTCCAGCTGGACCCCCACACGAAGGCCTGCAA	3944
	TTGCAGGCCTTCGTGTGGGGGTCCAGCTGGAAGCCTTCCTC ACACTGGCACTTGTAGCCACCTCCAGGTTACGCAGAGCTG GCTGCAGGTGTCGGGATCCTGACACTCATCGATATCTG	3945

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCTGGAGGGTGGCTACA	3946
	TGTAGCCACCCTCCAGG	3947
Hypercholesterolaemia Tyr354Cys TAC-TGC	TCGATGAGTGTGAGGATCCCGACACCTGCAGCCAGCTCTGC GTGAACCTGGAGGGTGGCTACAAGTGCCAGTGTGAGGAAGG CTTCCAGCTGGACCCCCACACGAAGGCCTGCAAGGCTGT	3948
	ACAGCCTTGCAGGCCTTCGTGTGGGGGTCCAGCTGGAAGCC TTCCTCACACTGGCACTTGTAGCCACCCTCCAGGTTACGCA GAGCTGGCTGCAGGTGTCGGGATCCTGACACTCATCGA	3949
	GGGTGGCTACAAGTGCC	3950
	GGCACTTGTAGCCACCC	3951
Hypercholesterolaemia Cys358Arg gTGT-CGT	CAGGATCCCGACACCTGCAGCCAGCTCTGCGTGAACCTGGA GGGTGGCTACAAGTGCCAGTGTGAGGAAGGCTTCCAGCTGG ACCCCCACACGAAGGCCTGCAAGGCTGTGGGTGAGCACG	3952
	CGTGCTACCCACAGCCTTGCAGGCCTTCGTGTGGGGGTCC AGCTGGAAGCCTTCCTCACACTGGCACTTGTAGCCACCCTCC AGGTTACGCAGAGCTGGCTGCAGGTGTCGGGATCCTG	3953
	AGTGCCAGTGTGAGGAA	3954
	TTCCTCACACTGGCACT	3955
Hypercholesterolaemia Gln363Term cCAG-TAG	TGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACAAGTG CCAGTGTGAGGAAGGCTTCCAGCTGGACCCCCACACGAAGG CCTGCAAGGCTGTGGGTGAGCACGGGAAGGCGGCGGGTG	3956
	CACCCGCCGCTTCCCGTGCTACCCACAGCCTTGCAGGCC TTCGTGTGGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCA CTTGTAGCCACCCTCCAGGTTACGCAGAGCTGGCTGCA	3957
	AAGGCTTCCAGCTGGAC	3958
	GTCCAGCTGGAAGCCTT	3959

EXAMPLE 23

UDP-glucuronosyltransferase - UGT1

[0236] Mutations in the human UGT1 gene result in a range of disease syndromes, ranging from relatively common diseases such as Gilbert's syndrome, which effects up to 7% of the population, to rare disorders such as Crigler-Najjar syndrome. Symptoms of these diseases are the result of diminished bilirubin conjugation and typically present with jaundice or, when mild, as an incidental finding during routing laboratory analysis. Severe cases of Crigler-Najjar syndrome are caused by an absence of UGT1 activity and the majority of these patients die in the neonatal period. The only known treatment is liver transplant. The attached table discloses the correcting oligonucleotide base sequences for the UGT1 oligonucleotides of the invention.

Table 25

UGT1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Crigler-Najjar syndrome 2 Leu15Arg CTG-CGG	GCAGGAGCAAAGGCGCCATGGCTGTGGAGTCCCAGGGCGG ACGCCCACCTTGTCTGGGCC <u>T</u> GCTGCTGTGTGTGCTGGGCC CAGTGGTGTCCCATGCTGGGAAGATACTGTTGATCCCAGT	3960
	ACTGGGATCAACAGTATCTTCCCAGCATGGGACACCACTGGG CCCAGCACACACAGCAGC <u>A</u> GGCCCAGGACAAGTGGGCGTCC GCCCTGGGACTCCACAGCCATGGCGCCTTTGCTCCTGC	3961
	CCTGGGCC <u>T</u> GCTGCTGT	3962
	ACAGCAGC <u>A</u> GGCCCAGG	3963
Crigler-Najjar syndrome 1 Gln49Term CAG-TAG	GGAAGATACTGTTGATCCCAGTGGATGGCAGCCACTGGCT GAGCATGCTTGGGGCCATC <u>C</u> AGCAGCTGCAGCAGAGGGGAC ATGAAATAGTTGTCTAGCACCTGACGCCTCGTTGTACA	3964
	TGTACAACGAGGCGTCAGGTGCTAGGACAACATTTTCATGTC CCCTCTGCTGCAGCTGCT <u>G</u> GATGGCCCCAAGCATGCTCAGC CAGTGGCTGCCATCCACTGGGATCAACAGTATCTTCCC	3965
	GGGCCATC <u>C</u> AGCAGCTG	3966
	CAGCTGCT <u>G</u> GATGGCCC	3967
Crigler-Najjar syndrome 1 Gly71Arg GGA-AGA	CAGCAGAGGGGACATGAAATAGTTGTCTAGCACCTGACGCC TCGTTGTACATCAGAGAC <u>G</u> GAGCATTTTACACCTTGAAGACG TACCCTGTGCCATTCCAAAGGGAGGATGTGAAAGAGT	3968
	ACTCTTTCACATCCTCCCTTTGGAATGGCACAGGGTACGTCTT CAAGGTGTAAAATGCTC <u>C</u> GTCTCTGATGTACAACGAGGCGTC AGGTGCTAGGACAACATTTTCATGTCCCCTCTGCTG	3969
	TCAGAGAC <u>G</u> GAGCATTT	3970
	AAATGCTC <u>C</u> GTCTCTGA	3971
Gilbert syndrome Pro229Gln CCG-CAG	GGGTGAAGAACATGCTCATTGCCTTTTACAGAACTTTCTGTG CGACGTGGTTTATTCCC <u>C</u> GTATGCAACCCTTGCCTCAGAATTC CTTCAGAGAGAGGTGACTGTCCAGGACCTATTGAG	3972
	CTCAATAGGTCCTGGACAGTCACCTCTCTCTGAAGGAATTCT GAGGCAAGGGTTGCATAC <u>G</u> GGGAATAAACCACGTGCGACAG AAAGTTCTGTGAAAAGGCAATGAGCATGTTCTTCACCC	3973
	TTATTCCC <u>C</u> GTATGCAA	3974
	TTGCATAC <u>G</u> GGGAATAA	3975
Crigler-Najjar syndrome 1 Cys280Term TGC-TGA	TGTGAAGGATTACCCTAGGCCCATCATGCCCAATATGGTTTTT GTTGGTGGAAATCAACTG <u>C</u> CTTCACCAAAATCCACTATCCCAG GTGTGTATTGGAGTGGGACTTTTACATGCGTATATT	3976
	AATATACGCATGTAAAAGTCCCACTCCAATACACACCTGGGAT AGTGGATTTTGGTGAAG <u>G</u> CAGTTGATTCCACCAACAAAAACC ATATTGGGCATGATGGGCCTAGGGTAATCCTTCACA	3977

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATCAACTG <u>C</u> CTTCACCA	3978
	TGGTGAAG <u>G</u> CAGTTGAT	3979
Crigler-Najjar syndrome 1 Ala292Val GCC-GTC	ATCAAAGAATATGAGAAAAAATTAAGTAAAATTTTTCTTCTGGCTCTAGGAATTTGAAG <u>C</u> CTACATTAATGCTTCTGGAGAACATGGAATTGTGGTTTTCTCTTTGGGATCAATGGTCTC	3980
	GAGACCATTGATCCCAAAGAGAAAACCACAATTCCATGTTCTCAGAAAGCATTAAATGTAG <u>G</u> CTTCAAATTCCTAGAGCCAGAAGAAAATTTTCAGTTAATTTTTTCTCATATTCTTTGAT	3981
	ATTTGAAG <u>C</u> CTACATTA	3982
	TAATGTAG <u>G</u> CTTCAAAT	3983
Crigler-Najjar syndrome 1 Gly308Glu GGA-GAA	AGGAATTTGAAGCCTACATTAATGCTTCTGGAGAACATGGAATGTGGTTTTCTCTTTGG <u>G</u> ATCAATGGTCTCAGAAATTCAGAGAAGAAAGCTATGGCAATTGCTGATGCTTTGGGCAA	3984
	TTGCCCAAAGCATCAGCAATTGCCATAGCTTTCTTCTCTGGAA TTTCTGAGACCATTGAT <u>C</u> CCCAAAGAGAAAACCACAATTCCATGTTCTCCAGAAGCATTAAATGTAGGCTTCAAATTCCT	3985
	CTCTTTGG <u>G</u> ATCAATGG	3986
	CCATTGAT <u>C</u> CCCAAAGAG	3987
Crigler-Najjar syndrome 1 Gln331Term CAG-TAG	GTCTCAGAAATTCAGAGAAGAAAGCTATGGCAATTGCTGATGCTTTGGGCAAAATCCCT <u>C</u> AGACAGTAAGAAGATTCTATACCATGGCCTCATATCTATTTTCACAGGAGCGCTAATCCC	3988
	GGGATTAGCGCTCCTGTGAAAATAGATATGAGGCCATGGTATAGAATCTTCTTACTGTCT <u>G</u> AGGGATTTTGCCCAAAGCATCAGCAATTGCCATAGCTTTCTTCTCTGGAATTTCTGAGAC	3989
	AAATCCCT <u>C</u> AGACAGTA	3990
	TACTGTCT <u>G</u> AGGGATTT	3991
Crigler-Najjar syndrome 1 Trp335Term TGG-TGA	TCTAATCATATTATGTTCTTTCTTTACGTTCTGCTCTTTTTGCCCTCCCAGGTCCTGTG <u>G</u> CGGTACACTGGAACCCGACCATCGAATCTTGCGAACAACACGATACTTGTTAAGTGGCTA	3992
	TAGCCACTTAACAAGTATCGTGTTGTTGCAAGATTTCGATGGTCGGGTTCCAGTGTACCG <u>C</u> CACAGGACCTGGGAGGGGGCAAAAAGAGCAGAACGTAAAGAAAGAACATAATATGATTAGA	3993
	GTCCTGTG <u>G</u> CGGTACAC	3994
	GTGTACCG <u>C</u> CACAGGAC	3995
Crigler-Najjar syndrome 1 Gln357Arg	ACACTGGAACCCGACCATCGAATCTTGCGAACAACACGATAC TTGTTAAGTGGCTACCCC <u>A</u> AAACGATCTGCTTGGTATGTTGGCGGATTGGATGTATAGGTCAAACCAGGGTCAAATTA	3996

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
CAA-CGA	TAATTTGACCCTGGTTTGACCTATACATCCAATCCGCCCAACA TACCAAGCAGATCGTTTTGGGGTAGCCACTTAACAAGTATCG TGTTGTTTCGCAAGATTCGATGGTCGGGTTCCAGTGT	3997
	GCTACCCC <u>A</u> AAACGATC	3998
	GATCGTTTT <u>T</u> GGGGTAGC	3999
Crigler-Najjar syndrome 1 Gln357Term CAA-TAA	TACACTGGAACCCGACCATCGAATCTTGCGAACAACACGATA CTTGTTAAGTGGCTACCCC <u>C</u> AAAACGATCTGCTTGGTATGTTG GGCGGATTGGATGTATAGGTCAAACCAGGGTCAAATT	4000
	AATTTGACCCTGGTTTGACCTATACATCCAATCCGCCCAACAT ACCAAGCAGATCGTTTT <u>G</u> GGGTAGCCACTTAACAAGTATCGT GTTGTTTCGCAAGATTCGATGGTCGGGTTCCAGTGTA	4001
	GGCTACCCC <u>C</u> AAAACGAT	4002
	ATCGTTTT <u>G</u> GGGTAGCC	4003
Gilbert syndrome Arg367Gly CGT-GGT	AACTCAGAGATGTAAGTCTGACATCCTCCCTATTTTGCATCT CAGGTACCCGATGACCC <u>G</u> TGCCTTTATCACCCATGCTGGTT CCCATGGTGTATGAAAGCATATGCAATGGCGTTC	4004
	GAACGCCATTGCATATGCTTTCATAAACACCATGGGAACCAG CATGGGTGATAAAGGCAC <u>G</u> GGTCATCGGGTGACCTGAGATG CAAAATAGGGAGGATGTCAGCAGTTACATCTCTGAGTT	4005
	CGATGACCC <u>G</u> TGCCTTT	4006
	AAAGGCAC <u>G</u> GGTCATCG	4007
Crigler-Najjar syndrome 1 Ala368Thr GCC-ACC	TCAGAGATGTAAGTCTGACATCCTCCCTATTTTGCATCTCAG GTCACCCGATGACCCG <u>T</u> GCCTTTATCACCCATGCTGGTTCCC ATGGTGTATGAAAGCATATGCAATGGCGTTCCCA	4008
	TGGGAACGCCATTGCATATGCTTTCATAAACACCATGGGAAC CAGCATGGGTGATAAAGGC <u>C</u> ACGGGTCATCGGGTGACCTGAG ATGCAAAATAGGGAGGATGTCAGCAGTTACATCTCTGA	4009
	TGACCCG <u>T</u> GCCTTTATC	4010
	GATAAAGGC <u>C</u> ACGGGTCA	4011
Crigler-Najjar syndrome 1 Ser375Phe TCC-TTC	CCTCCCTATTTTGCATCTCAGGTACCCGATGACCCGTCCT TTATCACCCATGCTGGTT <u>C</u> CCATGGTGTTTATGAAAGCATATG CAATGGCGTTCCCATGGTGATGATGCCCTTGTTTGG	4012
	CCAAACAAGGGCATCATCACCATGGGAACGCCATTGCATATG CTTTCATAAACACCATGG <u>G</u> AACCAGCATGGGTGATAAAGGCA CGGGTCATCGGGTGACCTGAGATGCAAAATAGGGAGG	4013
	TGCTGGTT <u>C</u> CCATGGTG	4014
	CACCATGG <u>G</u> AACCAGCA	4015

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Crigler-Najjar syndrome 1 Ser381Arg AGC-AGG	AGGTCACCCGATGACCCGTGCCTTTATCACCCATGCTGGTTC CCATGGTGTTCATGAAAGCATATGCAATGGCGTTCCCATGGT GATGATGCCCTTGTTTGGTGATCAGATGGACAATGCA	4016
	TGCATTGTCCATCTGATCACCAAACAAGGGCATCATCACCAT GGGAACGCCATTGCATATGCTTTTCATAAACACCATGGGAACC AGCATGGGTGATAAAGGCACGGGTCATCGGGTGACCT	4017
	TATGAAAGCATATGCAA	4018
	TTGCATATGCTTTTCATA	4019
Crigler-Najjar syndrome 1 Ala401Pro GCA-CCA	AGCATATGCAATGGCGTTCCCATGGTGATGATGCCCTTGTTT GGTGATCAGATGGACAATGCAAAGCGCATGGAGACTAAGGG AGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCTG	4020
	CAGAAGTCATTTCCAGAACATTCAGGGTCACTCCAGCTCCCT TAGTCTCCATGCGCTTTGCATTGTCCATCTGATCACCAAACAA GGGCATCATCACCATGGGAACGCCATTGCATATGCT	4021
	TGGACAATGCAAAGCGC	4022
	GCGCTTTGCATTGTCCA	4023
Crigler-Najjar syndrome 1 Lys428Glu AAA-GAA	GGAGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCTGAA GATTTAGAAAATGCTCTAAAGCAGTCATCAATGACAAAAGGT AAGAAAGAAGATACAGAAGAATACTTTGGTCATGGC	4024
	GCCATGACCAAAGTATTCTTCTGTATCTTCTTTCTTACCTTTTG TCATTGATGACTGCTTTAGAGCATTCTTCTAAATCTTCAGAAGT CATTTCCAGAACATTCAGGGTCACTCCAGCTCC	4025
	ATGCTCTAAAGCAGTC	4026
	GACTGCTTTAGAGCAT	4027
Crigler-Najjar syndrome 1 Tyr486Asp TAC-GAC	ATGAGGCACAAGGGCGCGCCACACCTGCGCCCCGCAGCCCA CGACCTCACCTGGTACCAGTACCATTCTTGGACGTGATTGG TTTCCTCTTGGCCGTCGTGCTGACAGTGGCCTTCATCA	4028
	TGATGAAGGCCACTGTCAGCACGACGGCCAAGAGGAAACCA ATCACGTCCAAGGAATGGTACTGGTACCAGGTGAGGTCGTG GGCTGCGGGGCGCAGGTGTGGCGCGCCCTTGTGCCTCAT	4029
	GGTACCAGTACCATTCC	4030
	GGAATGGTACTGGTACC	4031
Crigler-Najjar syndrome 1 Ser488Phe TCC-TTC	ACAAGGGCGCGCCACACCTGCGCCCCGCAGCCACGACCTC ACCTGGTACCAGTACCATTCTTGGACGTGATTGGTTTCCTCT TGGCCGTCGTGCTGACAGTGGCCTTCATCACCTTTAA	4032
	TTAAAGGTGATGAAGGCCACTGTCAGCACGACGGCCAAGAG GAAACCAATCACGTCCAAGGAATGGTACTGGTACCAGGTGAG GTCGTGGGCTGCGGGGCGCAGGTGTGGCGCGCCCTTGT	4033
	GTACCATTCTTGGACG	4034

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGTCCAAGGAATGGTAC	4035

EXAMPLE 24

Alzheimer's Disease - Amyloid precursor protein (APP)

[0237] Over the past few decades Alzheimer's disease (AD), once considered a rare disorder, has become recognized as a major public health problem. Although there is no agreement on the exact prevalence of Alzheimer's disease, in part due to difficulties of diagnosis, studies consistently point to an exponential rise in prevalence of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

[0238] Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest tasks. Anatomic changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and internal neurofibrillary tangles.

[0239] At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with a particular allele of APOE (see Example 20); AD3 is caused by mutation in a gene encoding a 7-transmembrane domain protein, presenilin-1 (PSEN1), and AD4 is caused by mutation in a gene that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2). The attached table discloses the correcting oligonucleotide base sequences for the APP oligonucleotides of the invention.

Table 26

APP Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Glu665Asp GAG-GAC	CTGCATACTTTAATTATGATGTAATACAGGTTCTGGGTTGACA AATATCAAGACGGAGGAGATCTCTGAAGTGAAGATGGATGCA GAATTCCGACATGACTCAGGATATGAAGTTCATCAT	4036

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGATGAACTTCATATCCTGAGTCATGTCGGAATTCTGCATCC ATCTTCACTTCAGAGATCTCCTCCGTCTTGATATTTGTCAACC CAGAACCTGTATTACATCATAATTAAAGTATGCAG	4037
	ACGGAGGAGATCTCTGA	4038
	TCAGAGATCTCCTCCGT	4039
Alzheimer disease Ala692Gly GCA-GGA	ATTATATTGCATTTAGAAATTAATAATTCTTTTTCTTAATTTGTTT TCAAGGTGTTCTTTGCGAGAAGATGTGGGTTCAAACAAAGGTG CAATCATTGGACTCATGGTGGGCGGTGTTGTCAT	4040
	ATGACAACACCGCCACCATGAGTCCAATGATTGCACCTTTG TTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAAATT AAGAAAAAGAATTTTAATTTCTAAATGCAATATAAT	4041
	GTTCTTTGCGAGAAGATG	4042
	CATCTTCTGCAAAGAAC	4043
Alzheimer disease Glu693Gln GAA-CAA	TATATTGCATTTAGAAATTAATAATTCTTTTTCTTAATTTGTTTT AAGGTGTTCTTTGCGAGAAGATGTGGGTTCAAACAAAGGTGCA ATCATTGGACTCATGGTGGGCGGTGTTGTCATAG	4044
	CTATGACAACACCGCCACCATGAGTCCAATGATTGCACCTT TGTTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAAA TTAAGAAAAAGAATTTTAATTTCTAAATGCAATATA	4045
	TCTTTGCGAGAAGATGTG	4046
	CACATCTTCTGCAAAGA	4047
Alzheimer disease Glu693Gly GAA-GGA	ATATTGCATTTAGAAATTAATAATTCTTTTTCTTAATTTGTTTTCA AGGTGTTCTTTGCGAGAAGATGTGGGTTCAAACAAAGGTGCAA TCATTGGACTCATGGTGGGCGGTGTTGTCATAGC	4048
	GCTATGACAACACCGCCACCATGAGTCCAATGATTGCACCT TTGTTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAA ATTAAGAAAAAGAATTTTAATTTCTAAATGCAATAT	4049
	CTTTGCGAGAAGATGTGG	4050
	CCACATCTTCTGCAAAG	4051
Alzheimer disease Ala713Thr GCG-ACG	GAAGATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATG GTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTG GTGATGCTGAAGAAGAAACAGTACACATCCATTCATC	4052
	GATGAATGGATGTGTACTGTTTCTTCTCAGCATCACCAAGGT GATGACGATCACTGTGCTATGACAACACCGCCACCATGAG TCCAATGATTGCACCTTTGTTTGAACCCACATCTTC	4053
	TTGTCATAGCGACAGTG	4054
	CACTGTCGCTATGACAA	4055
Schizophrenia Ala713Val GCG-GTG	AAGATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGG TGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGG TGATGCTGAAGAAGAAACAGTACACATCCATTCATCA	4056

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGG TGATGACGATCACTGTCGCTATGACAACACCGCCCACCATGA GTCCAATGATTGCACCTTTGTTTGAACCCACATCTT	4057
	TGTCATAGCGACAGTGA	4058
	TCACTGTCGCTATGACA	4059
Alzheimer disease Val715Met GTG-ATG	GTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGC GGTGTGTGCATAGCGACAGTGATCGTCATCACCTTGGTGATG CTGAAGAAGAAACAGTACACATCCATTTCATCATGGTG	4060
	CACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCAC CAAGGTGATGACGATCACTGTCGCTATGACAACACCGCCCAC CATGAGTCCAATGATTGCACCTTTGTTTGAACCCAC	4061
	TAGCGACAGTGATCGTC	4062
	GACGATCACTGTCGCTA	4063
Alzheimer disease Ile716Val ATC-GTC	GGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGT GTTGTGCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTG AAGAAGAAACAGTACACATCCATTTCATCATGGTGTGG	4064
	CCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCAT CACCAAGGTGATGACGATCACTGTCGCTATGACAACACCGCC CACCATGAGTCCAATGATTGCACCTTTGTTTGAACC	4065
	CGACAGTGATCGTCATC	4066
	GATGACGATCACTGTGCG	4067
Alzheimer disease Val717Gly GTC-GGC	CAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTTG TCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGA AGAAACAGTACACATCCATTTCATCATGGTGTGGTGG	4068
	TCCACCACCATGATGAATGGATGTGTACTGTTTCTTCTTCA GCATCACCAAGGTGATGACGATCACTGTCGCTATGACAACAC CGCCACCATGAGTCCAATGATTGCACCTTTGTTTG	4069
	AGTGATCGTCATCACCT	4070
	AGGTGATGACGATCACT	4071
Alzheimer disease Val717Ile GTC-ATC	TCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTT GTCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAG AAGAAACAGTACACATCCATTTCATCATGGTGTGGTGG	4072
	CCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAG CATCACCAAGGTGATGACGATCACTGTCGCTATGACAACACC GCCCACCATGAGTCCAATGATTGCACCTTTGTTTGA	4073
	CAGTGATCGTCATCACC	4074
	GGTGATGACGATCACTG	4075
Alzheimer disease Val717Phe GTC-TTC	TCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTT GTCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAG AAGAAACAGTACACATCCATTTCATCATGGTGTGGTGG	4076

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAG CATCACCAAGGTGATGACGATCACTGTCGCTATGACAACACC GCCCACCATGAGTCCAATGATTGCACCTTTGTTTGA	4077
	CAGTGATCGTCATCACC	4078
	GGTGATGACGATCACTG	4079
Alzheimer disease Leu723Pro CTG-CCG	TTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCG TCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCAT TCATCATGGTGTGGTGGAGGTAGGTAAACTTGACTG	4080
	CAGTCAAGTTTACCTACCTCCACCACACCATGATGAATGGAT GTGTACTGTTTCTTCTTCAGCATCACCAAGGTGATGACGATCA CTGTCGCTATGACAACACCGCCCACCATGAGTCCAA	4081
	GGTGATGCTGAAGAAGA	4082
	TCTTCTTCAGCATCACC	4083

EXAMPLE 25

Alzheimer's Disease - presenilin-1 (PSEN1)

[0240] The attached table discloses the correcting oligonucleotide base sequences for the PSEN1 oligonucleotides of the invention.

5

Table 27

PSEN1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Ala79Val GCC-GTC	CCCGGCAGGTGGTGGAGCAAGATGAGGAAGAAGATGAGGAG CTGACATTGAAATATGGCGCCAAGCATGTGATCATGCTCTTTG TCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTAC	4084
	GTAGCCACGACCACCACCATGCAGAGAGTCACAGGGACAAA GAGCATGATCACATGCTTGCGCCATATTTCAATGTCAGCTC CTCATCTTCTTCCTCATCTTGCTCCACCACCTGCCGGG	4085
	ATATGGCGCCAAGCATG	4086
	CATGCTTGCGCCATAT	4087
Alzheimer disease Val82Leu tGTG-CTG	GTGGTGGAGCAAGATGAGGAAGAAGATGAGGAGCTGACATT GAAATATGGCGCCAAGCATGTGATCATGCTCTTTGTCCCTGT GACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGT	4088
	ACTTAATGGTAGCCACGACCACCACCATGCAGAGAGTCACAG GGACAAAGAGCATGATCAATGCTTGCGCCATATTTCAATG TCAGCTCCTCATCTTCTTCCTCATCTTGCTCCACCAC	4089
	CCAAGCATGTGATCATG	4090
	CATGATCAATGCTTG	4091

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Val96Phe gGTC-TTC	AAATATGGCGCCAAGCATGTGATCATGCTCTTTGTCCCTGTG ACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTC AGCTTTTATACCCGGAAGGATGGGCAGCTGTACGTAT	4092
	ATACGTACAGCTGCCCATCCTCCGGGTATAAAAGCTGACTG ACTTAATGGTAGCCACGACCACCACCATGCAGAGAGTCACAG GGACAAAGAGCATGATCACATGCTTGGCGCCATATTT	4093
	TGGTGGTGGTCGTGGCT	4094
	AGCCACGACCACCACCA	4095
Alzheimer disease Phe105Leu TTTt-TTG	CTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTAC CATTAAAGTCAGTCAGCTTTTATACCCGGAAGGATGGGCAGCT GTACGTATGAGTTTTGTTTTATTATTCTCAAAGCCAG	4096
	CTGGCTTTGAGAATAATAAAACAAACTCATACGTACAGCTGC CCATCCTTCCGGGTATAAAGCTGACTGACTTAATGGTAGCC ACGACCACCACCATGCAGAGAGTCACAGGGACAAAG	4097
	GTCAGCTTTTATACCCG	4098
	CGGGTATAAAGCTGAC	4099
Alzheimer disease Thr116Asn ACC-AAC	TGGTGATCTCCATTAACTGACCTAGGGCTTTTGTGTTTGT TTATTGTAGAATCTATACCCATTACAGAAGATAACCGAGACT GTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGC	4100
	GCATTACAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCG GTATCTTCTGTGAATGGGGTATAGATTCTACAATAAAACAAAC ACAAAAGCCCTAGGTCAGTGTTAATGGAGATCACCA	4101
	AATCTATACCCATTCA	4102
	TGAATGGGGTATAGATT	4103
Alzheimer disease Pro117Leu CCA-CTA	TGATCTCCATTAACTGACCTAGGGCTTTTGTGTTTGT TGTAAGATCTATACCCATTACAGAAGATAACCGAGACTGTG GGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGC	4104
	GCAGCATTACAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTC TCGGTATCTTCTGTGAATGGGGTATAGATTCTACAATAAAACA AACACAAAAGCCCTAGGTCAGTGTTAATGGAGATCA	4105
	CTATACCCATTACAG	4106
	CTGTGAATGGGGTATAG	4107
Alzheimer disease Glu120Asp GAAg-GAT	TAACACTGACCTAGGGCTTTTGTGTTTGT ATACCCATTACAGAAAGATACCGAGACTGTGGGCCAGAGAG CCCTGCACTCAATTCTGAATGCTGCCATCATGATC	4108
	GATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTG GCCACAGTCTCGGTATCTTCTGTGAATGGGGTATAGATTCT ACAATAAAACAAACACAAAAGCCCTAGGTCAGTGTTA	4109
	TTCACAGAAAGATACCGA	4110
	TCGGTATCTTCTGTGAA	4111

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Glu120Asp GAAg-GAC	TAACACTGACCTAGGGCTTTTGTGTTTGTTTTATTGTAGAATCT ATACCCCATTCACAGAAGATACCGAGACTGTGGGCCAGAGAG CCCTGCACTCAATTCTGAATGCTGCCATCATGATC	4112
	GATCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTG GCCCACAGTCTCGGTATCTTCTGTGAATGGGGTATAGATTCT ACAATAAAACAAACACAAAAGCCCTAGGTCAGTGTTA	4113
	TTCACAGAAGATACCGA	4114
	TCGGTATCTTCTGTGAA	4115
Alzheimer disease Glu120Lys aGAA-AAA	ATTAACACTGACCTAGGGCTTTTGTGTTTGTTTTATTGTAGAAT CTATACCCCATTCACAGAAGATACCGAGACTGTGGGCCAGAG AGCCCTGCACTCAATTCTGAATGCTGCCATCATGA	4116
	TCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGC CCACAGTCTCGGTATCTTCTGTGAATGGGGTATAGATTCTACA ATAAAACAAACACAAAAGCCCTAGGTCAGTGTTAAT	4117
	CATTCACAGAAGATACC	4118
	GGTATCTTCTGTGAATG	4119
Alzheimer disease Glu123Lys cGAG-AAG	GACCTAGGGCTTTTGTGTTTGTTTTATTGTAGAATCTATACCC CATTCACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTG CACTCAATTCTGAATGCTGCCATCATGATCAGTGTC	4120
	TGACACTGATCATGATGGCAGCATTGAGAATTGAGTGCAGGG CTCTCTGGCCCACAGTCTCGGTATCTTCTGTGAATGGGGTAT AGATTCTACAATAAAACAAACACAAAAGCCCTAGGTC	4121
	AAGATACCGAGACTGTG	4122
	CACAGTCTCGGTATCTT	4123
Alzheimer disease Asn135Asp gAAT-GAT	TATACCCCATTCACAGAAGATACCGAGACTGTGGGCCAGAGA GCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTC ATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATA	4124
	TATACAGAACCACCAGGAGGATAGTCATGACAACAATGACAC TGATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCT GGCCCACAGTCTCGGTATCTTCTGTGAATGGGGTATA	4125
	CAATTCTGAATGCTGCC	4126
	GGCAGCATTCAGAATTG	4127
Alzheimer disease Met139Ile ATGa-ATA	AGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAA TTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGAC TATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTAT	4128
	ATAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCAT GACAACAATGACACTGATCATGATGGCAGCATTGAGAATTGA GTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTTCT	4129
	GCCATCATGATCAGTGT	4130
	ACACTGATCATGATGGC	4131

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Met139Lys ATG-AAG	CAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCA ATTCTGAATGCTGCCATCATGATCAGTGTCAATTGTTGTCATGA CTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTA	4132
	TAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATG ACAACAATGACACTGATCATGATGGCAGCATTGAGAATTGAG TGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTG	4133
	TGCCATCATGATCAGTG	4134
	CACTGATCATGATGGCA	4135
Alzheimer disease Met139Thr ATG-ACG	CAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCA ATTCTGAATGCTGCCATCATGATCAGTGTCAATTGTTGTCATGA CTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTA	4136
	TAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATG ACAACAATGACACTGATCATGATGGCAGCATTGAGAATTGAG TGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTG	4137
	TGCCATCATGATCAGTG	4138
	CACTGATCATGATGGCA	4139
Alzheimer disease Met139Val cATG-GTG	ACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTC AATTCTGAATGCTGCCATCATGATCAGTGTCAATTGTTGTCATG ACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCT	4140
	AGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGA CAACAATGACACTGATCATGATGGCAGCATTGAGAATTGAGT GCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTGT	4141
	CTGCCATCATGATCAGT	4142
	ACTGATCATGATGGCAG	4143
Alzheimer disease Ile143Phe cATT-TTT	GAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCT GCCATCATGATCAGTGTCAATTGTTGTCATGACTATCCTCCTGG TGGTTCTGTATAAATACAGGTGCTATAAGGTGAGCA	4144
	TGCTCACCTTATAGCACCTGTATTTATACAGAACCACCAGGAG GATAGTCATGACAACAATGACACTGATCATGATGGCAGCATT CAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCTC	4145
	TCAGTGTCAATTGTTGTC	4146
	GACAACAATGACACTGA	4147
Alzheimer disease Ile143Thr ATT-ACT	AGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTG CCATCATGATCAGTGTCAATTGTTGTCATGACTATCCTCCTGGT GGTTCTGTATAAATACAGGTGCTATAAGGTGAGCAT	4148
	ATGCTCACCTTATAGCACCTGTATTTATACAGAACCACCAGGA GGATAGTCATGACAACAATGACACTGATCATGATGGCAGCAT TCAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCT	4149
	CAGTGTCAATTGTTGTCA	4150
	TGACAACAATGACACTG	4151
Alzheimer disease Met146Ile ATGa-ATA	CCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGAT CAGTGTCAATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTAT AAATACAGGTGCTATAAGGTGAGCATGAGACACAGA	4152

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGA ACCACCAGGAGGATAGT <u>C</u> ATGACAACAATGACACTGATCATG ATGGCAGCATTGAGATTGAGTGCAGGGCTCTCTGG	4153
	GTTGT <u>C</u> ATGACTATCCT	4154
	AGGATAGT <u>C</u> ATGACAAC	4155
Alzheimer disease Met146Ile ATGa-ATC	CCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGAT CAGTGTCAATTGTTGTCAT <u>G</u> ACTATCCTCCTGGTGGTTCTGTAT AAATACAGGTGCTATAAGGTGAGCATGAGACACAGA	4156
	TCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGA ACCACCAGGAGGATAGT <u>C</u> ATGACAACAATGACACTGATCATG ATGGCAGCATTGAGATTGAGTGCAGGGCTCTCTGG	4157
	GTTGT <u>C</u> ATGACTATCCT	4158
	AGGATAGT <u>C</u> ATGACAAC	4159
Alzheimer disease Met146Leu cATG-TTG	GGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATG ATCAGTGTCAATTGTTGTC <u>A</u> TGACTATCCTCCTGGTGGTTCTGT ATAAATACAGGTGCTATAAGGTGAGCATGAGACACA	4160
	TGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGAAC CACCAGGAGGATAGTCAT <u>G</u> ACAACAATGACACTGATCATGAT GGCAGCATTGAGATTGAGTGCAGGGCTCTCTGGCC	4161
	TTGTTGTC <u>A</u> TGACTATC	4162
	GATAGTCATGACAACAA	4163
Alzheimer disease Met146Val cATG-GTG	GGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATG ATCAGTGTCAATTGTTGTC <u>A</u> TGACTATCCTCCTGGTGGTTCTGT ATAAATACAGGTGCTATAAGGTGAGCATGAGACACA	4164
	TGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGAAC CACCAGGAGGATAGTCAT <u>G</u> ACAACAATGACACTGATCATGAT GGCAGCATTGAGATTGAGTGCAGGGCTCTCTGGCC	4165
	TTGTTGTC <u>A</u> TGACTATC	4166
	GATAGTCATGACAACAA	4167
Alzheimer disease Thr147Ile ACT-ATT	AGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCA GTGTCATTGTTGTCATG <u>A</u> TATCCTCCTGGTGGTTCTGTATAA ATACAGGTGCTATAAGGTGAGCATGAGACACAGATC	4168
	GATCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACA GAACCACCAGGAGGATAGT <u>G</u> TCATGACAACAATGACACTGATCA TGATGGCAGCATTGAGATTGAGTGCAGGGCTCTCT	4169
	TGTCATG <u>A</u> TATCCTCC	4170
	GGAGGATAGT <u>G</u> TCATGACA	4171
Alzheimer disease His163Arg CAT-CGT	CTTTTAAAGGGTTGTGGGACCTGTTAATTATATTGAAATGCTTT CTTTTCTAGGTCATCC <u>A</u> TGCCTGGCTTATTATATCATCTCTATT GTTGCTGTTCTTTTTTTCATTCACTTACTTGGG	4172
	CCCAAGTAAATGAATGAAAAAAGAACAGCAACAATAGAGAT GATATAATAAGCCAGGCAT <u>G</u> GATGACCTAGAAAAGAAAGCAT TTCAATATAATTAACAGGTCCCACAACCCTTAAAAAG	4173

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGTCATCC <u>A</u> TGCCTGGC	4174
	GCCAGGCATGGATGACC	4175
Alzheimer disease His163Tyr cCAT-TAT	ACTTTTTAAGGGTTGTGGGACCTGTTAATTATATTGAAATGCT TTCTTTTCTAGGTCATCC <u>A</u> TGCCTGGCTTATTATATCATCTCTA TTGTTGCTGTTCTTTTTTTCATTCATTTACTTGG	4176
	CCAAGTAAATGAATGAAAAAAGAACAGCAACAATAGAGATGA TATAATAAGCCAGGCAT <u>G</u> GATGACCTAGAAAAGAAAGCATTTC AATATAATTAACAGGTCCCACAACCCTTAAAAAGT	4177
	AGGTCATCC <u>A</u> TGCCTGG	4178
	CCAGGCAT <u>G</u> GATGACCT	4179
Alzheimer disease Trp165Cys TGGc-TGC	AGGGTTGTGGGACCTGTTAATTATATTGAAATGCTTTCTTTTC TAGGTCATCCATGCCTG <u>G</u> CTTATTATATCATCTCTATTGTTGCT GTTCTTTTTTTCATTCATTTACTTGGGGTAAGTT	4180
	AACCTACCCCAAGTAAATGAATGAAAAAAGAACAGCAACAAT AGAGATGATATAATAAG <u>C</u> CAGGCATGGATGACCTAGAAAAGA AAGCATTTCAATATAATTAACAGGTCCCACAACCCT	4181
	CATGCCTG <u>G</u> CTTATTAT	4182
	ATAATAAG <u>C</u> CAGGCATG	4183
Alzheimer disease Ser169Leu TCA-TTA	ACCTGTTAATTATATTGAAATGCTTTCTTTTCTAGGTCATCCAT GCCTGGCTTATTATAT <u>C</u> ATCTCTATTGTTGCTGTTCTTTTTTTC ATTCATTTACTTGGGGTAAGTTGTGAAATTTTT	4184
	AAAAATTTCACAACTTACCCCAAGTAAATGAATGAAAAAAGA ACAGCAACAATAGAGAT <u>G</u> ATATAATAAGCCAGGCATGGATGA CCTAGAAAAGAAAGCATTTCAATATAATTAACAGGT	4185
	TATTATAT <u>C</u> ATCTCTAT	4186
	ATAGAGAT <u>G</u> ATATAATA	4187
Alzheimer disease Leu171Pro CTA-CCA	TAATTATATTGAAATGCTTTCTTTTCTAGGTCATCCATGCCTGG CTTATTATATCATCTC <u>T</u> ATTGTTGCTGTTCTTTTTTTCATTCATT TACTTGGGGTAAGTTGTGAAATTTTTGGTCTG	4188
	CAGACCAAAAATTTCACAACTTACCCCAAGTAAATGAATGAAA AAAAGAACAGCAACAAT <u>A</u> AGAGATGATATAATAAGCCAGGCAT GGATGACCTAGAAAAGAAAGCATTTCATATAATTA	4189
	ATCATCTC <u>T</u> ATTGTTGC	4190
	GCAACAAT <u>A</u> AGAGATGAT	4191
Alzheimer disease Leu173Trp TTG-TGG	TATTGAAATGCTTTCTTTTCTAGGTCATCCATGCCTGGCTTATT ATATCATCTCTATTGT <u>T</u> GCTGTTCTTTTTTTCATTCATTTACTTG GGGTAAGTTGTGAAATTTTTGGTCTGTCTTTC	4192
	GAAAGACAGACCAAAAATTTCACAACTTACCCCAAGTAAATGA ATGAAAAAAGAACAGC <u>A</u> ACAATAGAGATGATATAATAAGCCA GGCATGGATGACCTAGAAAAGAAAGCATTTCATA	4193
	TCTATTGT <u>T</u> GCTGTTCT	4194

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGAACAGC <u>A</u> ACAATAGA	4195
Alzheimer disease Gly209Arg gGGA-AGA	TATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGA	4196
	TCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAATCATTCCACCACACCAAAATTCCAGATCAGGAGTGCAACAGTAATGTAGTCCACAGCAACGTTATA	4197
	GTGTGGTGGGAATGATT	4198
	AATCATTCCACCACAC	4199
Alzheimer disease Gly209Val GGA-GTA	ATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGAT	4200
	ATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCAGTGAATGGAAATCATTCCACCACACCAAAATTCCAGATCAGGAGTGCAACAGTAATGTAGTCCACAGCAACGTTAT	4201
	TGTGGTGGGAATGATT	4202
	AAATCATTCCACCACA	4203
Alzheimer disease Ile213Thr ATT-ACT	TGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGATTAGTGCCCTCAT	4204
	ATGAGGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAATCATTCCACCACACCAAAATTCCAGATCAGGAGTGCAACAGTAATGTAGTCCA	4205
	GATTTCCATTCACTGGA	4206
	TCCAGTGAATGGAAATC	4207
Alzheimer disease Leu219Pro CTT-CCT	CACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATATGATTAGTGCCCTCATGGCCCTGGTGTATCAA	4208
	TTGATAAACACCAGGGCCATGAGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAATCATTCCACCACACCAAAATTCCAGATCAGGAGTG	4209
	AGGTCCACTTCGACTCC	4210
	GGAGTCGAAGTGGACCT	4211
Alzheimer disease Ala231Thr tGCC-ACC	ATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCAATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTATCAAGTACCTCCCTGAATGGACTGCGTGGCTCATCTTGG	4212
	CCAAGATGAGCCACGCAGTCCATTCCAGGGAGGTACTTGATAAACACCAGGGCCATGAGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAAT	4213
	TGATTAGTGCCCTCATG	4214
	CATGAGGGCACTAATCA	4215

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Ala231Val GCC-GTC	TTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCAT ATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTCATCAA GTACCTCCCTGAATGGACTGCGTGGCTCATCTTGGC	4216
	GCCAAGATGAGCCACGCAGTCCATTGAGGGAGGTACTTGATA AACACCAGGGCCATGAGGGCACTAATCATAATGAGATATGCC TGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAA	4217
	GATTAGTGCCCTCATGG	4218
	CCATGAGGGCACTAATC	4219
Alzheimer disease Met233Thr ATG-ACG	TTCAGTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCA TTATGATTAGTGCCCTCATGGCCCTGGTGTTCATCAAGTACCT CCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGAT	4220
	ATCACAGCCAAGATGAGCCACGCAGTCCATTGAGGGAGGTAC TTGATAAACACCAGGGCCATGAGGGCACTAATCATAATGAGA TATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAA	4221
	TGCCCTCATGGCCCTGG	4222
	CCAGGGCCATGAGGGCA	4223
Alzheimer disease Leu235Pro CTG-CCG	GGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGA TTAGTGCCCTCATGGCCCTGGTGTTCATCAAGTACCTCCCTG AATGGACTGCGTGGCTCATCTTGGCTGTGATTTTCAGT	4224
	ACTGAAATCACAGCCAAGATGAGCCACGCAGTCCATTGAGGG AGGTACTTGATAAACACCAGGGCCATGAGGGCACTAATCATA ATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCC	4225
	CATGGCCCTGGTGTTC	4226
	TAAACACCAGGGCCATG	4227
Alzheimer disease Ala246Glu GCG-GAG	TCATTATGATTAGTGCCCTCATGGCCCTGGTGTTCATCAAGTA CCTCCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGATTTTC AGTATATGGTAAAACCCAAGACTGATAATTTGTTTG	4228
	CAAACAAATTATCAGTCTTGGGTTTTACCATATACTGAAATCA CAGCCAAGATGAGCCACGCAGTCCATTGAGGGAGGTACTTGA TAAACACCAGGGCCATGAGGGCACTAATCATAATGA	4229
	ATGGACTGCGTGGCTCA	4230
	TGAGCCACGCAGTCCAT	4231
Alzheimer disease Leu250Ser TTG-TCG	GTGCCCTCATGGCCCTGGTGTTCATCAAGTACCTCCCTGAAT GGACTGCGTGGCTCATCTTGGCTGTGATTTTCAGTATATGGTA AAACCCAAGACTGATAATTTGTTTGTCACAGGAATGC	4232
	GCATTCCTGTGACAAACAAATTATCAGTCTTGGGTTTTACCAT ATACTGAAATCACAGCCAGATGAGCCACGCAGTCCATTGAG GGAGGTACTTGATAAACACCAGGGCCATGAGGGCAC	4233
	GCTCATCTTGGCTGTGA	4234
	TCACAGCCAGATGAGC	4235
Alzheimer disease Ala260Val GCT-GTT	AGTTTAGCCCATACATTTTATTAGATGTCTTTTATGTTTTCTTT TTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCG TATGCTGGTTGAAACAGCTCAGGAGAGAAATGA	4236

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGAC CTTTCGGACACAAAACA <u>G</u> CCACTAAATCTAGAAAAAGAAAAAC ATAAAAGACATCTAATAAAATGTATGGGCTAAACT	4237
	TTTAGTGGCTGTTTTGT	4238
	ACAAAACA <u>G</u> CCACTAAA	4239
Alzheimer disease Leu262Phe TTGt-TTC	CCCATACATTTTATTAGATGTCTTTTATGTTTTCTTTTTCTAGA TTTAGTGGCTGTTTT <u>G</u> TGTCCGAAAGGTCCACTTCGTATGCTG GTTGAAACAGCTCAGGAGAGAAATGAAACGCTT	4240
	AAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGA AGTGGACCTTTTCGGACACA <u>A</u> AAACAGCCACTAAATCTAGAAAA AGAAAAACATAAAAGACATCTAATAAAATGTATGGG	4241
	GCTGTTTT <u>G</u> TGTCCGAA	4242
	TTCGGACACA <u>A</u> AAACAGC	4243
Alzheimer disease Cys263Arg gTGT-CGT	CCATACATTTTATTAGATGTCTTTTATGTTTTCTTTTTCTAGAT TTAGTGGCTGTTTTG <u>I</u> GTCGAAAGGTCCACTTCGTATGCTG GTTGAAACAGCTCAGGAGAGAAATGAAACGCTTT	4244
	AAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACG AAGTGGACCTTTTCGGACA <u>A</u> AAACAGCCACTAAATCTAGAAA AAGAAAAACATAAAAGACATCTAATAAAATGTATGG	4245
	CTGTTTTG <u>T</u> GTCGAAA	4246
	TTTCGGACA <u>A</u> AAACAG	4247
Alzheimer disease Pro264Leu CCG-CTG	ACATTTTATTAGATGTCTTTTATGTTTTCTTTTTCTAGATTTAG TGGCTGTTTTGTGTCC <u>G</u> GAAAGGTCCACTTCGTATGCTGGTTG AAACAGCTCAGGAGAGAAATGAAACGCTTTTTTCC	4248
	GGAAAAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCA TACGAAGTGGACCTTTCC <u>G</u> GACACAAAACAGCCACTAAATCTA GAAAAAGAAAAACATAAAAGACATCTAATAAAATGT	4249
	TTTGTGTCC <u>G</u> GAAAGGTC	4250
	GACCTTTC <u>G</u> GACACAAA	4251
Alzheimer disease Arg269Gly tCGT-GGT	GTCTTTTATGTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTG TCCGAAAGGTCCACTTC <u>G</u> TATGCTGGTTGAAACAGCTCAGGA GAGAAATGAAACGCTTTTTCCAGCTCTCATTACT	4252
	AGTAAATGAGAGCTGGAAAAAGCGTTTCATTTCTCTCCTGAGC TGTTCACCAGCATAC <u>G</u> AAGTGGACCTTTTCGGACACAAAAC AGCCACTAAATCTAGAAAAAGAAAAACATAAAAGAC	4253
	GTCCACTTC <u>G</u> TATGCTG	4254
	CAGCATAC <u>G</u> AAGTGGAC	4255
Alzheimer disease Arg269His CGT-CAT	TCTTTTATGTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTGTC CGAAAGGTCCACTTC <u>G</u> TATGCTGGTTGAAACAGCTCAGGAGA GAAATGAAACGCTTTTTCCAGCTCTCATTACTC	4256
	GAGTAAATGAGAGCTGGAAAAAGCGTTTCATTTCTCTCCTGA GCTGTTTCAACCAGCATAC <u>G</u> AAGTGGACCTTTTCGGACACAAA ACAGCCACTAAATCTAGAAAAAGAAAAACATAAAAGA	4257

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCCA <u>CTTC</u> GATGCTGG	4258
	CCAGCATA <u>C</u> GAAAGTGGA	4259
Alzheimer disease Arg278Thr AGA-ACA	TAGTGGCTGTTTTGTGTCCGAAAGGTCCA <u>CTTC</u> GATGCTGG TTGAAACAGCTCAGGAGAG <u>G</u> AAATGAAACGCTTTTTCCAGCTCT CATTACTCCTGTAAGTATTTGAGAATGATATTGAA	4260
	TTCAATATCATTCTCAA <u>TA</u> CTTACAGGAGTAAATGAGAGCTG GAAAAAGCGTTTCATTT <u>C</u> TCTCCTGAGCTGTTTCAACCAGCAT ACGAAGTGGACCTTTCGGACACAAAACAGCCACTA	4261
	TCAGGAGAG <u>G</u> AAATGAAA	4262
	TTTCATTT <u>C</u> TCTCCTGA	4263
Alzheimer disease Glu280Ala GAA-GCA	CTGTTTTGTGTCCGAAAGGTCCA <u>CTTC</u> GATGCTGGTTGAAAC AGCTCAGGAGAGAAATG <u>A</u> AACGCTTTTTCCAGCTCTCATTAC TCCTGTAAGTATTTGAGAATGATATTGAATTAGTA	4264
	TACTAATTCAATATCATTCTCAA <u>TA</u> CTTACAGGAGTAAATGAG AGCTGGAAAAAGCGTTT <u>C</u> ATTTCTCTCCTGAGCTGTTTCAACC AGCATACGAAGTGGACCTTTCGGACACAAAACAG	4265
	GAGAAATG <u>A</u> AACGCTTT	4266
	AAAGCGTTT <u>C</u> ATTTCTC	4267
Alzheimer disease Glu280Gly GAA-GGA	CTGTTTTGTGTCCGAAAGGTCCA <u>CTTC</u> GATGCTGGTTGAAAC AGCTCAGGAGAGAAATG <u>A</u> AACGCTTTTTCCAGCTCTCATTAC TCCTGTAAGTATTTGAGAATGATATTGAATTAGTA	4268
	TACTAATTCAATATCATTCTCAA <u>TA</u> CTTACAGGAGTAAATGAG AGCTGGAAAAAGCGTTT <u>C</u> ATTTCTCTCCTGAGCTGTTTCAACC AGCATACGAAGTGGACCTTTCGGACACAAAACAG	4269
	GAGAAATG <u>A</u> AACGCTTT	4270
	AAAGCGTTT <u>C</u> ATTTCTC	4271
Alzheimer disease Leu282Arg CTT-CGT	TGTGTCCGAAAGGTCCA <u>CTTC</u> GATGCTGGTTGAAACAGCTC AGGAGAGAAATGAAACGCTTTTTCCAGCTCTCATTACTCCTG TAAGTATTTGAGAATGATATTGAATTAGTAATCAGT	4272
	ACTGATTACTAATTCAATATCATTCTCAA <u>TA</u> CTTACAGGAGTA AATGAGAGCTGGAAAA <u>A</u> GCGTTTCATTTCTCTCCTGAGCTGTT TCAACCAGCATACGAAGTGGACCTTTCGGACACA	4273
	TGAAACGCTTTTTCCAG	4274
	CTGGAAAA <u>A</u> GCGTTTCA	4275
Alzheimer disease Ala285Val GCT-GTT	AAGGTCCA <u>CTTC</u> GATGCTGGTTGAAACAGCTCAGGAGAGAA ATGAAACGCTTTTTCCAG <u>C</u> TCTCATTACTCCTGTAAGTATTTG AGAATGATATTGAATTAGTAATCAGTGTAGAATTT	4276
	AAATTCTACACTGATTACTAATTCAATATCATTCTCAA <u>TA</u> CTT ACAGGAGTAAATGAGAG <u>G</u> CTGGAAAAAGCGTTTCATTTCTCTC CTGAGCTGTTTCAACCAGCATACGAAGTGGACCTT	4277
	TTTTCCAG <u>C</u> TCTCATT	4278
	AAATGAGAG <u>G</u> CTGGAAAA	4279

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Leu286Val tCTC-GTC	GGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAAT GAAACGCTTTTTCCAGCTCTCATTACTCCTGTAAGTATTTGA GAATGATATTGAATTAGTAATCAGTGTAGAATTTAT	4280
	ATAAATTCTACACTGATTACTAATTCAATATCATTCTCAAATAC TTACAGGAGTAAATGAGAGCTGGAAAAAGCGTTTCATTTCTCT CCTGAGCTGTTTCAACCAGCATACGAAGTGGACC	4281
	TTCCAGCTCTCATTAC	4282
	GTAAATGAGAGCTGGAA	4283
Alzheimer disease Gly384Ala GGA-GCA	GTGACCAACTTTTTAATATTTGTAACCTTTCCTTTTAGGGGGA GTAAACTTGGATTGGGAGATTTTCTACAGTGTCTGG TTGGTAAAGCCTCAGCAACAGCCAGTGGAGACTG	4284
	CAGTCTCCACTGGCTGTTGCTGAGGCTTTACCAACCAGAACA CTGTAGAAAATGAAATCTCCCAATCCAAGTTTTACTCCCCCTA AAAAGGAAAGGTTACAAATATTAAGGTTGGTCAC	4285
	TGGATTGGGAGATTTCA	4286
	TGAAATCTCCCAATCCA	4287
Alzheimer disease Ser390Ile AGT-ATT	TTTGTAACCTTTCCTTTTAGGGGGAGTAAACTTGGATTGGG AGATTTTCTATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCA ACAGCCAGTGGAGACTGGAACACAACCATAGCCTG	4288
	CAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTGCTGAG GCTTTACCAACCAGAACACTGTAGAAAATGAAATCTCCCAATC CAAGTTTTACTCCCCCTAAAAAGGAAAGTTACAAA	4289
	TTTCTACAGTGTCTGG	4290
	CCAGAACACTGTAGAAA	4291
Alzheimer disease Leu392Val tCTG-GTG	AACCTTTCCTTTTAGGGGGAGTAAACTTGGATTGGGAGATT TCATTTTCTACAGTGTCTGTTGGTAAAGCCTCAGCAACAGC CAGTGGAGACTGGAACACAACCATAGCCTGTTTCG	4292
	CGAAACAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTG CTGAGGCTTTACCAACCAGAACACTGTAGAAAATGAAATCTCC CAATCCAAGTTTTACTCCCCCTAAAAAGGAAAGGTT	4293
	ACAGTGTCTGTTGGT	4294
	ACCAACCAGAACACTGT	4295
Alzheimer disease Asn405Ser AAC-AGC	ATTCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAAC AGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGC CATATTAATTGTAAGTATACATAATAAGAATGTGT	4296
	ACACATTCTTATTAGTGTATACTTACAATTAATATGGCTACGAA ACAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTGCTGA GGCTTTACCAACCAGAACACTGTAGAAAATGAAAT	4297
	AGACTGGAACACAACCA	4298
	TGGTTGTGTTCCAGTCT	4299

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Ala409Thr aGCC-ACC	TACAGTGGTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGA GACTGGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTG TAAGTATACTAATAAGAATGTGTCAGAGCTCTTA	4300
	TAAGAGCTCTGACACATTCTTATTAGTGTATACTTACAATTAAT ATGGCTACGAAACAGGCATATGGTTGTGTTCCAGTCTCCACTG GCTGTTGCTGAGGCTTTACCAACCAGAACACTGTA	4301
	CAACCATAGCCTGTTTC	4302
	GAAACAGGCATATGGTTG	4303
Alzheimer disease Cys410Tyr TGT-TAT	GTGTTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGAGACT GGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTGTAAG TATACACTAATAAGAATGTGTCAGAGCTCTTAATGT	4304
	ACATTAAGAGCTCTGACACATTCTTATTAGTGTATACTTACAAT TAATATGGCTACGAAACAGGCTATGGTTGTGTTCCAGTCTCCA CTGGCTGTTGCTGAGGCTTTACCAACCAGAACAC	4305
	CATAGCCTGTTTCGTAG	4306
	CTACGAAACAGGCTATG	4307
Alzheimer disease Ala426Pro tGCC-CCC	TGTGAATGTGTGTCTTTCCCATCTTCTCCACAGGGTTTGTGCC TTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGC TCTTCCAATCTCCATCACCTTTGGGCTTGTCT	4308
	AGAAAACAAGCCCAAAGGTGATGGAGATTGGAAGAGCTGGC AATGCTTTCTTGAAAATGGCAAGGAGTAATAATGTAAGGCACA AACCCTGTGGAGAAGATGGGAAAGACACACATTCACA	4309
	TACTCCTTGCCATTTTC	4310
	GAAAATGGCAAGGAGTA	4311
Alzheimer disease Pro436Gln CCA-CAA	AGGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAA AGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTCTACTTTGCCACAGATTATCTTGTACAGCCTTT	4312
	AAAGGCTGTACAAGATAATCTGTGGCAAAGTAGAAAACAAGC CCAAAGGTGATGGAGATTGGAAGAGCTGGCAATGCTTTCTTG AAAATGGCAAGGAGTAATAATGTAAGGCACAAACCCT	4313
	AGCTCTTCCAATCTCCA	4314
	TGGAGATTGGAAGAGCT	4315
Alzheimer disease Pro436Ser tCCA-TCA	CAGGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGA AAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTACAGCCTT	4316
	AAGGCTGTACAAGATAATCTGTGGCAAAGTAGAAAACAAGCC CAAAGGTGATGGAGATTGGAAGAGCTGGCAATGCTTTCTTG AAATGGCAAGGAGTAATAATGTAAGGCACAAACCCTG	4317
	CAGCTCTTCCAATCTCC	4318
	GGAGATTGGAAGAGCTG	4319

EXAMPLE 26

Alzheimer's Disease - presenilin-2 (PSEN2)

[0241] The attached table discloses the correcting oligonucleotide base sequences for the PSEN2 oligonucleotides of the invention.

Table 28

5

PSEN2 Mutations And Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Arg62His CGC-CAC	GATGTGGTTTCCCACAGAGAAGCCAGGAGAACGAGGAGGAC GGTGAGGAGGACCCTGACC <u>G</u> CTATGTCTGTAGTGGGGTTCC CGGGCGGCCGCCAGGCCTGGAGGAAGAGCTGACCCTCAA	4320
	TTGAGGGTCAGCTCTTCTCCAGGCCTGGCGGCCGCCCGGG AACCCCACTACAGACATAGC <u>G</u> GTTCAGGGTCCTCCTACCGTC CTCCTCGTTCTCCTGGCTTCTCTGTGGGAAACACATC	4321
	CCCTGACC <u>G</u> CTATGTCT	4322
	AGACATAGC <u>G</u> GTTCAGGG	4323
Alzheimer disease Thr122Pro cACG-CCG	GCCTCGAGGAGCAGTCAGGGCCGGGAGCATCAGCCCTTTGC CTTCTCCCTCAGCATCTAC <u>A</u> CGACATTCACTGAGGACACACC CTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACA	4324
	TGTTCAACACGGAGTTGAGGAGGCGCTGGCCCACCGAGGGT GTGTCTCAGTGAATGTCTG <u>T</u> GTAGATGCTGAGGGAGAAGGCA AAGGGCTGATGCTCCCGGCCCTGACTGCTCCTCGAGGC	4325
	GCATCTAC <u>A</u> CGACATT	4326
	GAATGTCTG <u>T</u> GTAGATGC	4327
Alzheimer disease Asn141Ile AAC-ATC	ACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGCGC CTCCTCAACTCCGTGCTGA <u>A</u> CACCCTCATCATGATCAGCGTC ATCGTGGTTATGACCATCTTCTTGGTGGTGTCTCTACAA	4328
	TTGTAGAGCACCACCAAGAAGATGGTCATAACCACGATGACG CTGATCATGATGAGGGTGT <u>T</u> CAGCACGGAGTTGAGGAGGCG CTGGCCCACCGAGGGTGTGTCCTCAGTGAATGGCGTGT	4329
	CGTGCTGA <u>A</u> CACCCTCA	4330
	TGAGGGTGT <u>T</u> CAGCACG	4331
Alzheimer disease Met239Ile ATGg-ATA	CCACTGGAAGGGCCCTCTGGTGTGTCAGCAGGCCTACCTCAT CATGATCAGTGCCTCAT <u>G</u> CCCTAGTGTTTCATCAAGTACCTC CCAGAGTGGTCCGCGTGGGTCATCCTGGGCGCCATC	4332
	GATGGCGCCCAGGATGACCCACGCGGACCACTCTGGGAGGT ACTTGATGAACACTAGGGC <u>C</u> ATGAGCGCACTGATCATGATGA GGTAGGCCTGCTGCAGCACCAAGAGGGCCCTTCCAGTGG	4333
	GCGCTCAT <u>G</u> CCCTAGT	4334
	ACTAGGGC <u>C</u> ATGAGCGC	4335

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Met239Val cATG-GTG	ATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTC ATCATGATCAGTGCCTC <u>A</u> TGGCCCTAGTGTTCAAGTAC CTCCAGAGTGGTCCGCGTGGGTCATCCTGGGCGCCA	4336
	TGGCGCCCAGGATGACCCACGCGGACCACTCTGGGAGGTAC TTGATGAACACTAGGGCCA <u>T</u> GAGCGCACTGATCATGATGAGG TAGGCCTGCTGCAGCACCAGAGGGCCCTTCCAGTGGAT	4337
	GTGCGCTC <u>A</u> TGGCCCTA	4338
	TAGGGCCAT <u>G</u> AGCGCAC	4339

Example 26
Engineering herbicide resistant plants

[242] Chemical weed control is an important tool of modern agriculture and many herbicides have been developed for this purpose. Their use has resulted in substantial increases in the yields of many crops, including, for example, maize, soybeans, and cotton. Thus while the use of fertilizers and new high-yielding crop varieties have contributed greatly to the "green revolution," chemical weed control has also been at the forefront of technological achievement.

[243] Herbicides having broad-spectrum activity are particularly useful because they obviate the need for multiple herbicides targeting different classes of weeds. The problem with such herbicides is that they typically also affect crops which are exposed to the herbicide. One way to overcome this is to generate plants which are resistant to one or more broad-spectrum herbicides. Such herbicide-tolerant plants may reduce the need for tillage to control weeds, thereby effectively reducing soil erosion and can reduce the quantity and number of different herbicides applied in the field.

[244] Common herbicides used, for example, include those that inhibit the enzyme 5-enolpyruvyl-3-phosphoshikimic acid synthase (EPSPS), for example N-phosphonomethyl-glycine (e.g. glyphosate), those that inhibit acetolactate synthase (ALS) activity, for example the sulfonylureas and related herbicides, and those that inhibit dihydropteroate synthase, for example methyl[(4-amino-phenyl)sulfonyl]carbamate (e.g. Asulam). Herbicide-tolerant plants can be produced by several methods, including, for example, introducing into the genome of the plant the ability to degrade the herbicide, the capacity to produce a higher level of the targeted enzyme, and/or expressing an herbicide-tolerant allele of the enzyme.

[245] The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes that confer herbicide resistance.

Table 28
Genome-Altering Oligos Conferring Glyphosate Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Glyphosate Resistance EPSPS <i>Arabidopsis thaliana</i> Gly97Ala GGC-GCC	AAGCGTCGGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTC TTATTAAGCTTCCTG <u>C</u> CTCCAAGTCTCTATCAAATCGGATCCTGC TTCTCGCTGCTCTGTCTGAGGTATATATCAC	4341
	GTGATATATACCTCAGACAGAGCAGCGAGAAGCAGGATCCGATT TGATAGAGACTTGGAG <u>G</u> CAGGAAGCTTAATAAGACCGGAGATTT CTCTAATGGGTTGAAGTACAATCTCCGACGCTT	4342
	GCTTCCTG <u>C</u> CTCCAAGT	4343
	ACTTGGAG <u>G</u> CAGGAAGC	4344
Glyphosate Resistance EPSPS <i>Brassica napus</i> Gly93Ala GGA-GCA	AAGCTTCAGAGATTGTGCTTCAACCAATCAGAGAAATCTCGGGTC TCATTAAGCTACCCG <u>C</u> ATCCAAATCTCTCTCCAATCGGATCCTCC TTCTTGCCGCTCTATCTGAGGTACATATACT	4345
	AGTATATGTACCTCAGATAGAGCGGCAAGAAGGAGGATCCGATT GGAGAGAGATTTGGAT <u>G</u> CGGGTAGCTTAATGAGACCCGAGATTT CTCTGATTGGTTGAAGCACAATCTCTGAAGCTT	4346
	GCTACCCG <u>C</u> ATCCAAAT	4347
	ATTTGGAT <u>G</u> CGGGTAGC	4348
Glyphosate Resistance EPSPS 1 <i>Nicotiana tabacum</i> Gly95Ala GGT-GCT	AGCCCAACGAGATTGTGCTGCAACCCATCAAAGATATATCAGGC ACTGTTAAATTGCCTG <u>C</u> TTCTAAATCCCTTTCCAATCGTATTCTCC TTCTTGCTGCCCTTTCTAAGGGAAGGACTGT	4349
	ACAGTCCTTCCCTTAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTTAGAA <u>G</u> CAGGCAATTTAACAGTGCCTGATATATC TTTGATGGGTTGCAGCACAATCTCGTTGGGCT	4350
	ATTGCCTG <u>C</u> TTCTAAAT	4351
	ATTTAGAA <u>G</u> CAGGCAAT	4352
Glyphosate Resistance EPSPS 2 <i>Nicotiana tabacum</i> Gly62Ala GGA-GCA	ATTGTTTCCTTGGTACGAAATGTCCTCCTGTTCAATTGTCAGCA AGGGAGGCCTTCCCG <u>C</u> AGGGAAGGTAAAGCTCTCTGGATCAATT AGCAGCCAGTACTTGACTGCTCTGCTTATGGC	4353
	GCCATAAGCAGAGCAGTCAAGTACTGGCTGCTAATTGATCCAGA GAGCTTTACCTTCCCT <u>G</u> CGGGAAGGCCTCCCTTGCTGACAATTC GAACAGGAGGACATTTTCGTACCAAGGAAACAAT	4354
	CCTTCCCG <u>C</u> AGGGAAGG	4355
	CCTTCCCT <u>G</u> CGGGAAGG	4356
Glyphosate Resistance EPSPS <i>Zea mays</i> Gly168Ala GGT-GCT	ATTGTTTCCTTGGCACTGACTGCCACCTGTTTCGTGTCAATGGAA TCGGAGGGCTACCTG <u>C</u> TGGCAAGGTCAAGCTGTCTGGCTCCATC AGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	4357
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAGCCAGA CAGCTTGACCTTGCCAG <u>G</u> CAGGTAGCCCTCCGATTCCATTGACAC GAACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	4358

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCTACCTG <u>C</u> TGGCAAGG	4359
	CCTTGCCAG <u>C</u> CAGGTAGC	4360
Glyphosate Resistance EPSPS <i>Oryza sativa</i> Gly115Ala GGT-GCT	ACTGTTTCCTTGGCACTGAATGCCCACCTGTTTCGTGTCAAGGGA ATTGGAGGACTTCCTG <u>C</u> TGGCAAGGTTAAGCTCTCTGGTTCCAT CAGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	4361
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAACCAGA GAGCTTAACCTTGCCAGCAGGAAGTCCTCCAATTCCTTGACAC GAACAGGTGGGCATTCAGTGCCAAGGAAACAGT	4362
	ACTTCCTG <u>C</u> TGGCAAGG	4363
	CCTTGCCAG <u>C</u> CAGGAAGT	4364
Glyphosate Resistance EPSPS <i>Petunia x hybrida</i> Gly93Ala GGC-GCC	AGCCTTCTGAGATAGTGTTGCAACCCATTAAAGAGATTTCAAGGCA CTGTTAAATTGCCTG <u>C</u> CTCTAAATCATTATCTAATAGAATTCTCCT TCTTGCTGCCTTATCTGAAGGAACAACGTGT	4365
	ACAGTTGTTTCCTTCAGATAAGGCAGCAAGAAGGAGAATTCTATTA GATAATGATTTAGAG <u>G</u> CAGGCAATTTAACAGTGCCTGAAATCTCT TTAATGGGTGCAACACTATCTCAGAAGGCT	4366
	ATTGCCTG <u>C</u> CTCTAAAT	4367
	ATTTAGAG <u>G</u> CAGGCAAT	4368
Glyphosate Resistance EPSPS <i>Lycopersicon esculentum</i> Gly97Ala GGT-GCT	AACCCCATGAGATTGTGCTAGNACCCATCAAAGATATATCTGGTA CTGTTAAATTACCCG <u>C</u> TTCGAAATCCCTTTCCAATCGTATTCTCCT TCTTGCTGCCCTTTCTGAGGGAAGGACTGT	4369
	ACAGTCCTTCCCTCAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTTTGAAG <u>C</u> GGGTAATTTAACAGTACCAGATATATC TTTGATGGGTNCTAGCACAATCTCATGGGGTT	4370
	ATTACCCG <u>C</u> TTCGAAAT	4371
	ATTTCGAAG <u>C</u> GGGTAAT	4372
Glyphosate Resistance EPSPS <i>Lolium rigidum</i> Gly107Ala GGT-GCT	ATTGTTTCCTTGGCACTGACTGCCCACCTGTTTCGKATCAACGGCA TTGGAGGGCTACCTG <u>C</u> TGGCAAGGTTAAGCTGTCTGGTTCCATC AGCAGCCAATACTTGAGTTCCTTGCTGATGGC	4373
	GCCATCAGCAAGGAACTCAAGTATTGGCTGCTGATGGAACCAGA CAGCTTAACCTTGCCAG <u>C</u> CAGGTAGCCCTCCAATGCCGTTGATCG AACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	4374
	GCTACCTG <u>C</u> TGGCAAGG	4375
	CCTTGCCAG <u>C</u> CAGGTAGC	4376

Table 29
Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Ser CCT-TCT	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCCTCTTGTAGCA ATCACAGGACAAGTCTCTCGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4377
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGAGAGACTTGTCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	4378
	GACAAGTCTCTCGTCGT	4379
	ACGACGAGAGACTTGTC	4380
Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Gln CCT-CAG	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCCTCTTGTAGCA ATCACAGGACAAGTCCAGCGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4381
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGCTGGACTTGTCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	4382
	ACAAGTCCAGCGTCGTC	4383
	TACGACGCTGGACTTGT	4384
Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Gln CCT-CAA	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCCTCTTGTAGCA ATCACAGGACAAGTCCAAACGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4385
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGTTGGACTTGTCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	4386
	ACAAGTCCAAACGTCGTA	4387
	TACGACGTTGGACTTGT	4388
Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAC	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGAACGGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4389
	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACCGTTTCGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	4390
	GATCCCGAACGGTGGCA	4391
	TGCCACCGTTTCGGGATC	4392

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAT	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGAATGGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4393
	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACCATTCTGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	4394
	GATCCCGAATGGTGGCA	4395
	TGCCACCATTCTGGGATC	4396
Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGGCCAGGTCTCCCGCCGCATGATCGGCACCGACGCCT TCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	4397
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGGAGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	4398
	GCCAGGTCTCCCGCCGC	4399
	GCGGCGGGAGACCTGGC	4400
Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAA	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGGCCAGGTCCAAAGCGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4401
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4402
	CCAGGTCCAAAGCGCCGA	4403
	TGCGGCGTTGGACCTGG	4404
Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAG	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGGCCAGGTCCAGCGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4405
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGCTGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4406
	CCAGGTCCAGCGCCGA	4407
	TGCGGCGCTGGACCTGG	4408
Imidazolinone Resistance ALS <i>Oryza sativa</i> Ile627Asn ATT-AAT	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCCTATGATCCCAAATGGGGGGCGCATTC AAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4409
	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCATTTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC	4410
	GATCCCAAATGGGGGCG	4411

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCCCCCA <u>T</u> TTGGGATC	4412
Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG	TCCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGC CATCACGGGACAGGTG <u>T</u> CGCGACGCATGATTGGCACCGACGCCT TCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4413
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGGT GCCAATCATGCGTCGCG <u>A</u> CACCTGTCCCGTGATGGCGACCATGG GGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	4414
	GACAGGTG <u>T</u> CGCGACGC	4415
	GCGTCGCG <u>A</u> CACCTGTC	4416
Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG	CCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGCC ATCACGGGACAGGTG <u>C</u> AGCGACGCATGATTGGCACCGACGCCTT CCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4417
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGG TGCCAATCATGCGTCGCT <u>G</u> CACCTGTCCCGTGATGGCGACCATG GGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGG	4418
	ACAGGTG <u>C</u> AGCGACGCA	4419
	TGCGTCGCT <u>G</u> CACCTGT	4420
Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAT	GGCCGTACCTCTTGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTA <u>A</u> TGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4421
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT TGAAAGCCCCACC <u>A</u> TAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4422
	GATCCCTA <u>A</u> TGGTGGGG	4423
	CCCCACC <u>A</u> TAGGGATC	4424
Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAC	GGCCGTACCTCTTGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTA <u>A</u> CGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4425
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT TGAAAGCCCCACC <u>G</u> TAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4426
	GATCCCTA <u>A</u> CGGTGGGG	4427
	CCCCACC <u>G</u> TAGGGATC	4428
Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Ser CCG-TCG	TCCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGC CATCACGGGGCAGGTG <u>T</u> CGCGCCGCATGATCGGCACGGACGCCT TCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4429
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGTG CCGATCATGCGGCGCG <u>A</u> GACCTGCCCCGTGATGGCCACCATGG GGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGGA	4430

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGCAGGTC <u>T</u> CGCGCCGC	4431
	GCGGCGCG <u>A</u> GACCTGCC	4432
Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Gln CCG-CAG	CCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTGGCC ATCACGGGGCAGGTCC <u>A</u> GCGCCGCATGATCGGCACGGACGCCTT CCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4433
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGT GCCGATCATGCGGCGC <u>T</u> GGACCTGCCCGTGATGGCCACCATGG GGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGG	4434
	GCAGGTCC <u>A</u> GCGCCGCA	4435
	TGCGGCGC <u>T</u> GGACCTGC	4436
Imidazolinone Resistance ALS <i>Lolium multiflorum</i> Ser623Asn AGC-AAC	CTGGGCCATACTTGTTGGATATCATCGTCCCTCACCAGGAGCATG TGCTGCCTATGATCCCTA <u>A</u> CGGTGGTGCTTTCAAGGACATTATCA TGGAAGGTGATGGCAGGATTTCTGATTAAAC	4437
	GTTTAATACGAAATCCTGCCATCACCTTCCATGATAATGTCCTTGA AAGCACCACCG <u>T</u> TAGGGATCATAGGCAGCACATGCTCCTGGTGA GGGACGATGATATCCAACAAGTATGGCCAG	4438
	GATCCCTA <u>A</u> CGGTGGTG	4439
	CACCACCG <u>T</u> TAGGGATC	4440
Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Ser CCA-TCA	TCCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGC CATCACGGGGCAGGTCT <u>C</u> CACGCCGCATGATCGGCACGGACGCGT TCCAGGAGACGCCCATAGTGAGGTCACGCGCT	4441
	AGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGTG CCGATCATGCGGCGTG <u>A</u> GACCTGGCCCGTGATGGCGACCATGG GGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGGA	4442
	GCCAGGTC <u>T</u> CACGCCGC	4443
	GCGGCGTG <u>A</u> GACCTGGC	4444
Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Gln CCA-CAA	CCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGCC ATCACGGGGCAGGTCC <u>A</u> ACGCCGCATGATCGGCACGGACGCGTT CCAGGAGACGCCCATAGTGAGGTCACGCGCTC	4445
	GAGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGT GCCGATCATGCGGCGT <u>T</u> GGACCTGGCCCGTGATGGCGACCATGG GGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGG	4446
	CCAGGTCC <u>A</u> ACGCCGCA	4447
	TGCGGCGT <u>T</u> GGACCTGG	4448

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Imidazolinone Resistance ALS <i>Hordeum vulgare</i> Ser524Asn AGC-AAC	CCCAGGGCCGTACCTGCTGGATATCATTGTCCC GCATCAGGAGC ACGTGCTGCCTATGATCCCAA A CGGTGGTGCTTTCAAGGACATGA TCATGGAGGGTGATGGCAGGACCTCGTACTGA	4449
	TCAGTACGAGGTCCTGCCATCACCTCCATGATCATGTCCTTGAA AGCACCACCG I TTGGGATCATAGGCAGCACGTGCTCCTGATGCG GGACAATGATATCCAGCAGGTACGGCCCTGGG	4450
	GATCCCAA A CGGTGGTG	4451
	CACCACCG I TTGGGATC	4452
Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTCT C TCGTCGGATGATCGGTACCGATGCTTTC CAGGAACTCCAATTGTTGAGGTAACAAGGT	4453
	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC CGATCATCCGACGAG A AGACTTGACCAGTGATCGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT	4454
	GTCAAGTCT C TCGTCGG	4455
	CCGACGAG A AGACTTGAC	4456
Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCC A ACGTCGGATGATCGGTACCGATGCTTTC AGGAACTCCAATTGTTGAGGTAACAAGGTC	4457
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACG T TTGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4458
	TCAAGTCC A ACGTCGGA	4459
	TCCGACG T TTGGACTTGA	4460
Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCC A ACGTCGGATGATCGGTACCGATGCTTTC AGGAACTCCAATTGTTGAGGTAACAAGGTC	4461
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACG C TGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4462
	TCAAGTCC A ACGTCGGA	4463
	TCCGACG C TGGACTTGA	4464
Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT	GACCTTACTTGTTGGATGTGATTGTCCACATCAAGAACATGTCCT GCCTATGATCCCCA A TGGAGGCGCTTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	4465
	TGAGGTCAATATTGTGTTCTTCCATCACCTCTGTGATCACATCTT TGAAAGCGCCTCCAT T TGGGGATCATAGGCAGGACATGTTCTTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	4466

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GATCCCCA <u>A</u> TGGAGGCG	4467
	CGCCTCCA <u>T</u> TGGGGATC	4468
Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTT <u>I</u> CCCGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACGAT	4469
	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC AATCATACGCCGGG <u>A</u> AACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4470
	GGCAAGTT <u>I</u> CCCGGCGT	4471
	ACGCCGGG <u>A</u> AACTTGCC	4472
Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCA <u>A</u> ACGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACGATC	4473
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>T</u> TGAAGTTGCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAG	4474
	GCAAGTTC <u>A</u> ACGGCGTA	4475
	TACGCCG <u>T</u> TGAAGTTGC	4476
Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCA <u>A</u> CGGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACGATC	4477
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>C</u> TGAAGTTGCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4478
	GCAAGTTC <u>A</u> CGGGCGTA	4479
	TACGCCG <u>C</u> TGAAGTTGC	4480
Imidazolinone Resistance ALS <i>Amaranthus retroflexus</i> Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC TGCCTATGATCCCTA <u>A</u> CGGTGCCGCTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4481
	ACCAACTAATAAGCCCTTCTTCCATCACCCCTCTGTTATGGTGTCT TGAAGGCGGCACCG <u>T</u> TAGGGATCATAGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATACGGTC	4482
	GATCCCTA <u>A</u> CGGTGCCG	4483
	CGGCACCG <u>T</u> TAGGGATC	4484

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Ser CCA-TCA	AGCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGC TATAACAGGTCAAGTGTCACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAAGTAGAT	4485
	ATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTACC TATCATCCTACGTGACACTTGACCTGTTATAGCAACAATGGGGAC GCTATCCAGTAGCGCGTCAGCGAGGCCGCT	4486
	GTCAAGTGTCACGTAGG	4487
	CCTACGTGACACTTGAC	4488
Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Gln CCA-CAA	GCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGCT ATAACAGGTCAAGTGCAACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAAGTAGATC	4489
	GATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTAC CTATCATCCTACGTGCACTTGACCTGTTATAGCAACAATGGGGA CGCTATCCAGTAGCGCGTCAGCGAGGCCGC	4490
	TCAAGTGCAACGTAGGA	4491
	TCCTACGTGCACTTGGA	4492
Imidazolinone Resistance ALS 1 <i>Nicotiana tabacum</i> Ser650Asn AGT-AAT	GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTTT ACCTATGATTCCCAATGGCGGAGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAAGTTCTATTGAGTTTG	4493
	CAAACCTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCTCCGCCATTGGGAATCATAGGTAAAACATGTTCTCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4494
	GATTCCCAATGGCGGAG	4495
	CTCCGCCATTGGGAATC	4496
Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Ser CCA-TCA	AGTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGC TATAACCGGTCAAGTGTCACGTAGGATGATCGGTACTGATGCTTT TCAGGAAACTCCGATTGTTGAGGTAAGTAGAT	4497
	ATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTACC GATCATCCTACGTGACACTTGACCGGTTATAGCAACAATGGGGAC GCTATCCAGTAGGGCGTCCGCGAGGCCACT	4498
	GTCAAGTGTCACGTAGG	4499
	CCTACGTGACACTTGAC	4500
Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Gln CCA-CAA	GTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGCT ATAACCGGTCAAGTGCAACGTAGGATGATCGGTACTGATGCTTTT CAGGAAACTCCGATTGTTGAGGTAAGTAGATC	4501
	GATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTAC CGATCATCCTACGTGCACTTGACCGGTTATAGCAACAATGGGGA CGCTATCCAGTAGGGCGTCCGCGAGGCCAC	4502
	TCAAGTGCAACGTAGGA	4503

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCTACGT <u>I</u> GCACTTGA	4504
Imidazolinone Resistance ALS 2 <i>Nicotiana tabacum</i> Ser647Asn AGT-AAT	GGCCATACTTGTGGATGTGATTGTACCTCATCAGGAACATGTTCT ACCTATGATTCCCA <u>A</u> TGGCGGGGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAGTTCTATTGACTTTG	4505
	CAAAGTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCCCCGCCA <u>T</u> TGGGAATCATAGGTAGAACATGTTCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4506
	GATCCCA <u>A</u> TGGCGGGG	4507
	CCCCGCCA <u>T</u> TGGGAATC	4508
Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Ser CCC-TCC	AGTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTA TTACTGGTCAAGTT <u>I</u> CCAGGAGAATGATTGGAACAGATGCGTTTC AAGAAACCCCTATTGTTGAGGTAACACGTT	4509
	AACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCC AATCATTCTCCTGG <u>A</u> AACTTGACCAGTAATAGCAACCATTGGAACA CTGTCTAATAAAGCATCAGCAAGACCACT	4510
	GTCAAGTT <u>I</u> CCAGGAGA	4511
	TCTCCTGG <u>A</u> AACTTGAC	4512
Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAA	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT TACTGGTCAAGTT <u>C</u> AAAGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTTT	4513
	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTT CAATCATTCTCCT <u>T</u> TGAACCTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC	4514
	TCAAGTT <u>C</u> AAAGGAGAA	4515
	TTCTCCT <u>T</u> TGAACCTTGA	4516
Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAG	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT TACTGGTCAAGTT <u>C</u> AGAGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTTT	4517
	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTT CAATCATTCTCCT <u>C</u> TGAACCTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC	4518
	TCAAGTT <u>C</u> AGAGGAGAA	4519
	TTCTCCT <u>C</u> TGAACCTTGA	4520
Imidazolinone Resistance ALS <i>Xanthium</i> spp. Ala631Asn GCT-AAT	GGGCCTTACTTGTGGATGTGATCGTGCCCCATCAAGAACATGTG TTGCCCATGATCCCG <u>A</u> ATGGTGGAGGTTTCATGGATGTGATCACC GAAGGCGACGGCAGAATGAAATATTGAGCTT	4521
	AAGCTCAATATTTCTTCTGCCGTCGCCTTCGGTGATCACATCCAT GAAACCTCCACCA <u>T</u> TCGGGATCATGGGCAACACATGTTCTTGATG GGGCACGATCACATCCAACAAGTAAGGCC	4522

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATCCCGAATGGTGA	4523
	TCCACCATTCGGGATCA	4524
Sulfonylurea Resistance ALS <i>Bassia scoparia</i> Pro189Ser CCG-TCG	TCCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCG ATCACGGGGCAGGTGTCGCGGCGAATGATTGGGACGGATGCTTT TCAGGAGACTCCTATTGTTGAGGTAACACGGT	4525
	ACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTCC CAATCATTCGCCGCGACACCTGCCCCGTGATCGCCACCAGTGA ACGGAATCGAGCAAAGCATCAGCAAACCCGGA	4526
	GGCAGGTGTCGCGGCGA	4527
	TCGCCGCGACACCTGCC	4528
Sulfonylurea Resistance ALS <i>Bassia scoparia</i> Pro189Gln CCG-CAG	CCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCGA TCACGGGGCAGGTGCAAGCGGCGAATGATTGGGACGGATGCTTTT CAGGAGACTCCTATTGTTGAGGTAACACGGTC	4529
	GACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTC CCAATCATTCGCCGCTGCACCTGCCCCGTGATCGCCACCAGTGG AACGGAATCGAGCAAAGCATCAGCAAACCCGG	4530
	GCAGGTGCAGCGGCGAA	4531
	TTCGCCGCTGCACCTGC	4532
Imidazolinone Resistance ALS <i>Bassia scoparia</i> Ser649Asn AGT-AAT	GACCTTACCTGCTTGATGTGATTGTACCTCATCAGGAGCATGTGC TGCCTATGATTCCTAATGGTGCAGCCTTCAAGGATATCATTAAACGA AGGTGATGGAAGAACAAGTTATTGATGTTT	4533
	GAACATCAATAACTTGTCTTCCATCACCTTCGTTAATGATATCCTT GAAGGCTGCACCATTAGGAATCATAGGCAGCACATGCTCCTGATG AGGTACAATCACATCAAGCAGGTAAGGTC	4534
	GATTCCTAATGGTGCAG	4535
	CTGCACCATTAGGAATC	4536
Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Ser CCT-TCT	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCTCTTGTGCGC ATTACAGGACAGGTCTCTCGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGT	4537
	ACCTCGTTACCTCAACGATTGGTGTCTCTTGAAGGCGTCAGTAC CGATCATCCGGCGAGAGACCTGTCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	4538
	GACAGGTCTCTCGCCGG	4539
	CCGGCGAGAGACCTGTC	4540

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAA	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCCTCTTGTCGCCA TTACAGGACAGGTCC A ACGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGTC	4541
	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTA CCGATCATCCGGCG T TGGACCTGTCCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCCGC	4542
	ACAGGTCC A ACGCCGGA	4543
	TCCGGCG T TGGACCTGT	4544
Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAG	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCCTCTTGTCGCCA TTACAGGACAGGTCC A GCGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGTC	4545
	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTA CCGATCATCCGGCG C TGGACCTGTCCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCCGC	4546
	ACAGGTCC A GCGCCGGA	4547
	TCCGGCG C TGGACCTGT	4548
Imidazolinone Resistance ALS 1 <i>Brassica napus</i> Ser638Asn AGT-AAT	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA A TGGTGGCACTTTCAAAGATGTAATAACAG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	4549
	ATCTCTCAGTACTTAGTGCGACCATCCCTTCTGTTATTACATCTTT GAAAGTGCCACCA T TTGGGATCATCGGTAACACATGTTCTTGGTG CGGACATATCACATCCAACAGGTATGGTC	4550
	GATCCCAA A TGGTGGCA	4551
	TGCCACCA T TTGGGATC	4552
Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Ser CCC-TCC	CAGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCCTCTTGTCGC CATTACAGGACAGGT T CCTCGCCGGATGATCGGTACTGACGCCTT CCAAGAGACACCAATCGTTGAGGTAACGAGG	4553
	CCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACC GATCATCCGGCGAGG A ACCTGTCCTGTAATGGCGACAAGAGGAA CACTGTCAAGCATCGCGTCTGCTAACCCGCTG	4554
	GGACAGGT T CCTCGCCG	4555
	CGGCGAGG A ACCTGTCC	4556
Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Gln CCC-CAG	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCCTCTTGTCGCC ATTACAGGACAGGT C ACTCGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGT	4557
	ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTAC CGATCATCCGGCGAG T GACCTGTCCTGTAATGGCGACAAGAGGA AACTGTCAAGCATCGCGTCTGCTAACCCGCT	4558
	GACAGGT C ACTCGCCGG	4559

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGGCGAG <u>I</u> GACCTGTC	4560
Imidazolinone Resistance ALS 2 <i>Brassica napus</i> Ser582Asn AGT-AAT	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA <u>A</u> TGGTGGCACTTTCAAAGATGTAATAACAG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	4561
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCTGTTATTACATCTTT GAAAGTGCCACCA <u>T</u> TTGGGATCATCGGTAACACATGTTCTTGGTG CGGACATATCACATCCAACAGGTATGGTC	4562
	GATCCCAA <u>A</u> TGGTGGCA	4563
	TGCCACCA <u>T</u> TTGGGATC	4564
Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Ser CCT-TCT	AGCGGGTTAGCCGACGCGATGCTTGACAGTGTTCTCTCGTCGC CATCACAGGACAGGT <u>C</u> TCTCGCCGGATGATCGGTACTGACGCGT TCCAAGAGACGCCAATCGTTGAGGTAACGAGGT	4565
	ACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTAC CGATCATCCGGCGAG <u>A</u> GACCTGTCCTGTGATGGCGACGAGAGGA AACTGTCAAGCATCGCGTCGGCTAACCCGCT	4566
	GACAGGT <u>C</u> TCTCGCCGG	4567
	CCGGCGAG <u>A</u> GACCTGTC	4568
Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAA	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCTCTCGTCGCC ATCACAGGACAGGTCC <u>A</u> ACGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	4569
	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCG <u>T</u> TGGACCTGTCCTGTGATGGCGACGAGAGG AACTGTCAAGCATCGCGTCGGCTAACCCGC	4570
	ACAGGTCC <u>A</u> ACGCCGGA	4571
	TCCGGCG <u>T</u> TGGACCTGT	4572
Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAG	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCTCTCGTCGCC ATCACAGGACAGGTCC <u>A</u> AGGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	4573
	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCG <u>C</u> TGGACCTGTCCTGTGATGGCGACGAGAGG AACTGTCAAGCATCGCGTCGGCTAACCCGC	4574
	ACAGGTCC <u>A</u> AGGCCGGA	4575
	TCCGGCG <u>C</u> TGGACCTGT	4576
Imidazolinone Resistance ALS 3 <i>Brassica napus</i> Ser635Asn AGT-AAT	GACCGTACCTGTTGGATGTCATCTGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA <u>A</u> TGGTGGCACTTTCAAAGATGTAATAACCG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	4577
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCGGTTATTACATCTT TGAAAGTGCCACCA <u>T</u> TTGGGATCATCGGTAACACATGTTCTTGGT GCGGACAGATGACATCCAACAGGTACGGTC	4578

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GATCCCAA <u>A</u> TGGTGGCA	4579
	TGCCACCA <u>T</u> TTGGGATC	4580
Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGGCCAGGTCT <u>C</u> CCCGCCGCATGATCGGCACCGACGCCT TCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	4581
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGG <u>A</u> GACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	4582
	GCCAGGTCT <u>C</u> CCCGCCGC	4583
	GCGGCGGG <u>A</u> GACCTGGC	4584
Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAA	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGGCCAGGTCC <u>A</u> ACGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4585
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGT <u>T</u> TGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4586
	CCAGGTCC <u>A</u> ACGCCGCA	4587
	TGCGGCGT <u>T</u> TGGACCTGG	4588
Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAG	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGGCCAGGTCC <u>A</u> AGCGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4589
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCG <u>C</u> TGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4590
	CCAGGTCC <u>A</u> AGCGCCGCA	4591
	TGCGGCG <u>C</u> TGGACCTGG	4592
Imidazolinone Resistance ALS <i>Oryza sativa</i> Ser627Asn AGT-AAT	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCCTATGATCCCAA <u>A</u> TGGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4593
	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCA <u>T</u> TTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC	4594
	GATCCCAA <u>A</u> TGGGGGCG	4595
	CGCCCCCA <u>T</u> TTGGGATC	4596

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG	TCTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGC CATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCCT TTCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4597
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGTG CCAATCATGCGTCGCGACACCTGTCCCGTGATGGCGACCATGGG GACGGAGTCGAGCAACGCGTCTGCGAGCGCAGA	4598
	GACAGGTGTCGCGACGC	4599
	GCGTCGCGACACCTGTC	4600
Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG	CTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGCC ATCACGGGACAGGTGACGCGACGCATGATTGGCACCGACGCCTT TCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4601
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGT GCCAATCATGCGTCGCTGCACCTGTCCCGTGATGGCGACCATGG GGACGGAGTCGAGCAACGCGTCTGCGAGCGCAG	4602
	ACAGGTGCAGCGACGCA	4603
	TGCGTCGCTGCACCTGT	4604
Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAT	GGCCGTACCTCTTGATATAATCGTCCCGCACCAGGAGCATGTGT TGCCATATGATCCCTAATGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTATTGATCCGT	4605
	ACGGATCAATACACAGTCCTGCCATCACCATCCAGGATCATATCC TTGAAAGCCCCACCAATTAGGGATCATAGGCAACACATGCTCCTGG TGCGGGACGATTATATCCAAGAGGTACGGCC	4606
	GATCCCTAATGGTGGGG	4607
	CCCCACCAATTAGGGATC	4608
Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTCTCTCGTCGGATGATCGGTACCGATGCTTTC CAGGAACTCCAATTGTTGAGGTAACAAGGT	4609
	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC CGATCATCCGACGAGAGACTTGACCAGTGATCGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT	4610
	GTCAAGTCTCTCGTCGG	4611
	CCGACGAGAGACTTGAC	4612
Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCCAAACGTCGGATGATCGGTACCGATGCTTTC AGGAACTCCAATTGTTGAGGTAACAAGGTC	4613
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACGTTGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4614
	TCAAGTCCAAACGTCGGA	4615

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACG <u>TT</u> GGACTTGA	4616
Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCC <u>AG</u> CGTCGGATGATCGGTACCGATGCTTTCC AGGAACTCCAATTGTTGAGGTAACAAGGTC	4617
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACG <u>CT</u> GGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4618
	TCAAGTCC <u>AG</u> CGTCGGA	4619
	TCCGACG <u>CT</u> GGACTTGA	4620
Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT	GACCTTACTTGTTGGATGTGATTGTCCACATCAAGAACATGTCCT GCCTATGATCCCCA <u>AT</u> GGAGGGGCTTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	4621
	TGAGGTCAATATTGTGTTCTTCCATCACCCCTCTGTGATCACATCTT TGAAAGCCCCCTCCA <u>TT</u> GGGGATCATAGGCAGGACATGTTCTTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	4622
	GATCCCCA <u>AT</u> GGAGGGG	4623
	CCCCTCCA <u>TT</u> GGGGATC	4624
Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTT <u>TC</u> CCCGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACCTCGAT	4625
	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC AATCATACGCCGGG <u>AA</u> ACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4626
	GGCAAGTT <u>TC</u> CCCGGCGT	4627
	ACGCCGGG <u>AA</u> ACTTGCC	4628
Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCA <u>AA</u> CGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACCTCGATC	4629
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>TT</u> GAACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAG	4630
	GCAAGTTC <u>AA</u> CGGCGTA	4631
	TACGCCG <u>TT</u> GAACTTGC	4632
Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCA <u>AG</u> CGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACCTCGATC	4633
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>CT</u> GAACTTGCCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4634

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCAAGTTC A GCGGCGTA	4635
	TACGCCG C TGAACTTGC	4636
Imidazolinone Resistance ALS <i>Amaranthus powellii</i> Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC TGCCTATGATCCCTA A CGGTGCCGCCTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4637
	ACCAACTAATAAGCCCTTCTTCCATCACCCCTCTGTTATGGTGTCTT TGAAGGCGGCACCG T TAGGGATCATAGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATACGGTC	4638
	GATCCCTA A CGGTGCCG	4639
	CGGCACCG T TAGGGATC	4640

Table 30
Genome-Altering Oligos Conferring Porphyric Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Porphyric Herbicide Resistant PPO <i>Arabidopsis thaliana</i> Val365Met GTT-ATG	TCTTGCGCCCTCTTTCTGAATCTGCTGCAAATGCACTCTCAAACT ATATTACCCACCAATGGCAGCAGTATCTATCTCGTACCCGAAAGA AGCAATCCGAACAGAATGTTTGATAGATGG	4641
	CCATCTATCAAACATTCTGTTGCGATTGCTTCTTTGCGGTACGAGA TAGATACTGCTGCCATTGGTGGGTAATATAGTTTTGAGAGTGCATT TGCAGCAGATTGAGAAAGAGGGCGCAAGA	4642
	CCCACCAATGGCAGCAG	4643
	CTGCTGCCATTGGTGGG	4644
Porphyric Herbicide Resistant PPO <i>Nicotiana tabacum</i> Val376Met GTT-ATG	TATTACGTCCTCTTTGCGTTGCCGAGCAGATGCACTTTCAAATTT CTACTATCCCCCAATGGGAGCAGTCACAATTTTCATATCCTCAAGAA GCTATTCGTGATGAGCGTCTGGTTGATGG	4645
	CCATCAACCAGACGCTCATCACGAATAGCTTCTTGAGGATATGAA ATTGTGACTGCTCCCATTTGGGGGATAGTAGAAATTTGAAAGTGCA TCTGCTGCGGCAACCGAAAGAGGACGTAATA	4646
	TCCCCCAATGGGAGCAG	4647
	CTGCTCCCATTTGGGGGA	4648
Porphyric Herbicide Resistant PPO <i>Cichorium intybus</i> Val383Met GTT-ATG	TGTTGCGTCCGCTTTTCGTTGGGTGCAGCAGATGCATTGTCAAAT TTTATTATCCTCCGATGGCAGCTGTATCAATTTTCATATCCAAAAGA CGCAATTCGTGCTGACCGGCTGATTGATGG	4649
	CCATCAATCAGCCGGTCAGCACGAATTGCGTCTTTTGGATATGAA ATTGATACAGCTGCCATCGGAGGATAATAAAATTTTGACAATGCAT CTGCTGCACCCAACGAAAGCGGACGCAACA	4650
	TCCTCCGATGGCAGCTG	4651
	CAGCTGCCATCGGAGGA	4652
Porphyric Herbicide Resistant PPO <i>Spinacia oleracea</i> Val390Met GTT-ATG	TCCTTCGTCCACTTTTCAGATGTCGCCGAGAATCTCTTTCAAATTT TCATTATCCACCAATGGCAGCTGTGTCACTTTTCCTATCCTAAAGAA GCAATTAGATCAGAGTGCTTGATTGACGG	4653
	CCGTCAATCAAGCACTCTGATCTAATTGCTTCTTTAGGATAGGAAA GTGACACAGCTGCCATTGGTGGATAATGAAATTTTGAAAGAGATT CTGCGGCGACATCTGAAAGTGGACGAAGGA	4654
	TCCACCAATGGCAGCTG	4655
	CAGCTGCCATTGGTGGG	4656

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Porphyric Herbicide Resistant PPO <i>Zea mays</i> Val363Met GTT-ATG	TTTTGCGTCCACTTTCAAGCGATGCTGCAGATGCTCTATCAAGATTCTATTATCCACCGATGGCTGCTGTAAGTGTTCGTATCCAAAGGAA GCAATTAGAAAAGAATGCTTAATTGATGG	4657
	CCATCAATTAAGCATTCTTTTCTAATTGCTTCCTTTGGATACGAAACAGTTACAGCAGCCATCGGTGGATAATAGAATCTTGATAGAGCATCTGCAGCATCGCTTGAAAGTGGACGCAAAA	4658
	TCCACCGATGGCTGCTG	4659
	CAGCAGCCATCGGTGGA	4660
Porphyric Herbicide Resistant PPO <i>Oryza sativa</i> Val364Met GTT-ATG	TCTTGCGGCCACTTTCAAGTGATGCAGCAGATGCTCTGTCAATATTCTATTATCCACCAATGGCTGCTGTAAGTGTTCATATCCAAAAGAA GCAATTAGAAAAGAATGCTTAATTGACGG	4661
	CCGTCAATTAAGCATTCTTTTCTAATTGCTTCCTTTGGATATGAAACAGTTACAGCAGCCATTGGTGGATAATAGAATATTGACAGAGCATCTGCTGCATCACTTGAAAGTGGCCGCAAGA	4662
	TCCACCAATGGCTGCTG	4663
	CAGCAGCCATTGGTGGGA	4664
Porphyric Herbicide Resistant PPO <i>Chlamydomonas reinhardtii</i> Val389Met GTG-ATG	CTGGTCAAGGAGCAGGCGCCCGCCGCGCCGAGGCCCTGGGCTCCTTCGACTACCCGCCGATGGGCGCCGTGACGCTGTCGTACCCGCTGAGCGCCGTGCGGGAGGAGCGCAAGGCCTCGG	4665
	CCGAGGCCTTGCGCTCCTCCCGCACGGCGCTCAGCGGGTACGACAGCGTCACGGCGCCCATCGGCGGGTAGTCGAAGGAGCCCAGGGCCTCGGCGGCGGGCGGCGCTGCTCCTTGACCAG	4666
	ACCCGCCGATGGGCGCC	4667
	GGCGCCCATCGGCGGGT	4668

Table 31
Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATTTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4669
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAAGTAGCATATTGGAAAATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4670

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATATGCTA <u>C</u> TTTCAACA	4671
	TGTTGAAA <u>G</u> TAGCATAT	4672
Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4673
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAAGTGAACGAA CGAGAGTTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	4674
	ATATGCTA <u>C</u> TTTCAACA	4675
	TGTTGAAA <u>G</u> TAGCATAT	4676
Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTTAACAACCTCTCGCTCTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG	4677
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG CGAGAGTTGTTAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4678
	ATATGCTA <u>C</u> TTTTAACA	4679
	TGTTAAA <u>G</u> TAGCATAT	4680
Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4681
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAAGTGAACGAA CGAGAGTTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4682
	ATATGCTA <u>C</u> TTTCAACA	4683
	TGTTGAAA <u>G</u> TAGCATAT	4684
Triazine Resistant D1 Protein <i>Magnolia pyramidata</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCCTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4685
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACGATATTATAAGTTT	4686
	ATATGCTA <u>C</u> TTTCAACA	4687
	TGTTGAAA <u>G</u> TAGCATAT	4688
Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCCTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4689
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAGTTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATATTATAGGTTT	4690

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATATGCTA <u>C</u> TTTCAACA	4691
	TGTTGAAAGTAGCATAT	4692
Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCA <u>A</u> CTTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG	4693
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTTGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACAATATTATAGGTTT	4694
	ATATGCA <u>A</u> CTTTCAACA	4695
	TGTTGAAAGTTGCATAT	4696
Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	4697
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATGTTGTAAGTTT	4698
	ATATGCTA <u>C</u> TTTCAACA	4699
	TGTTGAAAGTAGCATAT	4700
Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAAAT CTTCCAATATGCTA <u>C</u> TTTTAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTTG	4701
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCGGCCACAATATTATAAGTTT	4702
	ATATGCTA <u>C</u> TTTTAACA	4703
	TGTTAAAAGTAGCATAT	4704
Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAAAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	4705
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCAAAT AACCGTGAGCAGCCACAATATTATAAGTCT	4706
	ATATGCTA <u>C</u> TTTCAACA	4707
	TGTTGAAAGTAGCATAT	4708
Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCT AGCGGCTTGGCCGGTAGTAGGTATTTG	4709
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGAAAATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	4710
	ATATGCTA <u>C</u> TTTCAACA	4711

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTTGAAAGTAGCATAT	4712
Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4713
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	4714
	ATATGCTA <u>C</u> TTTCAACA	4715
	TGTTGAAAGTAGCATAT	4716
Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTTAACAACCTCTCGCTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG	4717
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG CGAGAGTTGTTAAAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4718
	ATATGCTA <u>C</u> TTTTAACA	4719
	TGTTAAAAGTAGCATAT	4720
Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4721
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4722
	ATATGCTA <u>C</u> TTTCAACA	4723
	TGTTGAAAGTAGCATAT	4724
Triazine Resistant D1 Protein <i>Magnolia pyramidata</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4725
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACGATATTATAAGTTT	4726
	ATATGCTA <u>C</u> TTTCAACA	4727
	TGTTGAAAGTAGCATAT	4728
Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCAGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4729
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATATTATAGGTTT	4730
	ATATGCTA <u>C</u> TTTCAACA	4731

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTTGAAAGTAGCATAT	4732
Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCAACTTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG	4733
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTTGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACAATATTATAGGTTT	4734
	ATATGCAACTTTCAACA	4735
	TGTTGAAAGTTGCATAT	4736
Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	4737
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATGTTGTAAGTTT	4738
	ATATGCTACTTTCAACA	4739
	TGTTGAAAGTAGCATAT	4740
Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAAAT CTTCCAATATGCTACTTTTAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTTG	4741
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCGGCCACAATATTATAAGTTT	4742
	ATATGCTACTTTTAACA	4743
	TGTTAAAAGTAGCATAT	4744
Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAAAT CTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	4745
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCAAAT AACCGTGAGCAGCCACAATATTATAAGTCT	4746
	ATATGCTACTTTCAACA	4747
	TGTTGAAAGTAGCATAT	4748
Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTTG	4749
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	4750
	ATATGCTACTTTCAACA	4751
	TGTTGAAAGTAGCATAT	4752

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein <i>Picea abies</i> Ser264Thr AGT-ACT	AAACCTACAATATTGTGGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAGTATGCTA <u>C</u> TTTCAACAACCTCCCGTTCTTTACATTTCTTCT TAGCTGCTTGGCCCGTAGCAGGTATCTG	4753
	CAGATACCTGCTACGGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGGGAGTTGTTGAAA <u>G</u> TAGCATACTGGAAGATCAATCGGCCGAAA TAACCGTGAGCAGCCACAATATTGTAGGTTT	4754
	GTATGCTA <u>C</u> TTTCAACA	4755
	TGTTGAAA <u>G</u> TAGCATAC	4756
Triazine Resistant D1 Protein <i>Vicia faba</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGCTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4757
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG CGAGAATTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATATTATAGGTTT	4758
	ATATGCTA <u>C</u> TTTCAACA	4759
	TGTTGAAA <u>G</u> TAGCATAT	4760
Triazine Resistant D1 Protein <i>Hordeum vulgare</i> Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCATGGTTATTTGGCCGATTAAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG	4761
	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAA TAACCATGAGCAGCCACAATATTATAAGTCT	4762
	ATATGCTACTTTCAACA	4763
	TGTTGAAAGTAGCATAT	4764
Triazine Resistant D1 Protein <i>Triticum aestivum</i> Ser264Thr AGT-ACT	AACTTATAATATTGTGGCTGCTCATGGTTATTTGGCCGATTAAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG	4765
	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAA <u>G</u> TAGCATATTGGAAGATTAATCGGCCAAAA TAACCATGAGCAGCCACAATATTATAAGTTT	4766
	ATATGCTA <u>C</u> TTTCAACA	4767
	TGTTGAAA <u>G</u> TAGCATAT	4768
Triazine Resistant D1 Protein <i>Vigna unguiculata</i> Ser264Thr AGT-ACT	AACTTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTAATC TTCCAATATGCA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCCT AGCTGCTTGGCCTGTAGTAGGTATTTG	4769
	CAAATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAA <u>G</u> TTGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCAGCTACAATATTATAAGTTT	4770
	ATATGCA <u>C</u> TTTCAACA	4771
	TGTTGAAA <u>G</u> TTGCATAT	4772

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein <i>Lotus japonicus</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCAAC <u>CTTT</u> CAACAACCTCTCGTTCTTTACACTTCTTCT TAGCTGCTTGGCCTGTTGTAGGTATCTG	4773
	CAGATACCTACAACAGGCCAAGCAGCTAAGAAGAAGTGTAAGAA CGAGAGTTGTTGAAAG <u>GTTG</u> CATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATATTATAGGTTT	4774
	ATATGCAAC <u>CTTT</u> CAACA	4775
	TGTTGAAAG <u>GTTG</u> CATAT	4776
Triazine Resistant D1 Protein <i>Sinapis alba</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTAC <u>CTTT</u> CAACAATTCTCGTTCTTTACATTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	4777
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAG <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATGTTGTAAGTTT	4778
	ATATGCTAC <u>CTTT</u> CAACA	4779
	TGTTGAAAG <u>G</u> TAGCATAT	4780
Triazine Resistant D1 Protein <i>Pisum sativum</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTAC <u>CTTT</u> CAACAATTCTCGCTCTTTACATTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4781
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG CGAGAATTGTTGAAAG <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATATTATAGGTTT	4782
	ATATGCTAC <u>CTTT</u> CAACA	4783
	TGTTGAAAG <u>G</u> TAGCATAT	4784
Triazine Resistant D1 Protein <i>Spinacia oleracea</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGTCGATTGAT CTTCCAATATGCTAC <u>CTTT</u> CAACAACCTCTCGTTCTTTACACTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG	4785
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAGTGTAAGAA CGAGAGTTGTTGAAAG <u>G</u> TAGCATATTGGAAGATCAATCGACCAAAA TAACCATGAGCAGCTACGATATTATAAGTTT	4786
	ATATGCTAC <u>CTTT</u> CAACA	4787
	TGTTGAAAG <u>G</u> TAGCATAT	4788
Triazine Resistant D1 Protein <i>Nicotiana debneyi</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTAC <u>CTTT</u> CAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4789
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAG <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	4790
	ATATGCTAC <u>CTTT</u> CAACA	4791
	TGTTGAAAG <u>G</u> TAGCATAT	4792

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein <i>Solanum nigrum</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4793
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAA <u>A</u> GTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4794
	ATATGCTA <u>C</u> TTTCAACA	4795
	TGTTGAA <u>A</u> GTAGCATAT	4796
Triazine Resistant D1 Protein <i>Nicotiana plumbaginifolia</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4797
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAA <u>A</u> GTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	4798
	ATATGCTA <u>C</u> TTTCAACA	4799
	TGTTGAA <u>A</u> GTAGCATAT	4800

Example 27
Engineering male- or female-sterile plants

[246] Flower development in distantly related dicot plant species is increasingly better understood and appears to be regulated by a family of genes which encode regulatory proteins. These genes include, for example, *AGAMOUS* (*AG*), *APETALA1* (*AP1*), and *APETALA3* (*AP3*) and *PISTILLATA* (*PI*) in *Arabidopsis thaliana*, and *DEFICIENS A* (*DEFA*), *GLOBOSA* (*GLO*), *SQUAMOSA* (*SQUA*), and *PLENA* (*PLE*) in *Antirrhinum majus*. Genetic studies have shown that the *DEFA*, *GLO* and *AP3* genes are essential for petal and stamen development. Sequence analysis of these genes revealed that the gene products contain a conserved MADS box region, a DNA-binding domain. Using these clones as probes, MADS box genes have also been isolated from other species including tomato, tobacco, petunia, *Brassica napus*, and maize.

[247] Altering the expression of these genes results in altered floral morphology. For example, mutations in *AP3* and *PI* result in male-sterile flowers because petals develop in place of stamens.

[248] The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer altered floral structures in plants.

Table 32
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AP3 <i>Arabidopsis thaliana</i> Arg3Term AGA-TGA	TTGTCCTCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAG AGAAGAATATGGCGT ^T GAGGGAAGATCCAGATCAAGAGGATAGAGA ACCAGACAAACAGACAAGTGACGTATTCAA	4801
	TTGAATACGTCAC ^T TTGTCTGTTTGTCTGGTTCTCTATCCTCTTGATC TGGATCTTCCCTC ^A CGCCATATTCTTCTCTTTGTTTAATCTTTTT GTTGAAGAGATTTGGTGGAGAGGACAA	4802
	ATATGGCGT ^T GAGGGAAG	4803
	CTTCCCTC ^A CGCCATAT	4804
Male-sterile AP3 <i>Arabidopsis thaliana</i> Lys5Term AAG-TAG	TCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGA ATATGGCGAGAGGGT ^T AGATCCAGATCAAGAGGATAGAGAACCAGA CAAACAGACAAGTGACGTATTCAAAGAGAA	4805
	TTCTCTTTGAATACGTCAC ^T TTGTCTGTTTGTCTGGTTCTCTATCCTC TTGATCTGGATCT ^A CCCTCTCGCCATATTCTTCTCTTTGTTTAAT CTTTTGTGAAGAGATTTGGTGGAGA	4806

	CGAGAGGGTAGATCCAG	4807
	CTGGATCTACCCTCTCG	4808
Male-sterile AP3 <i>Arabidopsis thaliana</i> Gln7Term CAG-TAG	CCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGG CGAGAGGGAAGATCTAGATCAAGAGGATAGAGAACCAGACAAACA GACAAGTGACGTATTCAAAGAGAAGGAATG	4809
	CATTCCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCT ATCCTCTTGATCTAGATCTTCCCTCTCGCCATATTCTTCTCTCTTTG TTTAATCTTTTTGTTGAAGAGATTTGG	4810
	GGAAGATCTAGATCAAG	4811
	CTTGATCTAGATCTTCC	4812
Male-sterile AP3 <i>Arabidopsis thaliana</i> Lys9Term AAG-TAG	CTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAG GGAAGATCCAGATCTAGAGGATAGAGAACCAGACAAACAGACAAG TGACGTATTCAAAGAGAAGGAATGGTTTAT	4813
	ATAAACCATTCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGG TTCTCTATCCTCTAGATCTGGATCTTCCCTCTCGCCATATTCTTCTC TCTTTGTTAATCTTTTTGTTGAAGAG	4814
	TCCAGATCTAGAGGATA	4815
	TATCCTCTAGATCTGGA	4816
Male-sterile AP3 <i>Brassica oleracea</i> Lys23Term AAG-TAG	AGAGGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCG ACAAGTGACGTATTCTTAGAGAAGAAATGGTTTGTTCAGAAAGCT CACGAGCTTACAGTTTTATGTGATGCTAGGG	4817
	CCCTAGCATCACATAAACTGTAAGCTCGTGAGCTTTCTTGAACAA ACCATTTCTTCTCTAGAATACGTCACTTGTCTGGTTGGTCTGGTTC TCTATCCTCTTGATCTGGATCTTCCCTCT	4818
	CGTATTCTTAGAGAAGA	4819
	TCTTCTCTAGAATACG	4820
Male-sterile AP3 <i>Brassica oleracea</i> Arg24Term AGA-TGA	GGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAA GTGACGTATTCTAAGTGAAGAAATGGTTTGTTCAGAAAGCTCACG AGCTTACAGTTTTATGTGATGCTAGGGTTT	4821
	AAACCCTAGCATCACATAAACTGTAAGCTCGTGAGCTTTCTTGAA CAAACCATTCTTCACTTAGAATACGTCACTTGTCTGGTTGGTCTGG TTCTCTATCCTCTTGATCTGGATCTTCCC	4822
	ATTCTAAGTGAAGAAAT	4823
	ATTTCTTCACTTAGAAT	4824
Male-sterile AP3 <i>Brassica oleracea</i> Arg25Term AGA-TGA	AAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAAAGTG ACGTATTCTAAGAGATGAAATGGTTTGTTCAGAAAGCTCACGAGC TTACAGTTTTATGTGATGCTAGGGTTTCTGA	4825
	TCGAAACCCTAGCATCACATAAACTGTAAGCTCGTGAGCTTTCTT GAACAAACCATTTCATCTCTTAGAATACGTCACTTGTCTGGTTGGTC TGGTTCTCTATCCTCTTGATCTGGATCTT	4826
	CTAAGAGATGAAATGGT	4827
	ACCATTTCACTCTCTTAG	4828

Male-sterile AP3 <i>Brassica oleracea</i> Leu28Term TTG-TAG	TCAAGAGGATAGAGAACCAGACCAACCGACAAGTGACGTATTCTA AGAGAAGAAATGGTTAGTTCAAGAAAGCTCACGAGCTTACAGTTTT ATGTGATGCTAGGGTTTCGATTATCATGTT	4829
	AACATGATAATCGAAACCCTAGCATCACATAAACTGTAAGCTCGT GAGCTTTCTTGAACTAACCATTTCTTCTCTTAGAATACGTCACTTGT CGGTTGGTCTGGTTCTCTATCCTCTTGA	4830
	AAATGGTTAGTTCAAGA	4831
	TCTTGAACTAACCATTT	4832
Male-sterile AP3 <i>Brassica napus</i> Tyr21Term TAC-TAG	GGCTCGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAA CAGGCAGGTCACCTAGTCCAAGAGAAGAAATGGTTTGTTCAGAA AGCACACGAGCTCTCTGTTCTCTGTGATGCT	4833
	AGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAAACC ATTTCTTCTCTTGGACTAGGTGACCTGCCTGTTTGTGTTGTTCTCTA TCCTCTTAATCTGGATCTTCCCTCGAGCC	4834
	GTCACCTAGTCCAAGAG	4835
	CTCTTGGACTAGGTGAC	4836
Male-sterile AP3 <i>Brassica napus</i> Lys23Term AAG-TAG	CGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGG CAGGTCACCTACTCCTAGAGAAGAAATGGTTTGTTCAGAAAGCAC ACGAGCTCTCTGTTCTCTGTGATGCTAAAG	4837
	CTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAA ACCATTTCTTCTCTAGGAGTAGGTGACCTGCCTGTTTGTGTTGTTT TCTATCCTCTTAATCTGGATCTTCCCTCG	4838
	CCTACTCCTAGAGAAGA	4839
	TCTTCTCTAGGAGTAGG	4840
Male-sterile AP3 <i>Brassica napus</i> Arg24Term AGA-TGA	GGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAG GTCACCTACTCCAAGTGAAGAAATGGTTTGTTCAGAAAGCACACG AGCTCTCTGTTCTCTGTGATGCTAAAGTTT	4841
	AAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAA CAAACCATTTCTTCACTTGGAGTAGGTGACCTGCCTGTTTGTGTTG TTCTCTATCCTCTTAATCTGGATCTTCCC	4842
	ACTCCAAGTGAAGAAAT	4843
	ATTTCTTCACTTGGAGT	4844
Male-sterile AP3 <i>Brassica napus</i> Arg25Term AGA-TGA	AAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTC ACCTACTCCAAGAGATGAAATGGTTTGTTCAGAAAGCACACGAG CTCTCTGTTCTCTGTGATGCTAAAGTTTCCA	4845
	TGGAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTT GAACAAACCATTTCATCTCTTGGAGTAGGTGACCTGCCTGTTTGT TGGTTCTCTATCCTCTTAATCTGGATCTT	4846
	CCAAGAGATGAAATGGT	4847
	ACCATTTCATCTCTTGG	4848

Male-sterile DEFA <i>Antirrhinum majus</i> Arg3Term CGA-TGA	GGAGAGAAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGG TAGTGGTTCGATGGCTT <u>G</u> AGGGGAAGATCCAGATTAAGAGGATAGA GAACCAAACAACAGGCAGGTCACCTACTCCA	4849
	TGGAGTAGGTGACCTGCCTGTTTGGTTCTCTATCCTCTTAAT CTGGATCTTCCCTC <u>A</u> AGCCATCGAACCCTACCCTACTGCTCTTG TTTTCTTCTTCCAGCTTTCTTTCTCTCC	4850
	CGATGGCTT <u>G</u> AGGGAAG	4851
	CTTCCCTC <u>A</u> AGCCATCG	4852
Male-sterile DEFA <i>Antirrhinum majus</i> Lys5Term AAG-TAG	AAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGT TCGATGGCTCGAGGGT <u>T</u> AGATCCAGATTAAGAGGATAGAGAACCAA ACAAACAGGCAGGTCACCTACTCCAAGAGAA	4853
	TTCTCTTGGAGTAGGTGACCTGCCTGTTTGGTTCTCTATCCT CTTAATCTGGATCT <u>A</u> CCCTCGAGCCATCGAACCCTACCCTACTG CTCTTGTTTTCTTCTTCCAGCTTTCTTT	4854
	CTCGAGGGT <u>T</u> AGATCCAG	4855
	CTGGATCT <u>A</u> CCCTCGAG	4856
Male-sterile DEFA <i>Antirrhinum majus</i> Gln7Term CAG-TAG	AAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATG GCTCGAGGGAAGATC <u>T</u> AGATTAAGAGGATAGAGAACCAAACAAC AGGCAGGTCACCTACTCCAAGAGAAGAAATG	4857
	CATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGGTTCTC TATCCTCTTAATCT <u>A</u> GATCTTCCCTCGAGCCATCGAACCCTACCA CTACTGCTCTTGTTTTCTTCTTCCAGCTT	4858
	GGAAGATC <u>T</u> AGATTAAG	4859
	CTTAATCT <u>A</u> GATCTTCC	4860
Male-sterile DEFA <i>Antirrhinum majus</i> Lys9Term AAG-TAG	GAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTCGA GGGAAGATCCAGATT <u>T</u> AGAGGATAGAGAACCAAACAACAGGCAG GTCACCTACTCCAAGAGAAGAAATGGTTTGT	4861
	ACAAACCATTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGGTTG GTTCTCTATCCTCT <u>A</u> AATCTGGATCTTCCCTCGAGCCATCGAACCA CTACCACTACTGCTCTTGTTTTCTTCTTC	4862
	TCCAGATT <u>T</u> AGAGGATA	4863
	TATCCTCT <u>A</u> AATCTGGA	4864
Male-sterile AP3 <i>Nicotiana tabacum</i> Lys5Term AAG-TAG	TCAGTAATTCTTAAGATCTCAAACCTTTGAGCAAAAAGAAAAAAAAAC TATGGCTCGTGGGT <u>T</u> AGATCCAGATCAAGAGAATAGAGAACCAAAC AAACAGACAAGTCACTTATTCTAAGAGAA	4865
	TTCTCTTAGAATAAGTGACTTGTCTGTTTGGTTCTCTATTCTC TTGATCTGGATCT <u>A</u> CCACGAGCCATAGTTTTTTTTCTTTTGCTC AAAGTTTGAGATCTTAAGAATTACTGA	4866
	CTCGTGGGT <u>T</u> AGATCCAG	4867
	CTGGATCT <u>A</u> CCACGAG	4868

Male-sterile AP3 <i>Nicotiana tabacum</i> Gln7Term CAG-TAG	ATTCTTAAGATCTCAAACCTTTGAGCAAAAAGAAAAAAACTATGGC TCGTGGGAAGATCTAGATCAAGAGAATAGAGAACCAAACAAACAG ACAAGTCACTTATTCTAAGAGAAGAAATG	4869
	CATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGGTTCTCT ATTCTCTTGATCTAGATCTCCACGAGCCATAGTTTTTTTTCTTT TTGCTCAAAGTTTGAGATCTTAAGAAT	4870
	GGAAGATCTAGATCAAG	4871
	CTTGATCTAGATCTTCC	4872
Male-sterile AP3 <i>Nicotiana tabacum</i> Lys9Term AAG-TAG	AAGATCTCAAACCTTTGAGCAAAAAGAAAAAAACTATGGCTCGTG GGAAGATCCAGATCTAGAGAATAGAGAACCAAACAAACAGACAAG TCACTTATTCTAAGAGAAGAAATGGACTTT	4873
	AAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGG TTCTCTATTCTCTAGATCTGGATCTTCCACGAGCCATAGTTTTTT TTCTTTTGCTCAAAGTTTGAGATCTT	4874
	TCCAGATCTAGAGAATA	4875
	TATTCTCTAGATCTGGA	4876
Male-sterile AP3 <i>Nicotiana tabacum</i> Arg10Term AGA-TGA	ATCTCAAACCTTTGAGCAAAAAGAAAAAAACTATGGCTCGTGGA AGATCCAGATCAAGTGAATAGAGAACCAAACAAACAGACAAGTCA CTTATTCTAAGAGAAGAAATGGACTTTTCA	4877
	TGAAAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGT TGGTTCTCTATTCACTTGATCTGGATCTTCCACGAGCCATAGTTT TTTTTCTTTTGCTCAAAGTTTGAGAT	4878
	AGATCAAGTGAATAGAG	4879
	CTCTATTCACTTGATCT	4880
Male-sterile AP3 <i>Medicago sativa</i> Tyr21Term TAC-TAG	GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAA CAGACAAGTAACTTAGTCAAACGAAGGGATGGTCTTTTCAAGAAG GCCAATGAGCTCACTGTTCTTTGTGATGCT	4881
	AGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGACCA TCCCTTCGTTTTGACTAAGTTACTTGTCTGTTTCGTTGTGTTCTCTAT TCTCTTGATCTGGATCTTTCCTCGAGCC	4882
	GTAACCTAGTCAAACG	4883
	CGTTTTGACTAAGTTAC	4884
Male-sterile AP3 <i>Medicago sativa</i> Ser22Term TCA-TGA	CTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACA GACAAGTAACTTACTGAAAACGAAGGGATGGTCTTTTCAAGAAGG CCAATGAGCTCACTGTTCTTTGTGATGCTAA	4885
	TTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGAC CATCCCTTCGTTTTAGTAAGTTACTTGTCTGTTTCGTTGTGTTCTCT ATTCTCTTGATCTGGATCTTTCCTCGAG	4886
	AACTTACTGAAAACGAA	4887
	TTCGTTTTAGTAAGTT	4888

Male-sterile AP3 <i>Medicago sativa</i> Lys23Term AAA-TAA	CGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGA CAAGTAACTTACTCAT <u>A</u> ACGAAGGGATGGTCTTTTCAAGAAGGCCA ATGAGCTCACTGTTCTTTGTGATGCTAAGG	4889
	CCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAG ACCATCCCTTCGTT <u>A</u> TGAGTAAGTTACTTGTCTGTTGTTGTTCT CTATTCTCTTGATCTGGATCTTTCCTCG	4890
	CTTACTCAT <u>A</u> ACGAAGG	4891
	CCTTCGTT <u>A</u> TGAGTAAG	4892
Male-sterile AP3 <i>Medicago sativa</i> Arg24Term CGA-TGA	GGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAA GTAACCTTACTCAAAATGAAGGGATGGTCTTTTCAAGAAGGCCAATG AGCTCACTGTTCTTTGTGATGCTAAGGTTT	4893
	AAACCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAA AAGACCATCCCTTC <u>A</u> TTTTGAGTAAGTTACTTGTCTGTTGTTGTT TCTCTATTCTCTTGATCTGGATCTTTC	4894
	ACTCAAAATGAAGGGAT	4895
	ATCCCTTC <u>A</u> TTTTGAGT	4896
Male-sterile DEF4 <i>Solanum tuberosum</i> Tyr21Term TAT-TAG	GGCTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAAT AGGCAAGTGACTTAGTCAAAGAGAAGAAATGGGCTATTCAAGAAG GCTAATGAACCTACAGTTCTTTGTGATGCT	4897
	AGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCA TTTCTTCTCTTTG <u>A</u> CTAAGTCACCTGCCTATTTGTTTGTTTTCTATT TTCTTGATCTGGATCTTACCACGAGCC	4898
	GTGACTTAGTCAAAGAG	4899
	CTCTTTG <u>A</u> CTAAGTCAC	4900
Male-sterile DEF4 <i>Solanum tuberosum</i> Ser22Term TCA-TGA	CTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAG GCAAGTGACTTATTGAAAGAGAAGAAATGGGCTATTCAAGAAGGC TAATGAACCTACAGTTCTTTGTGATGCTAA	4901
	TTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCC CATTTCTTCTCTTT <u>C</u> AATAAGTCACCTGCCTATTTGTTTGTTTTCTA TTTTCTTGATCTGGATCTTACCACGAG	4902
	GACTTATTGAAAGAGAA	4903
	TTCTCTTT <u>C</u> AATAAGTC	4904
Male-sterile DEF4 <i>Solanum tuberosum</i> Lys23Term AAG-TAG	CGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGG CAAGTGACTTATTCA <u>T</u> AGAGAAGAAATGGGCTATTCAAGAAGGCTA ATGAACCTACAGTTCTTTGTGATGCTAAAG	4905
	CTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAG CCCATTTCTTCTCT <u>A</u> TGAATAAGTCACCTGCCTATTTGTTTGTTTT CTATTTCTTGATCTGGATCTTACCACG	4906
	CTTATTCATAGAGAAGA	4907
	TCTTCTCT <u>A</u> TGAATAAG	4908

Male-sterile DEF4 <i>Solanum tuberosum</i> Arg24Term AGA-TGA	GGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAA GTGACTTATTCAAAGTGAAGAAATGGGCTATTCAAGAAGGCTAATG AACTTACAGTTCTTTGTGATGCTAAAGTTT	4909
	AACTTTAGCATCACAAAGAAGTGTAAAGTTTCATTAGCCTTCTTGAAT AGCCCATTTCTTC A CTTTGAATAAGTCACTTGCCTATTTGTTTGGTT TTCTATTTTCTTGATCTGGATCTTACC	4910
	ATTCAAAGTGAAGAAAT	4911
	ATTTCTTC A CTTTGAAT	4912
Male-sterile AP3 <i>Lycopersicon esculentum</i> Gly27Term GGA-TGA	GCTAATGAACCTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTAT GATTTCTAGTACTTGAAAACCTTCATGAGTTTATAAGTCCCTCTATCA CGACCAAACAATTGTTTCGATCTGTACC	4913
	GGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAA CTCATGAAGTTTTCAAGTACTAGAAATCATAACAATTGAACTTTAG CATCACAAAGAACAGTAAGTTCATTAGC	4914
	CTAGTACTTGAAAACCTT	4915
	AAGTTTTCAAGTACTAG	4916
Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys28Term AAA-TAA	AATGAACCTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGAT TTCTAGTACTGGATAAAGTTCATGAGTTTATAAGTCCCTCTATCACGA CCAAACAATTGTTTCGATCTGTACCAGA	4917
	TCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTAT AACTCATGAAGTTATCCAGTACTAGAAATCATAACAATTGAACTT TAGCATCACAAAGAACAGTAAGTTCATT	4918
	GTAAGTTAAGTTCAT	4919
	ATGAAGTTATCCAGTAC	4920
Male-sterile AP3 <i>Lycopersicon esculentum</i> Glu31Term GAG-TAG	ACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTAC TGAAAACCTTCATTAGTTTATAAGTCCCTCTATCACGACCAAACAAT TGTTTCGATCTGTACCAGAAGACTATTG	4921
	CAATAGTCTTCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGA GGGACTTATAAACTAATGAAGTTTCCAGTACTAGAAATCATAACA ATTGAACTTTAGCATCACAAAGAACAGT	4922
	AACTTCATTAGTTTATA	4923
	TATAAACTAATGAAGTT	4924
Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys40Term AAA-TAA	ATTGTTATGATTTCTAGTACTGAAAACCTTCATGAGTTTATAAGTCC CTCTATCACGACCTAACAATTGTTTCGATCTGTACCAGAAGACTATT GGAGTTGATATTTGGACTACTCACTATG	4925
	CATAGTGAGTAGTCCAAATATCAACTCCAATAGTCTTCTGGTACAG ATCGAACAATTGTTAGGTCGTGATAGAGGGACTTATAAACTCATGA AGTTTTCCAGTACTAGAAATCATAACAAT	4926
	TCACGACCTAACAATTG	4927
	CAATTGTTAGGTCGTGA	4928

Male-sterile AP3 <i>Triticum aestivum</i> Tyr21Term TAC-TAG	GGGGCGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCA ACAGGCAGGTGACCTAGTCCAAGCGCCGGTCGGGGATCATGAAG AAGGCGCGGGAGCTCACCCTGCTCTGCGACGCC	4929
	GGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATGATCC CCGACCGGCGCTTGGACTAGGTACCTGCCTGTTGGTGGCGTTCT CGATCCGCTTTATCTCAATCTTCCCCCGCCCC	4930
	GTGACCTAGTCCAAGCG	4931
	CGCTTGGACTAGGTAC	4932
Male-sterile AP3 <i>Triticum aestivum</i> Lys23Term AAG-TAG	CGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAG GCAGGTGACCTACTCTAGCGCCGGTCGGGGATCATGAAGAAGG CGCGGGAGCTCACCCTGCTCTGCGACGCCAGG	4933
	CCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATG ATCCCCGACCGGCGCTAGGAGTAGGTACCTGCCTGTTGGTGGC GTTCTCGATCCGCTTTATCTCAATCTTCCCCG	4934
	CCTACTCTAGCGCCGG	4935
	CCGGCGCTAGGAGTAGG	4936
Male-sterile AP3 <i>Triticum aestivum</i> Ser26Term TCG-TAG	TTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCT ACTCCAAGCGCCGGTAGGGGATCATGAAGAAGGCGCGGGAGCTC ACCGTGCTCTGCGACGCCAGGTGCGCATCAT	4937
	ATGATGGCGACCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGC CTTCTTCATGATCCCCTACCGGCGCTTGGAGTAGGTACCTGCCT GTTGGTGGCGTTCTCGATCCGCTTTATCTCAA	4938
	GCGCCGGTAGGGGATCA	4939
	TGATCCCCTACCGGCGC	4940
Male-sterile AP3 <i>Triticum aestivum</i> Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCCAAGCG CCGGTCGGGGATCATGTAGAAGGCGCGGGAGCTCACCCTGCTCT GCGACGCCAGGTGCGCATCATGTTCTCCT	4941
	AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG AGCTCCCGCGCCTTCTACATGATCCCCGACCGGCGCTTGGAGTAG GTCACCTGCCTGTTGGTGGCGTTCTCGATCCG	4942
	GGATCATGTAGAAGGCG	4943
	CGCCTTCTACATGATCC	4944
Male-sterile Silky1 <i>Zea mays</i> Tyr21Term TAC-TAG	GGGGCGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCA ACCGCCAGGTGACCTAGTCCAAGCGCCGGACGGGGATCATGAAG AAGGCACGCGAGCTCACCCTGCTCTGCGACGCC	4945
	GGCGTCGCAGAGCACGGTGAGCTGCGTGCCTTCTTCATGATCCC CGTCCGGCGCTTGGACTAGGTACCTGGCGGTTGGTGGCGTTCT CGATCCGCTTGATCTCGATCTTGCCGCGCCCC	4946
	GTGACCTAGTCCAAGCG	4947
	CGCTTGGACTAGGTAC	4948

Male-sterile Silky1 <i>Zea mays</i> Lys23Term AAG-TAG	CGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCG CCAGGTGACCTACTCCTAGCGCCGGACGGGGATCATGAAGAAGG CACGCGAGCTCACCGTGCTCTGCGACGCCCAGG	4949
	CCTGGGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATG ATCCCCGTCCGGCGCTAGGAGTAGGTCACCTGGCGGTTGGTGGC GTTCTCGATCCGCTTGATCTCGATCTTGCCGCG	4950
	CCTACTCCTAGCGCCGG	4951
	CCGGCGCTAGGAGTAGG	4952
Male-sterile Silky1 <i>Zea mays</i> Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCG CCGGACGGGGATCATGTAGAAGGCACGCGAGCTCACCGTGCTCT GCGACGCCCAGGTCGCCATCATCATGTTCTCCT	4953
	AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG AGCTCGCGTGCCTTCTACATGATCCCCGTCCGGCGCTTGAGTAG GTCACCTGGCGGTTGGTGGCGTTCTCGATCCG	4954
	GGATCATGTAGAAGGCA	4955
	TGCCTTCTACATGATCC	4956
Male-sterile Silky1 <i>Zea mays</i> Lys31Term AAG-TAG	ATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCGCCG GACGGGGATCATGAAGTAGGCACGCGAGCTCACCGTGCTCTGCG ACGCCCAGGTCGCCATCATCATGTTCTCCTCCA	4957
	TGGAGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACG GTGAGCTCGCGTGCCTACTTCATGATCCCCGTCCGGCGCTTGAG TAGGTACCTGGCGGTTGGTGGCGTTCTCGAT	4958
	TCATGAAGTAGGCACGC	4959
	GCGTGCCTACTTCATGA	4960
Male-sterile AP3 <i>Oryza sativa</i> Lys5Term AAG-TAG	GCTAGCTGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGC GGCCATGGGGAGGGGCTAGATCGAGATCAAGCGGATCGAGAACG CGACCAACAGGCAGGTGACCTACTCGAAGCGCC	4961
	GGCGCTTCGAGTAGGTCACCTGCCTGTTGGTTCGCGTTCTCGATCC GCTTGATCTCGATCTAGCCCCTCCCCATGGCCGCCCCCTGCAGCA GCTATCTCTCTCGCCGACAATGCAGCTAGC	4962
	GGAGGGGCTAGATCGAG	4963
	CTCGATCTAGCCCCTCC	4964
Male-sterile AP3 <i>Oryza sativa</i> Glu7Term GAG-TAG	TGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCAT GGGGAGGGGCAAGATCTAGATCAAGCGGATCGAGAACGCGACCA ACAGGCAGGTGACCTACTCGAAGCGCCGCACGG	4965
	CCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTTCGCGTTCT CGATCCGCTTGATCTAGATCTTGCCCCTCCCCATGGCCGCCCCCT GCAGCAGCTATCTCTCTCGCCGACAATGCA	4966
	GCAAGATCTAGATCAAG	4967
	CTTGATCTAGATCTTGC	4968

Male-sterile AP3 <i>Oryza sativa</i> Lys9Term AAG-TAG	GTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGA GGGGCAAGATCGAGATCTAGCGGATCGAGAACGCGACCAACAGG CAGGTGACCTACTCGAAGCGCCGCACGGGGATCA	4969
	TGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCG CGTTCTCGATCCGCTAGATCTCGATCTTGCCCCTCCCCATGGCCG CCCCCTGCAGCAGCTATCTCTCTCGCCGGAC	4970
	TCGAGATCTAGCGGATC	4971
	GATCCGCTAGATCTCGA	4972
Male-sterile AP3 <i>Oryza sativa</i> Glu12Term GAG-TAG	GAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCAAGA TCGAGATCAAGCGGATCTAGAACGCGACCAACAGGCAGGTGACCT ACTCGAAGCGCCGCACGGGGATCATGAAGAAGG	4973
	CCTTCTTCATGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCC TGTTGGTCGCGTTCTAGATCCGCTTGATCTCGATCTTGCCCCTCCC CATGGCCGCCCCCTGCAGCAGCTATCTCTC	4974
	AGCGGATCTAGAACGCG	4975
	CGCGTTCTAGATCCGCT	4976

Table 33
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG <i>Arabidopsis thaliana</i> Tyr35Term TAC-TAG	TCTGTACTAATCAAATTTTGGCCTAAACGTTTTTGGCTTTGGAGCA GCAATCACGGCGTAGCAATCGGAGCTAGGAGGAGATTCTCTCC CTTGAGGAAATCTGGGAGAGGAAAGATCGAA	4977
	TTCGATCTTCTCTCTCCAGATTTCTCAAGGGAGAGGAATCTCCT CCTAGCTCCGATTGCTACGCCGTGATTGCTGCTCCAAAGCCAAA ACGTTTAGGGCAAATTTGATTAGTACAGA	4978
	ACGGCGTAGCAATCGGA	4979
	TCCGATTGCTACGCCGT	4980
Male-sterile AG <i>Arabidopsis thaliana</i> Gln36Term CAA-TAA	CTGTACTAATCAAATTTTGGCCTAAACGTTTTTGGCTTTGGAGCAG CAATCACGGCGTACTAATCGGAGCTAGGAGGAGATTCTCTCCCT TGAGGAAATCTGGGAGAGGAAAGATCGAAA	4981
	TTTCGATCTTCTCTCTCCAGATTTCTCAAGGGAGAGGAATCTCC TCCTAGCTCCGATTAGTACGCCGTGATTGCTGCTCCAAAGCCAAA AACGTTTAGGGCAAATTTGATTAGTACAG	4982
	CGGCGTACTAATCGGAG	4983
	CTCCGATTAGTACGCCG	4984

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG <i>Arabidopsis thaliana</i> Ser37Term TCG-TAG	ACTAATCAAATTTTGGCCTAAACGTTTTTGGCTTTGGAGCAGCAAT CACGGCGTACCAATAGGAGCTAGGAGGAGATTCTCTCCCTTGA GGAAATCTGGGAGAGGAAAGATCGAAATCAA	4985
	TTGATTTGATCTTTCTCTCCAGATTTCTCAAGGGAGAGGAAT CTCCTCCTAGCTCCTATTGGTACGCCGTGATTGCTGCTCCAAAGC CAAAAACGTTTAGGGCAAATTTGATTAGT	4986
	GTACCAATAGGAGCTAG	4987
	CTAGCTCCTATTGGTAC	4988
Male-sterile AG <i>Arabidopsis thaliana</i> Glu38Term GAG-TAG	TAATCAAATTTTGGCCTAAACGTTTTTGGCTTTGGAGCAGCAATCA CGGCGTACCAATCGTAGCTAGGAGGAGATTCTCTCCCTTGAGGA AATCTGGGAGAGGAAAGATCGAAATCAAAC	4989
	GTTTGATTTGATCTTTCTCTCCAGATTTCTCAAGGGAGAGGA ATCTCCTCCTAGCTACGATTGGTACGCCGTGATTGCTGCTCCAAA GCCAAAACGTTTAGGGCAAATTTGATTA	4990
	ACCAATCGTAGCTAGGA	4991
	TCCTAGCTACGATTGGT	4992
Male-sterile AG <i>Brassica napus</i> Glu3Term GAA-TAA	CTCTCCCACTTCTTTTCGGTGGTTTATTCATTTGGTGACGATATCA CAGAAGCAATGGATTAAGGTGGGAGTAGTCACGATGCAGAGAGT AGCAAGAAGATAGGTAGAGGGAAGATAGAGA	4993
	TCTCTATCTTCCCTCTACCTATCTTCTTGCTACTCTCTGCATCGTGA CTACTCCACCTTAATCCATTGCTTCTGTGATATCGTCACCAAATG AATAAACCACCGAAAAGAAGTGGGAGAG	4994
	CAATGGATTAAGGTGGG	4995
	CCCACCTTAATCCATTG	4996
Male-sterile AG <i>Brassica napus</i> Glu11Term GAG-TAG	TATTCATTTGGTGACGATATCACAGAAGCAATGGATGAAGGTGGG AGTAGTCACGATGCATAGAGTAGCAAGAAGATAGGTAGAGGGAA GATAGAGATAAAGAGGATAGAGAACACAACAA	4997
	TTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCTCTACCTATC TTCTTGCTACTCTATGCATCGTGACTACTCCACCTTCATCCATTG CTTCTGTGATATCGTCACCAAATGAATA	4998
	ACGATGCATAGAGTAGC	4999
	GCTACTCTATGCATCGT	5000
Male-sterile AG <i>Brassica napus</i> Lys14Term AAG-TAG	GGTGACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCA CGATGCAGAGAGTAGCTAGAAGATAGGTAGAGGGAAGATAGAGA TAAAGAGGATAGAGAACACAACAAATCGTCAAG	5001
	CTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCT CTACCTATCTTCTAGCTACTCTCTGCATCGTGACTACTCCACCTT CATCCATTGCTTCTGTGATATCGTCACC	5002
	AGAGTAGCTAGAAGATA	5003
	TATCTTCTAGCTACTCT	5004

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG <i>Brassica napus</i> Lys15Term AAG-TAG	GACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGA TGCAGAGAGTAGCAAGTAGATAGGTAGAGGGAAGATAGAGATAAA GAGGATAGAGAACACAACAAATCGTCAAGTAA	5005
	TACTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTC CCTCTACCTATCTACTTGCTACTCTCTGCATCGTGACTACTCCCAC CTTCATCCATTGCTTCTGTGATATCGTC	5006
	GTAGCAAGTAGATAGGT	5007
	ACCTATCTACTTGCTAC	5008
Male-sterile AG <i>Lycopersicon esculentum</i> Glu4Term CAA-TAA	CAACCAAAAACTTAAAAATCTTCTCTTTCCTTTCCTTACAAGGTGA AGTAATGGACTTCTAAAGTGATCTAACCAGAGAGATCTCACCACAA AGGAACTAGGAAGGGGAAAATTGAGA	5009
	TCTCAATTTTCCCCCTTCTAGTTTCCTTGTGGTGAGATCTCTCT GGTTAGATCACTTTAGAAGTCCATTACTTCACCTTGTAAGGAAAGG AAAGAGAAGATTTTAAAGTTTTTGGTTG	5010
	TGGACTTCTAAAGTGAT	5011
	ATCACTTTAGAAGTCCA	5012
Male-sterile AG <i>Lycopersicon esculentum</i> Arg9Term AGA-TGA	AAAATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCC AAAGTGATCTAACCIGAGAGATCTCACCACAAAGGAAACTAGGAA GGGGGAAAATTGAGATCAAAGGATCGAAA	5013
	TTTCGATCCTTTTGATCTCAATTTCCCCCTTCTAGTTTCCTTGT GGTGAGATCTCTCAGGTTAGATCACTTTGGAAGTCCATTACTTCAC CTTGTAAGGAAAGGAAAGAGAAGATTTT	5014
	ATCTAACCIGAGAGATC	5015
	GATCTCTCAGGTTAGAT	5016
Male-sterile AG <i>Lycopersicon esculentum</i> Glu10Term GAG-TAG	ATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAA GTGATCTAACCAGATAGATCTCACCACAAAGGAACTAGGAAGGG GGAAAATTGAGATCAAAGGATCGAAAACA	5017
	TGTTTTCGATCCTTTTGATCTCAATTTCCCCCTTCTAGTTTCCTT TGTGGTGAGATCTATCTGGTTAGATCACTTTGGAAGTCCATTACTT CACCTTGTAAGGAAAGGAAAGAGAAGAT	5018
	TAACCAGATAGATCTCA	5019
	TGAGATCTATCTGGTTA	5020
Male-sterile AG <i>Lycopersicon esculentum</i> Ser12Term TCA-TGA	CTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCT AACCAGAGAGATCTGACCACAAAGGAACTAGGAAGGGGGAAAA TTGAGATCAAAGGATCGAAAACACGACGAA	5021
	TTTCGTCGTGTTTTCGATCCTTTTGATCTCAATTTCCCCCTTCTAG TTTCCTTTGTGGTCAGATCTCTCTGGTTAGATCACTTTGGAAGTCC ATTACTTCACCTTGTAAGGAAAGGAAAG	5022
	AGAGATCTGACCACAAA	5023

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTTGTGGT <u>C</u> AGATCTCT	5024
Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln4Term CAA-TAA	GTA <u>C</u> TCTCTATTTTCATCTTCCAACCCTTTCTTTCTTACCAGGTGA AAGTATGGACTTCTAAAGTGATCTAACAAGAGAGATCTCTCCACAA AGGAAACTGGGAAGAGGAAAGATTGAGA	5025
	TCTCAATCTTTCTCTTCCAGTTTCCTTTGTGGAGAGATCTCTCTT GTTAGATCACTTTA <u>A</u> GAAGTCCATACTTTACCTGGTAAGGAAAGAA AGGGTTGGAAGATGAAAATAGAGAGTAC	5026
	TGGACTTCTAAAGTGAT	5027
	ATCACTTTA <u>A</u> GAAGTCCA	5028
Male-sterile NAG1 <i>Nicotiana tabacum</i> Arg9Term AGA-TGA	ATCTTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTCC AAAGTGATCTAACA <u>T</u> GAGAGATCTCTCCACAAAGGAAACTGGGAA GAGGAAAGATTGAGATCAAACGGATCGAAA	5029
	TTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCAGTTTCCTTTGT GGAGAGATCTCTC <u>A</u> TGTTAGATCACTTTGGAAGTCCATACTTTCAC CTGGTAAGGAAAGAAAGGGTTGGAAGAT	5030
	ATCTAACA <u>T</u> GAGAGATC	5031
	GATCTCTC <u>A</u> TGTTAGAT	5032
Male-sterile NAG1 <i>Nicotiana tabacum</i> Glu10Term GAG-TAG	TTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTCCAAA GTGATCTAACAAGATAGATCTCTCCACAAAGGAAACTGGGAAGAG GAAAGATTGAGATCAAACGGATCGAAAACA	5033
	TGTTTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCAGTTTCCTT TGTGGAGAGATCTA <u>T</u> CTTGTAGATCACTTTGGAAGTCCATACTTT CACCTGGTAAGGAAAGAAAGGGTTGGAA	5034
	TAACAAGATAGATCTCT	5035
	AGAGATCTA <u>T</u> CTTGTTA	5036
Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln14Term CAA-TAA	CTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACA GAGAGATCTCTCCATAAAGGAAACTGGGAAGAGGAAAGATTGAGA TCAAACGGATCGAAAACACAACGAATCGTC	5037
	GACGATTGTTGTGTTTTCGATCCGTTTGATCTCAATCTTTCCTCTT CCCAGTTTCCTTTA <u>T</u> GGAGAGATCTCTCTTGTAGATCACTTTGGA AGTCCATACTTTCACCTGGTAAGGAAAG	5038
	TCTCTCCA <u>T</u> AAAGGAAA	5039
	TTTCCTTTA <u>T</u> GGAGAGA	5040
Male-sterile AG <i>Rosa hybrida</i> Gly22Term GGA-TGA	GCCTATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAA AGAAGATTGGGAAGGTGAAAGATCGAGATCAAGCGGATCGAAAA CACCACCAATCGTCAAGTCACCTTCTGCAAAA	5041
	TTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTCGATCCGCT TGATCTCGATCTTTCACCTTCCAATCTTCTTTGGGCATCAGCGTC CAGGACCGTGTTGGGTTGTTTTCATAGGC	5042
	TGGGAAGGTGAAAGATC	5043

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GATCTTTCACCTTCCCA	5044
Male-sterile AG <i>Rosa hybrida</i> Lys23Term AAG-TAG	TATGAAACAAACCCAAACACGGTCCTGGACGCTGATGCCCAAAGA AGATTGGGAAGGGGATAGATCGAGATCAAGCGGATCGAAAACAC CACCAATCGTCAAGTCACCTTCTGCAAAAGGC	5045
	GCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTCGATCC GCTTGATCTCGATCTATCCCCTTCCCAATCTTCTTTGGGCATCAGC GTCCAGGACCGTGTTGGGTTTGTTCATA	5046
	GAAGGGGATAGATCGAG	5047
	CTCGATCTATCCCCTTC	5048
Male-sterile AG <i>Rosa hybrida</i> Glu25Term GAG-TAG	AACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTG GGAAGGGGAAAGATCTAGATCAAGCGGATCGAAAACACCACCAA TCGTCAAGTCACCTTCTGCAAAAGGCGCAATG	5049
	CATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTC CGATCCGCTTGATCTAGATCTTCCCCTTCCCAATCTTCTTTGGGC ATCAGCGTCCAGGACCGTGTTGGGTTTGT	5050
	GAAAGATCTAGATCAAG	5051
	CTTGATCTAGATCTTTC	5052
Male-sterile AG <i>Rosa hybrida</i> Lys27 AAG-TAG	CCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAG GGGAAAGATCGAGATCTAGCGGATCGAAAACACCACCAATCGTCA AGTCACCTTCTGCAAAAGGCGCAATGGTTTGC	5053
	GCAAACCATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGG TGTTTCGATCCGCTAGATCTCGATCTTCCCCTTCCCAATCTTCT TTGGGCATCAGCGTCCAGGACCGTGTTGGG	5054
	TCGAGATCTAGCGGATC	5055
	GATCCGCTAGATCTCGA	5056
Male-sterile far <i>Antirrhinum majus</i> Gln7Term CAA-TAA	CAATTGCCTGTTTTATTTTTTTCTTTTTGACTAAGTAGAAATGGC GTCTCTAAGCGATTAATCGACCGAGGTATCGCCCGAGAGGAAAT CGGGAGAGGAAAGATCGAGATCAAACGGA	5057
	TCCGTTTGATCTCGATCTTCTCTCCCGATTTTCTCTCGGGCGA TACCTCGGTCGATTAAATCGCTTAGAGACGCCATTTCTACTTAGTCA AAAAGAAAAAAATAAAAAACAGGCAATTG	5058
	TAAGCGATTAAATCGACC	5059
	GGTCGATTAAATCGCTTA	5060
Male-sterile far <i>Antirrhinum majus</i> Glu10Term GAG-TAG	GTTTTATTTTTTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAG CGATCAATCGACCTAGGTATCGCCCGAGAGGAAATCGGGAGAG GAAAGATCGAGATCAAACGGATCGAAAACA	5061
	TGTTTCGATCCGTTTGATCTCGATCTTCTCTCCCGATTTTCTC TCGGGCGATACCTAGGTCGATTGATCGCTTAGAGACGCCATTTCT ACTTAGTCAAAAAGAAAAAAATAAAAAAC	5062
	AATCGACCTAGGTATCG	5063

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGATACCTAGGTCGATT	5064
Male-sterile far <i>Antirrhinum majus</i> Glu14Term GAG-TAG	TTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGA CCGAGGTATCGCCCAGAGGAAAATCGGGAGAGGAAAGATCGAG ATCAAACGGATCGAAAACAAAACAAATCAAC	5065
	GTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTC CCGATTTTCCTCTAGGGCGATACCTCGGTGCGATTGATCGCTTAGA GACGCCATTTCTACTTAGTCAAAAAGAAA	5066
	TATCGCCCTAGAGGAAA	5067
	TTTCCTCTAGGGCGATA	5068
Male-sterile far <i>Antirrhinum majus</i> Lys16Term AAA-TAA	TTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGACCGAG GTATCGCCCGAGAGGTAAATCGGGAGAGGAAAGATCGAGATCAA ACGGATCGAAAACAAAACAAATCAACAGGTTA	5069
	TAACCTGTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTT CCTCTCCCGATTTACCTCTCGGGCGATACCTCGGTGCGATTGATCG CTTAGAGACGCCATTTCTACTTAGTCAAA	5070
	CCGAGAGGTAAATCGGG	5071
	CCCGATTTACCTCTCGG	5072
Male-sterile AG <i>Cucumis sativus</i> Leu21Term TTG-TAG	TGTCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGA AGGAAAGGGTAAGTAGCAAATAAAGGGGATGTTCCAGAATCAAGA AGAGAAGATGTCAGACTCGCCTCAGAGGAA	5073
	TTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAACA TCCCCTTTATTTGCTACTTACCCTTTCTTCTTCTTAATCATTCTT GTGAGTGGTGACTGATAATGCTTGACA	5074
	GGGTAAGTAGCAAATAA	5075
	TTATTTGCTACTTACCC	5076
Male-sterile AG <i>Cucumis sativus</i> Gln22Term CAA-TAA	TCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAA GGAAAGGGTAAGTTGTAAATAAAGGGGATGTTCCAGAATCAAGAA GAGAAGATGTCAGACTCGCCTCAGAGGAAGA	5077
	TCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAA CATCCCCTTTATTTCAACTTACCCTTTCTTCTTCTTAATCATTCT TTGTGAGTGGTGACTGATAATGCTTGGA	5078
	GTAAGTTGTAAATAAAG	5079
	CTTTATTTCAACTTAC	5080
Male-sterile AG <i>Cucumis sativus</i> Lys24Term AAG-TAG	CATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAG GGTAAGTTGCAAATAAGGGGATGTTCCAGAATCAAGAAGAGAAG ATGTCAGACTCGCCTCAGAGGAAGATGGGAA	5081
	TTCCCATCTTCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATT CTGGAACATCCCCTATATTTGCAACTTACCCTTTCTTCTTCTTA TCATTCTTGTGAGTGGTGACTGATAATG	5082
	TGCAAATATAGGGGATG	5083

[illegible]

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTGCTCCT <u>A</u> GACCTTGG	5104
Male-sterile AG <i>Zea mays</i> Arg4Term CGA-TGA	TCCTACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACA AGAGCATGCACATCTGAGAAGAGGAGGCTACACCATCCACAGTAA CAGGCATCATGTGACCCCTGACTTCGGCGG	5105
	CCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGT GTAGCCTCCTCTTCTC <u>A</u> GATGTGCATGCTCTTGTTCTATCACACA GATTTTGAGGTCTGAAGGAGAAAAGGTAGGA	5106
	TGCACATCTGAGAAGAG	5107
	CTCTTCTC <u>A</u> GATGTGCA	5108
Male-sterile AG <i>Zea mays</i> Glu5Term GAA-TAA	TACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGA GCATGCACATCCGAT <u>A</u> AAGAGGAGGCTACACCATCCACAGTAACAG GCATCATGTGACCCCTGACTTCGGCGGGGC	5109
	GCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGAT GGTGTAGCCTCCTCTT <u>A</u> TCGGATGTGCATGCTCTTGTTCTATCAC ACAGATTTTGAGGTCTGAAGGAGAAAAGGTA	5110
	ACATCCGAT <u>A</u> AAGAGGAG	5111
	CTCCTCTT <u>A</u> TCGGATGT	5112
Male-sterile AG <i>Zea mays</i> Glu6Term GAG-TAG	CTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCA TGCACATCCGAGAATAGGAGGCTACACCATCCACAGTAACAGGCA TCATGTGACCCCTGACTTCGGCGGGGCAGC	5113
	GCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTG GATGGTGTAGCCTCCT <u>A</u> TTCTCGGATGTGCATGCTCTTGTTCTAT CACACAGATTTTGAGGTCTGAAGGAGAAAAG	5114
	TCCGAGAATAGGAGGCT	5115
	AGCCTCCT <u>A</u> TTCTCGGA	5116
Male-sterile AG <i>Zea mays</i> Glu7Term GAG-TAG	TTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATG CACATCCGAGAAGAGTAGGCTACACCATCCACAGTAACAGGCATC ATGTGACCCCTGACTTCGGCGGGGCAGCAGA	5117
	TCTGCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACT GTGGATGGTGTAGCCT <u>A</u> CTCTTCTCGGATGTGCATGCTCTTGTTCT CTATCACACAGATTTTGAGGTCTGAAGGAGAA	5118
	GAGAAGAGTAGGCTACA	5119
	TGTAGCCT <u>A</u> CTCTTCTC	5120
Male-sterile AG <i>Oryza sativa</i> Lys5Term AAG-TAG	GCTGGGTCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGC GAGAAGATGGGGAGGGGGT <u>I</u> AGATCGAGATAAAGCGGATCGAGAA CACGACGAACCGGCAGGTGACCTTCTGCAAGCGCC	5121
	GGCGCTTGCAAGAAGGTCACCTGCCGGTTCTGCTGTTCTCGATC CGCTTTATCTCGATCT <u>A</u> CCCCCTCCCCATCTTCTCGCTGCTCCCC GCCGCCACCGCCGCCGACGATCCTGACCCAGC	5122
	GGAGGGGGT <u>I</u> AGATCGAG	5123

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTCGATCT <u>A</u> CCCCCTCC	5124
Male-sterile AG <i>Oryza sativa</i> Glu7Term GAG-TAG	TCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGA TGGGGAGGGGGAAGATCTAGATAAAGCGGATCGAGAACACGACG AACCGGCAGGTGACCTTCTGCAAGCGCCGCAATG	5125
	CATTGCGGCGCTTGCAAGAAGGTCACCTGCCGGTTCGTCGTGTTCT CGATCCGCTTTATCTAGATCTTCCCCCTCCCCATCTTCTCGCTGCT CCCCGCCGCCACCGCCGCCGACGATCCTGA	5126
	GGAAGATCTAGATAAAG	5127
	CTTTATCTAGATCTTCC	5128
Male-sterile AG <i>Oryza sativa</i> Lys9Term AAG-TAG	TCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGG AGGGGGAAGATCGAGATAAGCGGATCGAGAACACGACGAACCG GCAGGTGACCTTCTGCAAGCGCCGCAATGGCCTCC	5129
	GGAGGCCATTGCGGCGCTTGCAAGAAGGTCACCTGCCGGTTCGTC GTGTTCTCGATCCGCTATATCTCGATCTTCCCCCTCCCCATCTTCT CGCTGCTCCCCGCCGCCACCGCCGCCGACGA	5130
	TCGAGATATAGCGGATC	5131
	GATCCGCTATATCTCGA	5132
Male-sterile AG <i>Oryza sativa</i> Glu12Term GAG-TAG	GCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAG ATCGAGATAAAGCGGATCTAGAACACGACGAACCGGCAGGTGAC CTTCTGCAAGCGCCGCAATGGCCTCCTGAAGAAGG	5133
	CCTTCTTCAGGAGGCCATTGCGGCGCTTGCAAGAAGGTCACCTGC CGGTTCTGTCGTGTTCTAGATCCGCTTTATCTCGATCTTCCCCCTCC CCATCTTCTCGCTGCTCCCCGCCGCCACCGC	5134
	AGCGGATCTAGAACACG	5135
	CGTGTTCTAGATCCGCT	5136

Table 34
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI <i>Cucumis sativus</i> Tyr21Term TAT-TAG	GGGAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAA TAGACAAGTTACATAGTCAAAGAGAAGAAATGGTATCATCAAAAAA GCCAAAGAAATTACTGTTCTTTGCGATGCT	5137
	AGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCAT TTCTTCTCTTTGACTATGTAACCTGTCTATTGCTTGAGTTCTCTATTC TTTTTATTTCTATTTTCCCTCTTCCC	5138
	GTTACATAGTCAAAGAG	5139
	CTCTTTGACTATGTAAC	5140
Male-sterile PI <i>Cucumis sativus</i> Ser22Term TCA-TGA	GAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATA GACAAGTTACATATTGAAAGAGAAGAAATGGTATCATCAAAAAAGC CAAAGAAATTACTGTTCTTTGCGATGCTCA	5141
	TGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATAC CATTTCTTCTCTTTCAATATGTAACCTGTCTATTGCTTGAGTTCTCTA TTCTTTTTATTTCTATTTTCCCTCTTC	5142
	TACATATTGAAAGAGAA	5143
	TTCTCTTTCAATATGTA	5144
Male-sterile PI <i>Cucumis sativus</i> Lys23Term AAG-TAG	AGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGAC AAGTTACATATTCATAGAGAAGAAATGGTATCATCAAAAAAGCCAA AGAAATTACTGTTCTTTGCGATGCTCAAG	5145
	CTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATA CCATTTCTTCTCTATGAATATGTAACCTGTCTATTGCTTGAGTTCTC TATTCTTTTTATTTCTATTTTCCCTCT	5146
	CATATTCATAGAGAAGA	5147
	TCTTCTCTATGAATATG	5148
Male-sterile PI <i>Cucumis sativus</i> Arg24Term AGA-TGA	GGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAG TTACATATTCAAAGTGAAGAAATGGTATCATCAAAAAAGCCAAAGA AATTACTGTTCTTTGCGATGCTCAAGTTT	5149
	AACTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATG ATACCATTTCTTCACTTTGAATATGTAACCTGTCTATTGCTTGAGTT CTCTATTCTTTTTATTTCTATTTTCCC	5150
	ATTCAAAGTGAAGAAAT	5151
	ATTTCTTCACTTTGAAT	5152
Male-sterile PI <i>Malus domestica</i> Tyr21Term TAC-TAG	GGGACGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAA CAGGCAGGTGACCTAGTCCAAGAGGAGGAATGGGATTATCAAGAA GGCAAAGGAGATCACTGTTCTATGTGATGCT	5153
	AGCATCACATAGAACAGTGATCTCCTTTGCCTTTTGATAATCCCA TTCTCCTCTTGGACTAGGTCACCTGCCTGTTACTTGAGTTCTCAA TCCTCTTGATCTCAACCTTCCCACGTCCC	5154

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTGACCTAGTCCAAGAG	5155
	CTCTTGGACTAGGTCAC	5156
Male-sterile PI <i>Malus domestica</i> Lys23Term AAG-TAG	CGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGG CAGGTGACCTACTCCTAGAGGAGGAATGGGATTATCAAGAAGGCA AAGGAGATCACTGTTCTATGTGATGCTAAAG	5157
	CTTTAGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATC CCATTCCTCCTCTAGGAGTAGGTCACCTGCCTGTTACTTGAGTTCT CAATCCTCTTGATCTCAACCTTCCCACG	5158
	CCTACTCCTAGAGGAGG	5159
	CCTCCTCTAGGAGTAGG	5160
Male-sterile PI <i>Malus domestica</i> Lys30Term AAG-TAG	AGGATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGG AGGAATGGGATTATCTAGAAGGCCAAAGGAGATCACTGTTCTATGT GATGCTAAAGTATCTCTTATCATTTATTCTA	5161
	TAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGTGAT CTCCTTTGCCTTCTAGATAATCCCATTCCCTCCTCTTGGAGTAGGTC ACCTGCCTGTTACTTGAGTTCTCAATCCT	5162
	GGATTATCTAGAAGGCA	5163
	TGCCTTCTAGATAATCC	5164
Male-sterile PI <i>Malus domestica</i> Lys31Term AAG-TAG	ATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGGAGG AATGGGATTATCAAGTAGGCCAAAGGAGATCACTGTTCTATGTGATG CTAAAGTATCTCTTATCATTTATTCTAGCT	5165
	AGCTAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGT GATCTCCTTTGCCTACTTGATAATCCCATTCCCTCCTCTTGGAGTAG GTCACCTGCCTGTTACTTGAGTTCTCAAT	5166
	TTATCAAGTAGGCCAAAG	5167
	CTTTGCCTACTTGATAA	5168
Male-sterile globosa <i>Antirrhinum majus</i> Gly2Term GGA-TGA	CATTTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAA AAACAAAAAATGTGAAGAGGAAAAATTGAGATCAAAAGAATTGAG AACTCAAGCAACAGGCAGGTTACTTACT	5169
	AGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTGATCTCA ATTTTTCCTCTTACATTTTTTTGTTTTTGTCTCTTGTGTTTTG TTTGCAGATAACTATTGTAAAAATG	5170
	AAAAAATGTGAAGAGGA	5171
	TCCTCTTACATTTTTT	5172

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile globosa <i>Antirrhinum majus</i> Arg3Term AGA-TGA	TTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAA CAAAAAATGGGATGAGGAAAAATTGAGATCAAAAGAATTGAGAAC TCAAGCAACAGGCAGGTTACTTACTCAA	5173
	TTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATC TCAATTTTTCCTCATCCCATTTTTTTGTTTTGTTTTCTCTCTTGT TTGTTTGCAGATAACTATTGTA	5174
	AAATGGGATGAGGAAAA	5175
	TTTTCCTCATCCCATTT	5176
Male-sterile globosa <i>Antirrhinum majus</i> Gly4Term GGA-TGA	TACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACA AAAAAATGGGAAGATGAAAAATTGAGATCAAAAGAATTGAGAACTC AAGCAACAGGCAGGTTACTTACTCAAAGA	5177
	TCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTG ATCTCAATTTTTCACTCTCCCATTTTTTTGTTTTGTTTTCTCTCTTG TTTTGTTTGCAGATAACTATTGTA	5178
	TGGGAAGATGAAAAATT	5179
	AATTTTTCACTCTCCCA	5180
Male-sterile globosa <i>Antirrhinum majus</i> Lys5Term AAA-TAA	AATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAA AAATGGGAAGAGGATAAATTGAGATCAAAAGAATTGAGAACTCAAG CAACAGGCAGGTTACTTACTCAAAGAGAA	5181
	TTCTCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTT TTGATCTCAATTTATCCTCTTCCCATTTTTTTGTTTTGTTTTCTCT CTTGTTTTGTTTGCAGATAACTATT	5182
	GAAGAGGATAAATTGAG	5183
	CTCAATTTATCCTCTTC	5184
Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG	GCTGAGCTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGC AGTATGGGGCGCGGCTAGATCAAGATCAAGAGGATCGAGAACTCT ACCAACCGGCAGGTGACCTTCTCCAAGCGCC	5185
	GGCGCTTGAGAAAGGTCACCTGCCGTTGGTAGAGTTCTCGATCC TCTTGATCTTGATCTAGCCGCGCCCCATACTGCGTTCTCCACTCCC AAACAGATCCAAGGGCAGCAAGAGCTCAGC	5186
	GGCGCGGCTAGATCAAG	5187
	CTTGATCTAGCCGCGCC	5188
Male-sterile PI <i>Zea mays</i> Lys7Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATG GGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5189
	CGGCCCGCGCTTGAGAAAGGTCACCTGCCGTTGGTAGAGTTC TCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTGCGTTCTC CACTCCCAAACAGATCCAAGGGCAGCAAGAG	5190

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCAAGATC <u>T</u> AGATCAAG	5191
	CTTGATCT <u>A</u> GATCTTGC	5192
Male-sterile PI <i>Zea mays</i> Lys9Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATG GGGCGCGGCAAGATC <u>T</u> AGATCAAGAGGATCGAGAAGCTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5193
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCT <u>A</u> GATCTTGCCGCGCCCCATACTGCGTTCTC CACTCCCAAACAGATCCAAGGGCAGCAAGAG	5194
	GCAAGATC <u>T</u> AGATCAAG	5195
	CTTGATCT <u>A</u> GATCTTGC	5196
Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG	GATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGAT CAAGATCAAGAGGATC <u>T</u> AGAACTCTACCAACCGGCAGGTGACCTT CTCCAAGCGCCGGGCCGACTGGTCAAGAAGG	5197
	CCTTCTTGACCACTCCGGCCCGCGCTTGGAGAAGGTCACCTGC CGGTTGGTAGAGTTCT <u>A</u> GATCCTCTTGATCTTGATCTTGCCGCGCC CCATACTGCGTTCTCCACTCCCAAACAGATC	5198
	AGAGGATC <u>T</u> AGAACTCT	5199
	AGAGTTCT <u>A</u> GATCCTCT	5200
Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG	GCTGAGCTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGG AGTATGGGGCGCGGCT <u>T</u> AGATCGAGATCAAGAGGATCGAGAAGCTCT ACCAACCGGCAGGTGACCTTCTCCAAGCGCC	5201
	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCC TCTTGATCTCGATCT <u>A</u> GCCGCGCCCCATACTCCGTTCTCCACTCCC TAACAGATTCAAGGGCAGCAAGAGCTCAGC	5202
	GGCGCGGCT <u>T</u> AGATCGAG	5203
	CTCGATCT <u>A</u> GCCGCGCC	5204
Male-sterile PI <i>Zea mays</i> Glu7Term GAG-TAG	CTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATG GGGCGCGGCAAGATC <u>T</u> AGATCAAGAGGATCGAGAAGCTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5205
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCT <u>A</u> GATCTTGCCGCGCCCCATACTCCGTTCTC CACTCCCTAACAGATTCAAGGGCAGCAAGAG	5206
	GCAAGATC <u>T</u> AGATCAAG	5207
	CTTGATCT <u>A</u> GATCTTGC	5208

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI <i>Zea mays</i> Lys9Term AAG-TAG	CTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCG CGGCAAGATCGAGATCTAGAGGATCGAGAACTCTACCAACCGGCA GGTGACCTTCTCCAAGCGCCGGGCGGACTGG	5209
	CCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTA GAGTTCTCGATCCTCTAGATCTCGATCTTGCCGCGCCCCATACTC CGTTCTCCACTCCCTAACAGATTCAAGGGCAG	5210
	TCGAGATCTAGAGGATC	5211
	GATCCTCTAGATCTCGA	5212
Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG	AATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGAT CGAGATCAAGAGGATCTAGA ACTCTACCAACCGGCAGGTGACCTT CTCCAAGCGCCGGGCGGACTGGTCAAGAAGG	5213
	CCTTCTTGACAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGC CGGTTGGTAGAGTTCTAGATCCTCTTGATCTCGATCTTGCCGCGC CCCATACTCCGTTCTCCACTCCCTAACAGATT	5214
	AGAGGATCTAGA ACTCT	5215
	AGAGTTCTAGATCCTCT	5216
Male-sterile PI <i>Oryza sativa</i> Lys5Term AAG-TAG	TTGCTGCTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGG CGGGATGGGGCGCGGGTAGATCGAGATCAAGAGGATCGAGAACT CCACCAACCGCCAGGTGACCTTCTCCAAGCGCA	5217
	TGCGCTTGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCC TCTTGATCTCGATCTACCCGCGCCCCATCCCGCCTCCTCCTCCTC CTCCTCCTCCTCCAGCTAGCTTAGCAGCAA	5218
	GGCGCGGGTAGATCGAG	5219
	CTCGATCTACCCGCGCC	5220
Male-sterile PI <i>Oryza sativa</i> Glu7Term GAG-TAG	CTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGA TGGGGCGCGGGAAGATCTAGATCAAGAGGATCGAGAACTCCACC AACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCG	5221
	CGTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCT CGATCCTCTTGATCTAGATCTTCCGCGCCCCATCCCGCCTCCTC CTCCTCCTCCTCCTCCTCCAGCTAGCTTAG	5222
	GGAAGATCTAGATCAAG	5223
	CTTGATCTAGATCTTCC	5224
Male-sterile PI <i>Oryza sativa</i> Lys9Term AAG-TAG	TAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGC GCGGGAAGATCGAGATCTAGAGGATCGAGAACTCCACCAACCGC CAGGTGACCTTCTCCAAGCGCAGGAGCGGGATCC	5225
	GGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTG GAGTTCTCGATCCTCTAGATCTCGATCTTCCGCGCCCCATCCCG CCTCCTCCTCCTCCTCCTCCTCCTCCTCCAGCTA	5226

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCGAGATC <u>T</u> AGAGGATC	5227
	GATCCTCT <u>A</u> GATCTCGA	5228
Male-sterile PI <i>Oryza sativa</i> Glu12Term GAG-TAG	GAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAG ATCGAGATCAAGAGGATC <u>T</u> AGAACTCCACCAACCGCCAGGTGACC TTCTCCAAGCGCAGGAGCGGGATCCTCAAGAAGG	5229
	CCTTCTTGAGGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGC GGTTGGTGGAGTTCT <u>A</u> GATCCTCTTGATCTCGATCTTCCCGCGCC CCATCCCGCCTCCTCCTCCTCCTCCTCCTC	5230
	AGAGGATC <u>T</u> AGAACTCC	5231
	GGAGTTCT <u>A</u> GATCCTCT	5232

Example 28

Engineering plants for abiotic stress tolerance

[249] Environmental stresses, such as drought, increased soil salinity, soil contamination with heavy metals, and extreme temperature, are major factors limiting plant growth and productivity. The worldwide loss in yield of three major cereal crops, rice, maize, and wheat due to water stress (drought) has been estimated to be over ten billion dollars annually and many currently marginal soils could be brought into cultivation if suitable plant varieties were available.

[250] Physiological and biochemical responses to high levels of ionic or nonionic solutes and decreased water potential have been studied in a variety of plants. It is known, for example, that increasing levels of alcohol dehydrogenase can confer enhanced flooding resistance in plants. There are also several possible mechanisms to enhance plant salt tolerance. For example, one mechanism underlying the adaptation or tolerance of plants to osmotic stresses is the accumulation of compatible, low molecular weight osmolytes such as sugar alcohols, special amino acids, and glycinebetaine. Such accumulation can be engineered, for example, by removing feedback inhibition on 1-pyrroline-t-carboxylate synthetase, which results in accumulation of proline. Additionally, recent experiments suggest that altering the expression or activity of specific sodium or potassium transporters can confer enhanced salt tolerance.

[251] Plant tolerance of contamination by heavy metals such as lead and aluminum in soils has also been investigated and one mechanism underlying tolerance is the production of dicarboxylic acids such as oxalate and citrate. In addition, individual genes involved in heavy metal sensitivity have been identified.

[252] The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer stress tolerance in plants.

Table 35
Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance P5CS <i>Arabidopsis thaliana</i> Phe128Ala TTT-GCT	CGTCTTTTTGTGTGGTAGTTGGATGTGACGGTTGCTCAAATGCTT GTGACCGATAGCAGT <u>GCT</u> AGAGATAAGGATTTTCAGGAAGCAACTT AGTGAAACTGTCAAAGCGATGCTGAGGATGA	5233
	TCATCCTCAGCATCGCTTTGACAGTTTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTAG <u>GC</u> ACTGCTATCGGTCACAAGCATTTGAGCAACC GTCACATCCAACCTACCACACAAAAAGACG	5234
	ATAGCAGT <u>GCT</u> AGAGAT	5235
	ATCTCTAG <u>GC</u> ACTGCTAT	5236
Salt Tolerance P5CS 1 <i>Brassica napus</i> Phe128Ala TTC-GCC	GAGACTATGTTTGACCAGCTGGATGTGACGGCTGCTCAGCTGCTG GTGAATGACAGTAGT <u>GCC</u> CAGAGACAAGGAGTTTCAGGAAGCAACTT AATGAGACAGTGAAGTCCATGCTTGATTTGA	5237
	TCAAATCAAGCATGGACTTCACTGTCTCATTAAAGTTGCTTCCTGAA CTCCTTGTCTCTG <u>GC</u> ACTACTGTCAATTCACCAGCAGCTGAGCAGC CGTCACATCCAGCTGGTCAAACATAGTCTC	5238
	ACAGTAGT <u>GCC</u> CAGAGAC	5239
	GTCTCTG <u>GC</u> ACTACTGT	5240
Salt Tolerance P5CS 2 <i>Brassica napus</i> Phe129Ala TTC-GCC	GAGACTATGTTTGACCAGATGGATGTGACGGTGGCTCAAATGCTG GTGACTGATAGCAGT <u>GTC</u> CAGAGATAAGGATTTTCAGGAAGCAACTT AGTGAGACAGTCAAAGCTATGCTGAAAATGA	5241
	TCATTTTCAGCATAGCTTTGACTGTCTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTGAC <u>ACT</u> GCTATCAGTCACCAGCATTTGAGCCACC GTCACATCCATCTGGTCAAACATAGTCTC	5242
	ATAGCAGT <u>GTC</u> CAGAGAT	5243
	ATCTCTGAC <u>ACT</u> GCTAT	5244
Salt Tolerance P5CS <i>Oryza sativa</i> Phe128Ala TTT-GCT	GATATGTTGTTTAACCAACTGGATGTCTCGTCATCTCAACTTCTTG TCACCGACAGTGAT <u>GCT</u> GAGAACCCAAAGTTCCGGGAGCAACTCA CTGAAACTGTTGAGTCATTATTAGATCTTA	5245
	TAAGATCTAATAATGACTCAACAGTTTCAGTGAGTTGCTCCCGGAA CTTTGGGTTCTCAG <u>GC</u> ATCACTGTCCGGTGACAAGAAGTTGAGATGA CGAGACATCCAGTTGGTTAAACAACATATC	5246
	ACAGTGAT <u>GCT</u> GAGAAC	5247
	GTTCTCAG <u>GC</u> ATCACTGT	5248

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance P5CS <i>Medicago sativa</i> Phe128Ala TTT-GCT	GATATTTTGTTCAGTCAGCTGGATGTGACATCTGCTCAGCTTCTTG TACTGACAATGATGCTAGAGACCAAGATTTTAGAAAGCAACTTTC TGAAACTGTGAGATCACTTCTAGCACTAA	5249
	TTAGTGCTAGAAGTGATCTCACAGTTTCAGAAAGTTGCTTTCTAAA ATCTTGGTCTCTAGCATCATTGTGAGTAACAAGAAGCTGAGCAGAT GTCACATCCAGCTGACTAAACAAAATATC	5250
	ACAATGATGCTAGAGAC	5251
	GTCTCTAGCATCATTGT	5252
Salt Tolerance P5CS <i>Actinidia deliciosa</i> Phe128Ala TTT-GCT	GATACATTGTTTAGTCAGCTGGATGTGACATCAGCTCAGCTACTC GTTACTGATAATGATGCTAGGGATCCAGAATTCAGGAAGCAACTT ACTGAACTGTAGAATCACTATTGAATTTGA	5253
	TCAAATTCAATAGTGATTCTACAGTTTCAGTAAGTTGCTTCCTGAAT TCTGGATCCCTAGCATCATTATCAGTAACGAGTAGCTGAGCTGAT GTCACATCCAGCTGACTAAACAATGTATC	5254
	ATAATGATGCTAGGGAT	5255
	ATCCCTAGCATCATTAT	5256
Salt Tolerance P5CS <i>Cichorium intybus</i> Phe122Ala TTC-GCC	GACACACTCTTCAGTCAACTGGATGTGACATCAGCACAGCTTCTT GTAACAGATAATGACGCCAGAAAGTCCAGAATTTAGAAAACAACCTTA CTGAAACAGTCGATTCTTTATTATCTTATA	5257
	TATAAGATAATAAAGAATCGACTGTTTCAGTAAGTTGTTTTCTAAAT TCTGGACTTCTGGCGTCATTATCTGTTACAAGAAGCTGTGCTGAT GTCACATCCAGTTGACTGAAGAGTGTGTC	5258
	ATAATGACGCCAGAAAGT	5259
	ACTTCTGGCGTCATTAT	5260
Salt Tolerance P5CS <i>Lycopersicon esculentum</i> Phe128Ala TTT-GCT	GATTCTTTGTTTCAGTCAGTTGGATGTGACATCAGCTCAGCTTCTGG TGACTGATAATGACGCTAGAGATCCAGATTTTAGGAGACAACCTCA ATGACACAGTAAATTCGTTGCTTTCTCTAA	5261
	TTAGAGAAAGCAACGAATTTACTGTGTCATTGAGTTGTCTCCTAAA ATCTGGATCTCTAGCGTCATTATCAGTCACCAGAAGCTGAGCTGA TGTCACATCCAACGACTGAACAAAGAATC	5262
	ATAATGACGCTAGAGAT	5263
	ATCTCTAGCGTCATTAT	5264
Salt Tolerance P5CS <i>Vigna unguiculata</i> Phe162Ala TTT-GCT	GATACCATGTTTCAGCCAGCTTGATGTGACTTCTTCCCAACTTCTTG TGAATGATGGATTTGCTAGGGATGCTGGCTTCAGAAAACAACCTT CGGACACAGTGAACGCGTTATTAGATTTAA	5265
	TTAAATCTAATAACGCGTTCACTGTGTCCGAAAGTTGTTTTCTGAA GCCAGCATCCCTAGCAAATCCATCATTACAAGAAGTTGGGAAGA AGTCACATCAAGCTGGCTGAACATGGTATC	5266
	ATGGATTTGCTAGGGAT	5267

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATCCCTAGC AAAT CCAT	5268
Salt Tolerance P5CS <i>Mesembryanthemum crystallinum</i> Phe125Ala TTT-GCT	GACACCTTGTTTAGTCAGTTGGATCTGACTGCTGCTCAGCTGCTT GTGACGGACAACGAC GCT AGAGATCCAAGTTTTAGAACACAACCTA ACTGAAACAGTGTATCAGTTGTTGGATCTAA	5269
	TTAGATCCAACAACCTGATACACTGTTTCAGTTAGTTGTGTTCTAAA ACTTGATCTCTAG CGT CGTTGTCCGTCACAAGCAGCTGAGCAGC AGTCAGATCCAACCTGACTAAACAAGGTGTC	5270
	ACAACGAC GCT AGAGAT	5271
	ATCTCTAG CGT CGTTGT	5272
Salt Tolerance P5CS <i>Vitis vinifera</i> Phe130Ala TTT-GCT	GACACATTATTTAGCCAGCTGGATGTGACATCAGCTCAGCTTCTT GTGACTGATAATGAT GCT AGGGATGAAGCTTTCCGAAATCAACTTA CTCAAACAGTGGATTCAATTGTTAGCTTTGA	5273
	TCAAAGCTAACAATGAATCCACTGTTTGAGTAAGTTGATTTCCGAA AGCTTCATCCCTAG GC ATCATTATCAGTCACAAGAAGCTGAGCTGAT GTCACATCCAGCTGGCTAAATAATGTGTC	5274
	ATAATGAT GCT AGGGAT	5275
	ATCCCTAG GC ATCATTAT	5276
Salt Tolerance P5CS <i>Vigna aconitifolia</i> Phe129Ala TTT-GCT	GATACGCTGTTCACTCAGCTCGATGTGACATCGGCTCAGCTTCTT GTGACGGATAACGAT GCT CGAGATAAGGATTTAGGAAGCAGCTT ACTGAGACTGTGAAGTCGCTGTTGGCGCTGA	5277
	TCAGCGCCAACAGCGACTTCACAGTCTCAGTAAGCTGCTTCCTGA AATCCTTATCTCGAG GC ATCGTTATCCGTCACAAGAAGCTGAGCCG ATGTCACATCGAGCTGAGTGAACAGCGTATC	5278
	ATAACGAT GCT CGAGAT	5279
	ATCTCGAG GC ATCGTTAT	5280
Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Ser207Val TCC-GTC	AGAGATGTTCTTAGTTCCAAAGAAATCTCACCTCTCACTTTCTCCG TCTTCACAACAGTT GT CACGTTTGCAAACCTGCGGATTTGCCCCAC GAATGAGAACATGATCATCTTTGCAAAA	5281
	TTTTGCGAAAGATGATCATGTTCTCATTCTGTTGGGGACAAATCCGC AGTTTGCAAACGTG ACA AACTGTTGTGAAGACGGAGAAAGTGAGAG GTGAGATTTCTTTGGAACCTAAGAACATCTCT	5282
	CAACAGTT GT CACGTTT	5283
	AAACGTG ACA AACTGTTG	5284
Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Gln237Leu CAA-CTA	CGAATGAGAACATGATCATCTTTGCAAAAACCTCTGGTCTCATCTG GCTCCTAATCCCTC T AGTACTGATGGGAAACACTTTGTTCCCTTGC TTCTTGTTTTGCTCATATGGGGACTTTA	5285
	TAAAGTCCCCATATGAGCAAAACCAAGAAGCAAGGGGAACAAAGTG TTTCCCATCAGTACT A GAGGGATTAGGAGCCAGATGAGACCAGAG TTTTTGCGAAAGATGATCATGTTCTCATTCTG	5286

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCCCTCTAGTACTGA	5287
	TCAGTACTAGAGGGATT	5288
Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Asn332Ser AAT-AGT	AGTCTCTAGAAGGAATGAGTTCGTACGAGAAGTTGGTTGGATCGT TGTTTCAAGTGGTGAAGTTCGCGACACACCGGAGAACTATAGTAG ACCTCTCTACACTTTCCCCAGCTATCTTGGT	5289
	ACCAAGATAGCTGGGGAAAGTGTAGAGAGGTCTACTATAGTTTCT CCGGTGTGTCGCGAACTCACCACCTGAAACAACGATCCAACCAAC TTCTCGTACGAACCTATTCTTCTAGAGACT	5290
	AGTGGTGAGTTCGCGAC	5291
	GTCGCGAACTCACCACCT	5292
Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Ser256Val TCG-GTG	AGAGATGTGCTAAAGAAGAAAGGTCTCAAAATGGTGACCTTTTCC GTCTTCACCACCGTGAGTACCTTTGCCAGTTGTGGGTTTGTCCCG ACCAATGAAAACATGATTATCTTCAGCAAAA	5293
	TTTTGCTGAAGATAATCATGTTTTATTGGTCGGGACAAACCCACA ACTGGCAAAGGTCACACCGGTGGTGAAGACGGAAAAGGTCACCA TTTTGAGACCTTTCTTCTTTAGCACATCTCT	5294
	CCACCGTGAGTACCTTT	5295
	AAAGGTCACACCGGTGG	5296
Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Gln286Leu CAG-CTG	CCAATGAAAACATGATTATCTTCAGCAAAAACCTCTGGCCTCCTCCT GATTCTCATCCCTCTGGCCCTTCTTGGGAACATGCTGTTCCCATC GAGCCTACGTTTGACGCTTTGGCTCATCGG	5297
	CCGATGAGCCAAAGCGTCAAACGTAGGCTCGATGGGAACAGCAT GTTCCCAAGAAGGGCCAGAGGGATGAGAATCAGGAGGAGGCCA GAGTTTTTGCTGAAGATAATCATGTTTTATTGG	5298
	CATCCCTCTGGCCCTTC	5299
	GAAGGGCCAGAGGGATG	5300
Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Asn381Ser AAC-AGC	AATCGTTGAATGGACTAAGCTCCTGTGAGAAAATCGTGGGCGCGC TGTTTCAGTGCGTGAGCAGCAGACATACCGGCGAGACGGTCGTC GATCTGTCCACAGTTGCTCCCGCCATCTTGGT	5301
	ACCAAGATGGCGGGAGCAACTGTGGACAGATCGACGACCGTCTC GCCGGTATGTCTGCTGCTCACGCACTGAAACAGCGCGCCACGA TTTTCTCACAGGAGCTTAGTCCATTCAACGATT	5302
	GTGCGTGAGCAGCAGAC	5303
	GTCTGCTGCTCACGCAC	5304

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance HKT1 <i>Oryza sativa</i> Ser238Val TCC-GTC	AAAGCTCCACTGAAGAAGAAAGGGATCAACATTGCACTCTTCTCA TTCTCGGTCACGGTC <u>G</u> TCTCGTTTGCGAATGTGGGGCTCGTGCC GACAAATGAGAACATGGCAATCTTCTCCAAGA	5305
	TCTTGAGAAGATTGCCATGTTCTCATTTGTGGGCACGAGCCCCA CATTCGCAAACGAG <u>A</u> CGACCGTGACCGAGAATGAGAAGAGTGCA ATGTTGATCCCTTTCTTCTTCAGTGGAGCTTT	5306
	TCACGGTC <u>G</u> TCTCGTTT	5307
	AAACGAG <u>A</u> CGACCGTGA	5308
Salt Tolerance HKT1 <i>Oryza sativa</i> Gln268Leu CAG-CTG	CAAATGAGAACATGGCAATCTTCTCCAAGAACCCGGGCCTCCTCC TCCTGTTTCATCGGCC <u>T</u> GATTCTTGCAAGCAATACACTTTACCTCT CTTCCTAAGGCTATTGATATGGTTCCCTGGG	5309
	CCCAGGAACCATATCAATAGCCTTAGGAAGAGAGGGTAAAGTGTA TTGCCTGCAAGAATC <u>A</u> GGCCGATGAACAGGAGGAGGAGGCCCGG GTTCTTGAGAAGATTGCCATGTTCTCATTTG	5310
	CATCGGCC <u>T</u> GATTCTTG	5311
	CAAGAATC <u>A</u> GGCCGATG	5312
Salt Tolerance HKT1 <i>Oryza sativa</i> Asn363Ser AAC-AGC	CAGTCTTTGATGGACTCAGCTCTTACCAGAAGATTATCAATGCATT GTTTCATGGCAGTGAG <u>C</u> CGCAAGGCACTCGGGGGAGAACTCCATCG ACTGCTCACTCATCGCCCCTGCTGTTCTAGT	5313
	ACTAGAACAGCAGGGGCGATGAGTGAGCAGTCGATGGAGTTCTC CCCCGAGTGCCTTGCG <u>C</u> TCACTGCCATGAACAATGCATTGATAAT CTTCTGGTAAGAGCTGAGTCCATCAAAGACTG	5314
	GGCAGTGAG <u>C</u> CGCAAGGC	5315
	GCCTTGCG <u>C</u> TCACTGCC	5316
Salt Tolerance HKT1 <i>Triticum aestivum</i> Ala240Val GCC-GTC	GTGCCCCACTGAACAAGAAAGGGATCAACATCGTGCTCTTCTCAC TATCAGTCACCGTTG <u>T</u> CTCCTGTGCGAATGCAGGACTCGTGCCCA CAAATGAGAACATGGTCATCTTCTCAAAGAA	5317
	TTCTTTGAGAAGATGACCATGTTCTCATTTGTGGGCACGAGTCCT GCATTGCGACAGGAG <u>A</u> CAACGGTGACTGATAGTGAGAAGAGCAC GATGTTGATCCCTTTCTTGTTTCAGTGGGGCAC	5318
	CACCGTTG <u>T</u> CTCCTGTG	5319
	CACAGGAG <u>A</u> CAACGGTG	5320
Salt Tolerance HKT1 <i>Triticum aestivum</i> Gln270Leu CAG-CTG	CAAATGAGAACATGGTCATCTTCTCAAAGAATTGAGGCCTCTTGTT GCTGCTGAGTGGCC <u>T</u> GATGCTCGCAGGCAATACATTGTTCCCTCT CTTCCTGAGGCTACTGGTGTGGTTCCCTGGG	5321
	CCCAGGAACCACACAGTAGCCTCAGGAAGAGAGGGGAACAATGT ATTGCCTGCGAGCATC <u>A</u> GGCCACTCAGCAGCAACAAGAGGCCTG AATTCTTTGAGAAGATGACCATGTTCTCATTTG	5322
	GAGTGGCC <u>T</u> GATGCTCG	5323

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGAGCATC <u>A</u> GGCCACTC	5324
Salt Tolerance HKT1 <i>Triticum aestivum</i> Asn365Ser AAT-AGT	CAGTCTTTGATGGGCTCAGCTCTTATCAGAAGACTGTCAATGCATT CTTCATGGTGGTGAGTGCGAGGCACTCAGGGGAGAATTCCATCG ACTGCTCGCTCATGTCCCCTGCCATTATAGT	5325
	ACTATAATGGCAGGGGACATGAGCGAGCAGTCGATGGAATTCTCC CCTGAGTGCCTCGCA <u>C</u> TACCACCATGAAGAATGCATTGACAGTC TTCTGATAAGAGCTGAGCCCATCAAAGACTG	5326
	GGTGGTGAGTGCGAGGC	5327
	GCCTCGCA <u>C</u> TACCACC	5328
Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg7Term CGA-TGA	TTTTTTTTGTTTTCGTTTTCAAAAACAAAATCTTTGAATTTTATGGCA ACCCGTCTTCTC <u>T</u> GAACAACTTTATCCGGCGATCTTACCGTTTAC CCGCTTTTAGCCCGGTGGGTCCTCCCA	5329
	TGGGAGGACCCACCGGGCTAAAAGCGGGTAAACGGTAAGATCGC CGGATAAAGTTTGTTC <u>A</u> GAGAAGACGGGTTGCCATAAAATTCAAA GATTTTGTTTTGA AACGAAAACAAAAAAA	5330
	GTCTTCTC <u>T</u> GAACAAAC	5331
	GTTTGTTCA <u>G</u> AGAAGAC	5332
Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg13Term CGA-TGA	TCAAAAACAAAATCTTTGAATTTTATGGCAACCCGTCTTCTCAGAA CAAACCTTATCCGG <u>I</u> GATCTTACCGTTTACCCGCTTTTAGCCCGGT GGGTCCTCCACCGTGACTGCTTCCACCG	5333
	CGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAAGC GGGTAAACGGTAAGATCA <u>A</u> CCGGATAAAGTTTGTTCGAGAAGACG GGTTGCCATAAAATTCAAAGATTTTGT TTTTGA	5334
	TTATCCGG <u>T</u> GATCTTAC	5335
	GTAAGATCA <u>A</u> CCGGATAA	5336
Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Tyr15Term TAC-TAG	AAAATCTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAACTTT ATCCGGCGATCTTAG <u>G</u> CGTTTACCCGCTTTTAGCCCGGTGGGTCCT CCCACCGTGACTGCTTCCACCGCCGTCGTC	5337
	GACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGG CTAAAAGCGGGTAAACG <u>C</u> TAAGATCGCCGGATAAAGTTTGTTCGG AGAAGACGGGTTGCCATAAAATTCAAAGATTTT	5338
	CGATCTTA <u>G</u> CGTTTACC	5339
	GGTAAACG <u>C</u> TAAGATCG	5340

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Leu17Term TTA-TAA	CTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAACTTTATCCG GCGATCTTACCGTTAACCCGCTTTTAGCCCGGTGGGTCCTCCCAC CGTGACTGCTTCCACCGCCGTCGTCCCGGA	5341
	TCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCA CCGGGCTAAAAGCGGGTTAACGGTAAGATCGCCGGATAAAGTTT GTTCCGAGAAGACGGGTTGCCATAAAATTCAAAG	5342
	TTACCGTTAACCCGCTT	5343
	AAGCGGGTTAACGGTAA	5344
Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Gly42Term GGA-TGA	CCGGTGGGTCCTCCACCGTGACTGCTTCCACCGCCGTCGTCCC GGAGATTCTCTCCTTTTGACAACAAGCACCGGAACCACCTCTTCA CCACCCAAAACCCACCGAGCAATCTCACGATG	5345
	CATCGTGAGATTGCTCGGTGGGTTTTGGGTGGTGAAGAGGTGGT TCCGGTGCTTGTGTCAAAAGGAGAGAATCTCCGGGACGACGGC GGTGGAAGCAGTCACGGTGGGAGGACCCACCGG	5346
	TCTCCTTTTGACAACAA	5347
	TTGTTGTCAAAAGGAGA	5348
Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Arg4Term CGA-TGA	ACATGAAGCAGTGAAATCTCTGTTTGATTGAATCTTATTAGTCTC AAACTATGAATTTCTGACAAGAGAAGTTTGTAAGGTCAGTGTTCCA GATTTGTCTCATTGAATTCTAAGTCGTGA	5349
	TCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTAC AAACTTCTCTTGTCAGAAATTCATAGTTTGAGACTAATAAGATTCAA TACAAACAGAGATTTCACTGCTTCATGT	5350
	TGAATTTCTGACAAGAG	5351
	CTCTTGTCAGAAATTCA	5352
Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Gln5Term CAA-TAA	TGAAGCAGTGAAATCTCTGTTTGATTGAATCTTATTAGTCTCAAA CTATGAATTTCCGATAAGAGAAGTTTGTAAGGTCAGTGTTCCAGAT TTGTCTCATTGAATTCTAAGTCGTGAAGC	5353
	GCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCT TACAACTTCTCTTATCGGAAATTCATAGTTTGAGACTAATAAGATT CAATACAAACAGAGATTTCACTGCTTCA	5354
	ATTTCCGATAAGAGAAG	5355
	CTTCTCTTATCGGAAAT	5356
Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG	AGCAGTGAAATCTCTGTTTGATTGAATCTTATTAGTCTCAAACTAT GAATTTCCGACAATAGAAGTTTGTAAGGTCAGTGTTCCAGATTTGT CTCATTGAATTCTAAGTCGTGAAGCTTA	5357
	TAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGA CCTTACAACTTCTATTGTGCGGAAATTCATAGTTTGAGACTAATAA GATTCAATACAAACAGAGATTTCACTGCT	5358

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACAATAGAAAGTTT	5359
	AAACTTCTATTGTCGGA	5360
Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Lys7Term AAG-TAG	AGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACATGAA TTTCCGACAAGAGTAGTTTGTAAAGTCAGTGTTCCAGATTTGTCTC ATTGAATTCTAAGTCGTGAAGCTTAATT	5361
	AATTAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACAC TGACCTTACAACTACTCTTGTCGGAAATTCATAGTTTGAGACTAA TAAGATTCAATACAAACAGAGATTTCACT	5362
	GACAAGAGTAGTTTGT	5363
	TACAACTACTCTTGTC	5364
Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Gln12Term CAA-TAA	CATTGAATTCTAAGTCGTGAAGCTTAATTCGATTCTTCTTCACTTTC TCGGATCAGGTTTAAAGATTGGAAGTCGGATAAGACTTCCTCCGA CGTGGAATATTCCGGTAAAAACGAGATTC	5365
	GAATCTCGTTTTTACCGGAATATTCCACGTCGGAGGAAGTCTTATC CGACTTCCAATCTTAAACCTGATCCGAGAAAGTGAAGAAGAATC GAATTAAGCTTCACGACTTAGAATTCAATG	5366
	TCAGGTTTAAAGATTGG	5367
	CCAATCTTAAACCTGA	5368
Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln5Term CAA-TAA	TGGAAGTCAATCCCCACGTTGAGCAGGTTGATGCATTGGCTAAA GTTATGAATCACCGCTAAGACGAGTTTGTGAGGTTTCAGGATTGG AAATCAGAGAGAAGCTCTGAGGGAAATTTTC	5369
	GAAAATTTCCCTCAGAGCTTCTCTCTGATTTCGAATCCTGAAACCT CACAACTCGTCTTAGCGGTGATTACATACTTTAGCCAATGCATCA ACCTGCTCAACGTGGGGGATTGACTTCCA	5370
	ATCACCGCTAAGACGAG	5371
	CTCGTCTTAGCGGTGAT	5372
Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gly7Term GAG-TAG	TCAATCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATG AATCACCGCCAAGACTAGTTTGTGAGGTTTCAGGATTGGAAATCA GAGAGAAGCTCTGAGGGAAATTTTCATGCTA	5373
	TAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTTCGAATCCTG AAACCTCACAACTAGTCTTGCGGTGATTACATACTTTAGCCAAT GCATCAACCTGCTCAACGTGGGGGATTGA	5374
	GCCAAGACTAGTTTGTG	5375
	CACAACTAGTCTTGGC	5376

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln12Term CAG-TAG	GAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGAC GAGTTTGTGAGGTTT <u>I</u> AGGATTGGAAATCAGAGAGAAGCTCTGAG GGAAATTTTCATGCTAAAGGTGGAGTCCACC	5377
	GGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTC TGATTTCCAATCCT <u>A</u> AAACCTCACAACTCGTCTTGGCGGTGATTG ATAACTTTAGCCAATGCATCAACCTGCTC	5378
	TGAGGTTT <u>I</u> AGGATTGG	5379
	CCAATCCT <u>A</u> AAACCTCA	5380
Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Trp14Term TGG-TGA	TGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGT GAGGTTTCAGGATTGT <u>I</u> AAATCAGAGAGAAGCTCTGAGGGAAATTT TCATGCTAAAGGTGGAGTCCACCGAAGTAAA	5381
	TTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAG CTTCTCTCTGATTT <u>A</u> CAATCCTGAAACCTCACAACTCGTCTTGGC GGTGATTCACTAATTTAGCCAATGCATCA	5382
	CAGGATTGT <u>I</u> AAATCAGA	5383
	TCTGATTT <u>A</u> CAATCCTG	5384
Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Lys15Term AAA-TAA	GATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTG AGGTTTCAGGATTGGT <u>I</u> AATCAGAGAGAAGCTCTGAGGGAAATTTT CATGCTAAAGGTGGAGTCCACCGAAGTAAAG	5385
	CTTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGA GCTTCTCTCTGATT <u>A</u> CCAATCCTGAAACCTCACAACTCGTCTTGG CGGTGATTCACTAATTTAGCCAATGCATC	5386
	AGGATTGGT <u>I</u> AATCAGAG	5387
	CTCTGATT <u>A</u> CCAATCCT	5388
Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu2Term GAA-TAA	CTTGAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTGCGCTGG TGGAGATAATGATGT <u>I</u> AAAGAGAGGACAGATATGTTAGATTTCAAG ACTGCAAATCAGAGCAATCTGTTATCTCAG	5389
	CTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAACATA TCTGTCCTCTCTTT <u>A</u> CATCATTATCTCCACCAGGCGAACAGTTAGC AGCTAAGAGTGGTAGATCAATTCTTCAAG	5390
	TAATGATGT <u>I</u> AAAGAGAG	5391
	CTCTCTTT <u>A</u> CATCATTA	5392

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg3Term AGA-TGA	GAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTGCGCTGGTG GAGATAATGATGGAATGAGAGGACAGATATGTTAGATTTTCAGGAC TGCAAATCAGAGCAATCTGTTATCTCAGAGA	5393
	TCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAAC ATATCTGTCCTCTCATTCCATCATTATCTCCACCAGGCGAACAGTT AGCAGCTAAGAGTGGTAGATCAATTCTTC	5394
	TGATGGAATGAGAGGAC	5395
	GTCCTCTCATTCCATCA	5396
Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu4Term GAG-TAG	GAATTGATCTACCACTCTTAGCTGCTAACTGTTGCGCTGGTGGAG ATAATGATGGAAAGATAGGACAGATATGTTAGATTTTCAGGACTGC AAATCAGAGCAATCTGTTATCTCAGAGAACG	5397
	CGTTCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCT AACATATCTGTCCTATCTTTCCATCATTATCTCCACCAGGCGAACCA GTTAGCAGCTAAGAGTGGTAGATCAATTC	5398
	TGGAAAGATAGGACAGA	5399
	TCTGTCCTATCTTTCCA	5400
Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg6Term AGA-TGA	ATCTACCACTCTTAGCTGCTAACTGTTGCGCTGGTGGAGATAATG ATGGAAAGAGAGGACTGATATGTTAGATTTTCAGGACTGCAAATCA GAGCAATCTGTTATCTCAGAGAACGCAGTTT	5401
	AACTGCGTTCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTG AAATCTAACATATCAGTCCTCTCTTTCCATCATTATCTCCACCAGG CGAACAGTTAGCAGCTAAGAGTGGTAGAT	5402
	GAGAGGACTGATATGTT	5403
	AACATATCAGTCCTCTC	5404
Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Tyr7Term TAT-TAG	CCACTCTTAGCTGCTAACTGTTGCGCTGGTGGAGATAATGATGGA AAGAGAGGACAGATAGGTTAGATTTTCAGGACTGCAAATCAGAGCA ATCTGTTATCTCAGAGAACGCAGTTTCACCA	5405
	TGGTGAAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTTGCA GTCCTGAAATCTAACCTATCTGTCCTCTCTTTCCATCATTATCTCCA CCAGGCGAACAGTTAGCAGCTAAGAGTGG	5406
	GACAGATAGGTTAGATT	5407
	AATCTAACCTATCTGTC	5408
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu2Term GAG-TAG	ATCCTTCTCTGAGAAAAACAACAGATCCGAATTTTATCTTTAATCA GCCGGAAAAATGTAGAAAGCGATCGAGAGACAACGCGTTCTTCT TGAGCATCTCCGACCTTCTTCTTCTTCTT	5409
	AAGAAGAAGAAGAGGTCGGAGATGCTCAAGAAGAACGCGTTGT CTCTCGATCGCTTTCTACATTTTTTCCGGCTGATTAAAGATAAAATT CGGATCTGTTGTTTTTCTCAGAGAAGGAT	5410

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAAATG <u>T</u> AGAAAGCG	5411
	CGCTTTCT <u>A</u> CATTTTTT	5412
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Lys3Term AAA-TAA	CTTCTCTGAGAAAAACAACAGATCCGAATTTTATCTTTAATCAGC CGGAAAAAATGGAG <u>T</u> AAGCGATCGAGAGACAACGCGTTCTTCTTG AGCATCTCCGACCTTCTTCTTCTTCTTCGC	5413
	GCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGT TGTCTCTCGATCGCTT <u>A</u> CTCCATTTTTTCCGGCTGATTAAAGATAA AATTCGGATCTGTTGTTTTTCTCAGAGAAG	5414
	AAATGGAG <u>T</u> AAGCGATC	5415
	GATCGCTT <u>A</u> CTCCATT	5416
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG	GAAAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAA TGGAGAAAGCGATC <u>T</u> AGAGACAACGCGTTCTTCTTGAGCATCTCC GACCTTCTTCTTCTTCTTCGCACAATTACG	5417
	CGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGA AGAACGCGTTGTCTCT <u>A</u> GATCGCTTTCTCCATTTTTTCCGGCTGAT TAAAGATAAAATTCGGATCTGTTGTTTTTC	5418
	AAGCGATC <u>T</u> AGAGACAA	5419
	TTGTCTCT <u>A</u> GATCGCTT	5420
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Arg7Term AGA-TGA	AAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGG AGAAAGCGATCGAG <u>T</u> GACAACGCGTTCTTCTTGAGCATCTCCGAC CTTCTTCTTCTTCTTCGCACAATTACGAGG	5421
	CCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAA GAAGAACGCGTTGTCT <u>A</u> CTCGATCGCTTTCTCCATTTTTTCCGGCT GATTAAAGATAAAATTCGGATCTGTTGTTTT	5422
	CGATCGAG <u>T</u> GACAACGC	5423
	GCGTTGTC <u>A</u> CTCGATCG	5424
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Gln8Term CAA-TAA	ACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGA AAGCGATCGAGAGAT <u>A</u> ACGCGTTCTTCTTGAGCATCTCCGACCTT CTTCTTCTTCTTCGCACAATTACGAGGCTT	5425
	AAGCCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGC TCAAGAAGAACGCGTT <u>A</u> TCTCTCGATCGCTTTCTCCATTTTTTCCG GCTGATTAAAGATAAAATTCGGATCTGTTGT	5426
	TCGAGAGAT <u>A</u> ACGCGTT	5427
	AACGCGTT <u>A</u> TCTCTCGA	5428

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Glu26Term GAA-TAA	GAGAGACAAAGAGTTCTTCTTGAACATCTCCGTCCTTCTTCTTCTT CCTCTCACAGCTTTAAGGCTCTCTCTGCTTCAGCTTGCTTGGC TGGGGACAGTGCTGCGTATCAGAGGACCT	5429
	AGGTCCTCTGATACGCAGCACTGTCCCCAGCCAAGCAAGCTGAA GCAGAGAGAGAGCCTTAAAAGCTGTGAGAGGAAGAAGAAGAAGG ACGGAGATGTTCAAGAAGAACTCTTTGTCTCTC	5430
	ACAGCTTTAAGGCTCT	5431
	AGAGCCTTAAAAGCTGT	5432
2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Ser32Term TCA-TGA	TTGAACATCTCCGTCCTTCTTCTTCTTCTCTCACAGCTTTGAAGG CTCTCTCTGCTTGAGCTTGCTTGGCTGGGGACAGTGCTGCGTA TCAGAGGACCTCTCTCTATGGAGATGATGT	5433
	ACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGCACTGTCC CCAGCCAAGCAAGCTCAAGCAGAGAGAGAGCCTTCAAAGCTGTG AGAGGAAGAAGAAGAAGGACGGAGATGTTCAA	5434
	CTCTGCTTGAGCTTGCT	5435
	AGCAAGCTCAAGCAGAG	5436
2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Cys34Term TGC-TGA	TCTCCGTCCTTCTTCTTCTTCTCTCACAGCTTTGAAGGCTCTCTC TCTGCTTCAGCTTGATTGGCTGGGGACAGTGCTGCGTATCAGAG GACCTCTCTCTATGGAGATGATGTAGTCATT	5437
	AATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGC ACTGTCCCCAGCCAATCAAGCTGAAGCAGAGAGAGAGCCTTCAAA GCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5438
	TCAGCTTGATTGGCTGG	5439
	CCAGCCAATCAAGCTGA	5440
2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Leu35Term TTG-TAG	TCCGTCCTTCTTCTTCTTCTCTCACAGCTTTGAAGGCTCTCTCTC TGCTTCAGCTTGCTAGGCTGGGGACAGTGCTGCGTATCAGAGGA CCTCTCTCTATGGAGATGATGTAGTCATTGT	5441
	ACAATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCA GCACTGTCCCCAGCCTAGCAAGCTGAAGCAGAGAGAGAGCCTTC AAAGCTGTGAGAGGAAGAAGAAGAAGGACGGA	5442
	AGCTTGCTAGGCTGGGG	5443
	CCCCAGCCTAGCAAGCT	5444

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Tyr42Term TAT-TAG	TCACAGCTTTGAAGGCTCTCTCTGCTTCAGCTTGCTTGGCTGG GGACAGTGCTGCGTAGCAGAGGACCTCTCTCTATGGAGATGATGT AGTCATTGTTGCGGCACATAGGACTGCACTA	5445
	TAGTGCAGTCCTATGTGCCGCAACAATGACTACATCATCTCCATA GAGAGAGGTCCTCTGCTACGCAGCACTGTCCCCAGCCAAGCAAG CTGAAGCAGAGAGAGAGCCTTCAAAGCTGTGA	5446
	GCTGCGTAGCAGAGGAC	5447
	GTCCTCTGCTACGCAGC	5448
2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr25Term TAC-TAG	CAACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTCT TTCTTCTCACAATTAGGAGTCCGCTCTTGCCGCATCAGTATGTGCT GCAGGGGATAGCGCCGCATATCATAGGGCT	5449
	AGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATGC GGCAAGAGCGGACTCCTAATTGTGAGAAGAAGAATTAGAAGGGC GGAGATGCTGGAGCAACACTTGCTGTCTGTTG	5450
	CACAATTAGGAGTCCGC	5451
	GCGGACTCCTAATTGTG	5452
2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Glu26Term GAG-TAG	AACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTCTT CTTCTCACAATTACTAGTCCGCTCTTGCCGCATCAGTATGTGCTGC AGGGGATAGCGCCGCATATCATAGGGCTT	5453
	AAGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATG CGGCAAGAGCGGACTAGTAATTGTGAGAAGAAGAATTAGAAGGG CGGAGATGCTGGAGCAACACTTGCTGTCTGTT	5454
	ACAATTACTAGTCCGCT	5455
	AGCGGACTAGTAATTGT	5456
2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Ser32Term TCA-TGA	TCCAGCATCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTC CGCTCTTGCCGCATGAGTATGTGCTGCAGGGGATAGCGCCGCAT ATCATAGGGCTTCTGTTTATGGAGACGATGT	5457
	ACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGCGCTATCC CCTGCAGCACATACTCATGCGGCAAGAGCGGACTCGTAATTGTGA GAAGAAGAATTAGAAGGGCGGAGATGCTGGA	5458
	TGCCGCATGAGTATGTG	5459
	CACATACTCATGCGGCA	5460

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Cys34Term TGT-TGA	TCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTCCGCTCTT GCCGCATCAGTATGAGCTGCAGGGGATAGCGCCGCATATCATAG GGCTTCTGTTTATGGAGACGATGTGGTGATT	5461
	AATCACCACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGC GCTATCCCCTGCAGCTCATACTGATGCGGCAAGAGCGGACTCGT AATTGTGAGAAGAAGAATTAGAAGGGCGGAGA	5462
	TCAGTATGAGCTGCAGG	5463
	CCTGCAGCTCATACTGA	5464
2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr42Term TAT-TAG	TCACAATTACGAGTCCGCTCTTGCCGCATCAGTATGTGCTGCAGG GGATAGCGCCGCATAGCATAGGGCTTCTGTTTATGGAGACGATGT GGTGATTGTGGCAGCTCATCGTACTGCACTT	5465
	AAGTGCAGTACGATGAGCTGCCACAATCACCACATCGTCTCCATA AACAGAAGCCCTATGCTATGCGGCGCTATCCCCTGCAGCACATAC TGATGCGGCAAGAGCGGACTCGTAATTGTGA	5466
	GCCGCATAGCATAGGGC	5467
	GCCCTATGCTATGCGGC	5468
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Tyr22Term TAC-TAG	GAAGGCGATCAACAGGCAGAGCATTGCTACATCATCTCCGGCC TTCTTCTTCCGCTTAGACAAATGAATCTTCGCTCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCTTCGTATCAA	5469
	TTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCAATTTGTCTAAGCGGAAGAAGAAGGCCGGAGATGATG TAGCAAAATGCTCTGCCTGTTGATCGCCTTC	5470
	TCCGCTTAGACAAATGA	5471
	TCATTTGTCTAAGCGGA	5472
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTGCTACATCATCTCCGGCCTTCTTCTT CCGCTTACACAAATTAATCTTCGCTCTCTGCATCGGTTTGTGCAGC TGGGGATAGTGCTTCGTATCAAAGGACAT	5473
	ATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAAATTTGTGTAAGCGGAAGAAGAAGGCCGG AGATGATGTAGCAAAATGCTCTGCCTGTTGAT	5474
	ACACAAATTAATCTTCG	5475
	CGAAGATTAAATTTGTGT	5476

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser27Term TCG-TAG	GGCAGAGCATTGCTACATCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATCTTCTGCTCTGCTATCGGTTTGTGCAGCTGGGGA TAGTGCTTCGTATCAAAGGACATCGGTGTT	5477
	AACACCGATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAGATTCAATTTGTGTAAGCGGAAGAAGAA GGCCGGAGATGATGTAGCAAAATGCTCTGCC	5478
	TGAATCTTAGCTCTCTG	5479
	CAGAGAGCTAAGATTCA	5480
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATC TTCGCTCTCTGCTATAGGTTTGTGCAGCTGGGGATAGTGCTTCGTA TCAAAGGACATCGGTGTTTGGAGATGATGT	5481
	ACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCACTATCCC CAGCTGCACAAACCTATGCAGAGAGCGAAGATTCAATTTGTGTAAG CGGAAGAAGAAGGCCGGAGATGATGTAGCA	5482
	CTCTGCATAGGTTTGTG	5483
	CACAAACCTATGCAGAG	5484
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Cys33Term TGT-TGA	TCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATCTTCGCTC TCTGCATCGGTTTGAGCAGCTGGGGATAGTGCTTCGTATCAAAGG ACATCGGTGTTTGGAGATGATGTCGTGATT	5485
	AATCACGACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCA CTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCAATTT GTGTAAGCGGAAGAAGAAGGCCGGAGATGA	5486
	TCGGTTTGAGCAGCTGG	5487
	CCAGCTGCTCAAACCGA	5488
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Tyr22Term TAT-TAG	GAAGGCAATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCC TTCATCTTCGGCTTAGAGCCATGAATCTTCGCTCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCCTCGTATCAA	5489
	TTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTATGGCTCTAAGCCGAAGATGAAGGCCGGAGATGAT GTAGCAGAATGCTCTGCCTGTTGATTGCCTTC	5490
	TCGGCTTAGAGCCATGA	5491
	TCATGGCTCTAAGCCGA	5492

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTT CGGCTTATAGCCATTAAATCTTCGCTCTCTGCATCGGTTTGTGCAGC TGGGGATAGTGCGTCGTATCAAAGAACGT	5493
	ACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAAATGGCTATAAGCCGAAGATGAAGGCCGG AGATGATGTAGCAGAATGCTCTGCCTGTTGAT	5494
	ATAGCCATTAAATCTTCG	5495
	CGAAGATTAAATGGCTAT	5496
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Ser27Term TCG-TAG	GGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTTCGGCTT ATAGCCATGAATCTTAAGCTCTCTGCATCGGTTTGTGCAGCTGGGG ATAGTGCGTCGTATCAAAGAACGTCGGTGTT	5497
	AACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAGATTCATGGCTATAAGCCGAAGATGAA GGCCGGAGATGATGTAGCAGAATGCTCTGCC	5498
	TGAATCTTAAGCTCTCTG	5499
	CAGAGAGCTAAGATTCA	5500
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATC TTCGCTCTCTGCATAGGTTTGTGCAGCTGGGGATAGTGCGTCGTA TCAAAGAACGTCGGTGTTTGGAGATGATGT	5501
	ACATCATCTCCAAACACCGACGTTCTTTGATACGACGCACTATCCC CAGCTGCACAAACCTATGCAGAGAGCGAAGATTCATGGCTATAAG CCGAAGATGAAGGCCGGAGATGATGTAGCA	5502
	CTCTGCATAGGTTTGTG	5503
	CACAAACCTATGCAGAG	5504
2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Cys33Term TGT-TGA	TCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTCGCTC TCTGCATCGGTTTGAAGCAGCTGGGGATAGTGCGTCGTATCAAAGA ACGTCGGTGTTTGGAGATGATGTCGTGATA	5505
	TATCACGACATCATCTCCAAACACCGACGTTCTTTGATACGACGCA CTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCATGG CTATAAGCCGAAGATGAAGGCCGGAGATGA	5506
	TCGGTTTGAAGCAGCTGG	5507
	CCAGCTGCTCAAACCGA	5508
2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln5Term CAG-TAG	TCATAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTG CTATGGCAACTCATTAGCAAACGCAACCTCCTTCCGATTTTCCCGC TCTTGCCGATGAAAATTCCCAGATTCCAG	5509
	CTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGGAA GGAGGTTGCGTTTGCTAATGAGTTGCCATAGCAGCTCACTAACCT TGGAAGAATCCAAGCGGCAAAAGAGACTATGA	5510

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAACTCAT <u>T</u> AGCAAACG	5511
	CGTTTGCT <u>A</u> ATGAGTTG	5512
2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln6Term CAA-TAA	TAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTA TGGCAACTCATCAGTAAACGCAACCTCCTTCCGATTTTCCCGCTCT TGCCGATGAAAATTCCAGATTCCAGGTT	5513
	AACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGG AAGGAGGTTGCGTTT <u>A</u> CTGATGAGTTGCCATAGCAGCTCACTAAC CTTGGAAGAATCCAAGCGGCAAAAGAGACTA	5514
	CTCATCAGTAAACGCAA	5515
	TTGCGTTT <u>A</u> CTGATGAG	5516
2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln8Term CAA-TAA	CTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTATGGCA ACTCATCAGCAAACGTAACCTCCTTCCGATTTTCCCGCTCTTGCCG ATGAAAATTTCCAGATTCCAGGTTCAATTT	5517
	AAATTGAACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAA AATCGGAAGGAGGTT <u>A</u> CGTTTGCTGATGAGTTGCCATAGCAGCTC ACTAACCTTGGAAGAATCCAAGCGGCAAAAG	5518
	AGCAAACGTAAACCTCCT	5519
	AGGAGGTT <u>A</u> CGTTTGCT	5520
2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Glu19Term GAA-TAA	GCTGCTATGGCAACTCATCAGCAAACGCAACCTCCTTCCGATTTT CCCGCTCTTGCCGATTAAATTTCCAGATTCCAGGTTCAATTTACA CCTTCTAATCATTATTTCTTAATTTTCTT	5521
	AAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAATTGAACCTGG AATCTGGGAATTTT <u>A</u> ATCGGCAAGAGCGGGAAAATCGGAAGGAG GTTGCGTTTGCTGATGAGTTGCCATAGCAGC	5522
	TTGCCGATTAAATTC	5523
	GGAATTTT <u>A</u> ATCGGCAA	5524
2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln22Term CAG-TAG	GCAACTCATCAGCAAACGCAACCTCCTTCCGATTTTCCCGCTCTT GCCGATGAAAATTCCTAGATTCCAGGTTCAATTTACACCTTCTAAT CATTATTTCTTAATTTTCTTTGGTGGATT	5525
	AATCCACCAAAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAAT TGAACCTGGAATCT <u>A</u> GGAATTTTCATCGGCAAGAGCGGGAAAATC GGAAGGAGGTTGCGTTTGCTGATGAGTTGC	5526
	AAAATTCCTAGATTCCA	5527
	TGGAATCT <u>A</u> GGAATTTT	5528

Example 29

Production of albino mutants for the analysis of photosynthetic processes

[253] Plant productivity is limited by resources available and the ability of plants to harness these resources. The conversion of light to chemical energy, which is then used to synthesize carbohydrates, fatty acids, sugars, amino acids and other compounds, requires a complex system which combines the light harvesting apparatus of pigments and proteins. The value of light energy to the plant can only be realized when it is efficiently converted into chemical energy by photosynthesis and fed into various biochemical processes. Significant effort has therefore been directed at studying photosynthetic processes in plants in order to improve productivity and/or the efficiency of photosynthesis. The analysis of the photosynthetic process is substantially aided by the ability to produce albino plants.

[254] The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 36
Oligonucleotides to produce albino plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
White leaves Immutans <i>Arabidopsis thaliana</i> Ser5Term TCA-TGA	TTCTTTCCTGTGAAATTATCTGCTCAAATCTTTGGTTCCTGACGGAG ATGGCGGCGATTTGAGGCATCTCCTCTGGTACGTTGACGATTTC CGGCCTTTGGTTACTCTTCGACGCTCTAG	5529
	CTAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTA CCAGAGGAGATGCCTCAAATCGCCGCCATCTCCGTCAGGAACCAA AGATTTGAGCAGATAATTTACAGGAAAGAA	5530
	GGCGATTTGAGGCATCT	5531
	AGATGCCTCAAATCGCC	5532
White leaves Immutans <i>Arabidopsis thaliana</i> Leu12Term TTG-TAG	GCTCAAATCTTTGGTTCCTGACGGAGATGGCGGCGATTTACAGGCA TCTCCTCTGGTACGTAGACGATTTACGGCCTTTGGTTACTCTTCG ACGCTCTAGAGCCGCCGTTTCGTACAGCTC	5533
	GAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAGAGTAACCAA GGCCGTGAAATCGTCTACGTACCAGAGGAGATGCCTGAAATCGCC GCCATCTCCGTCAGGAACCAAAGATTTGAGC	5534
	TGGTACGTAGACGATTT	5535
	AAATCGTCTACGTACCA	5536
White leaves Immutans <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA	TTTGGTTCCTGACGGAGATGGCGGCGATTTACAGGCATCTCCTCTG GTACGTTGACGATTTGACGGCCTTTGGTTACTCTTCGACGCTCTAG AGCCGCCGTTTCGTACAGCTCCTCTCACCG	5537
	CGGTGAGAGGAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAG AGTAACCAAAGGCCGTCAAATCGTCAACGTACCAGAGGAGATGCC TGAAATCGCCGCCATCTCCGTCAGGAACCAA	5538
	GACGATTTGACGGCCTT	5539
	AAGGCCGTCAAATCGTC	5540
White leaves Immutans <i>Arabidopsis thaliana</i> Arg22Term CGA-TGA	GCGGCGATTTACAGGCATCTCCTCTGGTACGTTGACGATTTACGG CCTTTGGTTACTCTTIGACGCTCTAGAGCCGCCGTTTCGTACAGCT CCTCTCACCGATTGCTTCATCATCTTCCTC	5541
	GAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTGTACGAAACG GCGGCTCTAGAGCGTCAAAGAGTAACCAAAGGCCGTGAAATCGTC AACGTACCAGAGGAGATGCCTGAAATCGCCGC	5542
	TTACTCTTIGACGCTCT	5543
	AGAGCGTCAAAGAGTAA	5544

White leaves Immutans <i>Arabidopsis thaliana</i> Arg25Term AGA-TGA	TCAGGCATCTCCTCTGGTACGTTGACGATTTACCGGCCTTTGGTTA CTCTTCGACGCTCTTGAGCCGCCGTTTCGTACAGCTCCTCTCACC GATTGCTTCATCATCTTCCTCTCTCTTCTC	5545
	GAGAAGAGAGAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTG TACGAAACGGCGGCTCAAGAGCGTCGAAGAGTAACCAAAGGCCG TGAAATCGTCAACGTACCAGAGGAGATGCCTGA	5546
	GACGCTCTTGAGCCGCC	5547
	GGCGGCTCAAGAGCGTC	5548
White leaves Immutans <i>Lycopersicon esculentum</i> Gly11Term GGA-TGA	GATTCTTGTGGGAAGGAAGAAGGATCAAGAATGGCGATTTTCGATT TCTGCTATGAGTTTTGAACCTCAGTTTCTTCATATTCTTGTTTTAG AGCTAGGAGTTTTGAGAAGTCATCAGTTT	5549
	AAACTGATGACTTCTCAAACTCCTAGCTCTAAAACAAGAATATGA AGAACTGAGGTTCAAAACTCATAGCAGAAATCGAAATCGCCATT CTTGATCCTTCTTCCTTCCACAAGAATC	5550
	TGAGTTTTGAACCTCA	5551
	TGAGGTTCAAAACTCA	5552
White leaves Immutans <i>Lycopersicon esculentum</i> Ser13Term TCA-TGA	GTGGGAAGGAAGAAGGATCAAGAATGGCGATTTTCGATTTCTGCTA TGAGTTTTGGAACCTGAGTTTCTTCATATTCTTGTTTTAGAGCTAGG AGTTTTGAGAAGTCATCAGTTTTATGCAA	5553
	TTGCATAAACTGATGACTTCTCAAACTCCTAGCTCTAAAACAAG AATATGAAGAACTCAGGTTCCAAACTCATAGCAGAAATCGAAAT CGCCATTCTTGATCCTTCTTCCTTCCAC	5554
	TGGAACCTGAGTTTCTT	5555
	AAGAACTCAGGTTCCA	5556
White leaves Immutans <i>Lycopersicon esculentum</i> Ser16Term TCA-TGA	AAGAAGGATCAAGAATGGCGATTTTCGATTTCTGCTATGAGTTTTGG AACCTCAGTTTCTTGATATTCTTGTTTTAGAGCTAGGAGTTTTGAGA AGTCATCAGTTTTATGCAATTCCCAGAA	5557
	TTCTGGGAATTGCATAAACTGATGACTTCTCAAACTCCTAGCTC TAAAACAAGAATATCAAGAACTGAGGTTCCAAACTCATAGCAGA AATCGAAATCGCCATTCTTGATCCTTCTT	5558
	AGTTTCTTGATATTCTT	5559
	AAGAATATCAAGAACT	5560
White leaves Immutans <i>Lycopersicon esculentum</i> Tyr17Term TAT-TAG	AGGATCAAGAATGGCGATTTTCGATTTCTGCTATGAGTTTTGGAACC TCAGTTTCTTCATAGTCTTGTTTTAGAGCTAGGAGTTTTGAGAAGTC ATCAGTTTTATGCAATTCCCAGAACCCA	5561
	TGGGTTCTGGGAATTGCATAAACTGATGACTTCTCAAACTCCTA GCTCTAAAACAAGACTATGAAGAACTGAGGTTCCAAACTCATAG CAGAAATCGAAATCGCCATTCTTGATCCT	5562
	TCTTCATAGTCTTGTTT	5563
	AAACAAGACTATGAAGA	5564

White leaves Immutans <i>Lycopersicon esculentum</i> Cys19Term TGT-TGA	AAGAATGGCGATTTCTGCTATGAGTTTTGGAACCTCAGTT TCTTCATATTCTTGATTTAGAGCTAGGAGTTTTGAGAAGTCATCAGT TTTATGCAATTCACAGAACCCATGTCGG	5565
	CCGACATGGGTTCTGGAATTGCATAAACTGATGACTTCTCAAAA CTCCTAGCTCTAAATCAAGAATATGAAGAACTGAGGTTCCAAAAC TCATAGCAGAAATCGAAATCGCCATTCTT	5566
	TATTCTTGATTTAGAGC	5567
	GCTCTAAATCAAGAATA	5568
White leaves Immutans <i>Capsicum annuum</i> Ser13Term TCA-TGA	CGCGTCCGATAAAAAAATCAAGAATGGCGATTTCCATATCTGCTAT GAGTTTTCGAAGTTGAGTTTCTTCTTCATATTCAGCATTTTTGTGCA ATTCCAAGAACCCATTTTGTGTTGAATTC	5569
	GAATTCAAACAAAATGGGTTCTTGAATTGCACAAAAATGCTGAAT ATGAAGAAGAACTCAAGTTCGAAAACATAGCAGATATGGAAAT CGCCATTCTTGATTTTTTATCGGACGCG	5570
	TCGAAGTTGAGTTTCTT	5571
	AAGAACTCAAGTTCTGA	5572
White leaves Immutans <i>Capsicum annuum</i> Ser17Term TCA-TGA	AAAAATCAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAAC TTCAGTTTCTTCTTGATATTCAGCATTTTTGTGCAATTCCAAGAACC CATTTTGTGTTGAATTCTCTATTTTCACT	5573
	AGTGAAGATAGAGAATTCAAACAAAATGGGTTCTTGAATTGCACA AAAATGCTGAATATCAAGAAGAACTGAAGTTCGAAAACATAGC AGATATGGAAATCGCCATTCTTGATTTTT	5574
	TTCTTCTTGATATTCAG	5575
	CTGAATATCAAGAAGAA	5576
White leaves Immutans <i>Capsicum annuum</i> Ser19Term TCA-TGA	CAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAAGTTTCTTCTTCA TATTCTTCTCATATTGAGCATTTTTGTGCAATTCCAAGAACCCATTTT GTTTGAATTCTCTATTTTCACTTAGGAA	5577
	TTCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGAAT TGCACAAAAATGCTCAATATGAAGAAGAACTGAAGTTCGAAAAC CATAGCAGATATGGAAATCGCCATTCTTG	5578
	TTTCATATTGAGCATTTT	5579
	AAAATGCTCAATATGAA	5580
White leaves Immutans <i>Capsicum annuum</i> Leu21Term TTG-TAG	CGATTTCCATATCTGCTATGAGTTTTCGAAGTTTCTTCTTCA TATTCAGCATTTTGTGCAATTCCAAGAACCCATTTTGTGTTGAATTC TCTATTTTCACTTAGGAATTCTCATAG	5581
	CTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGT TCTTGAATTGCACTAAAATGCTGAATATGAAGAAGAACTGAAGT TCGAAAACATAGCAGATATGGAAATCG	5582
	AGCATTTTGTGCAATT	5583
	AATTGCACTAAAATGCT	5584

White leaves Immutans <i>Capsicum annuum</i> Cys22Term TGC-TGA	TTCCATATCTGCTATGAGTTTTTCGAACTTCAGTTTCTTCTTCATATT CAGCATTTTTGTGA A AATTCCAAGAACCCATTTTGTGTAATTCTCTA TTTTCACTTAGGAATTCTCATAGAACT	5585
	AGTTCTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAAT GGGTTCTTGGAATTTCACAAAAATGCTGAATATGAAGAAGAACTG AAGTTCGAAAACATCATAGCAGATATGGAA	5586
	TTTTTGTGA A AATTCCAA	5587
	TTGGAATTTCACAAAAA	5588
White leaves Immutans <i>Oryza sativa</i> Glu22Term GAG-TAG	TTCGGCACGAGGGAGAAGGAGCAGACCGAGGTGGCCGTCGAGG AGTCCTTCCCCTTCAGGTAGACGGCTCCTCCTGACGAGCCACTGG TCACCGCCGAGGAGAGCTGGGTGGTTAAGCTCG	5589
	CGAGCTTAACCACCCAGCTCTCCTCGGCGGTGACCAGTGGCTCGT CAGGAGGAGCCGTCT A CCTGAAGGGGAAGGACTCCTCGACGGCC ACCTCGGTCTGCTCCTTCTCCCTCGTGCCGAA	5590
	CCTTCAGGTAGACGGCT	5591
	AGCCGTCT A CCTGAAGG	5592
White leaves Immutans <i>Oryza sativa</i> Glu28Term CAG-TAG	GAGCAGACCGAGGTGGCCGTCGAGGAGTCCTTCCCCTTCAGGGA GACGGCTCCTCCTGACTAGCCACTGGTCACCGCCGAGGAGAGCT GGGTGGTTAAGCTCGAGCAGTCCGTGAACATTT	5593
	AAATGTTACGGACTGCTCGAGCTTAACCACCCAGCTCTCCTCGG CGGTGACCAGTGGCT A GTCAAGGAGGAGCCGTCTCCCTGAAGGGG AAGGACTCCTCGACGGCCACCTCGGTCTGCTC	5594
	CTCCTGACTAGCCACTG	5595
	CAGTGGCT A GTCAAGGAG	5596
White leaves Immutans <i>Oryza sativa</i> Glu34Term GAG-TAG	GTCGAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGA GCCACTGGTCACCGCC T AGGAGAGCTGGGTGGTTAAGCTCGAGC AGTCCGTGAACATTTTCTCACGGAGTCAGTCA	5597
	TGACTGACTCCGTGAGGAAAATGTTACGGACTGCTCGAGCTTAA CCACCCAGCTCTCCT A GGCGGTGACCAGTGGCTCGTCAGGAGGA GCCGTCTCCCTGAAGGGGAAGGACTCCTCGAC	5598
	TCACCGCC T AGGAGAGC	5599
	GCTCTCCT A GGCGGTGA	5600
White leaves Immutans <i>Oryza sativa</i> Glu35Term GAG-TAG	GAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCC ACTGGTCACCGCCGAGTAGAGCTGGGTGGTTAAGCTCGAGCAGT CCGTGAACATTTTCTCACGGAGTCAGTCATCA	5601
	TGATGACTGACTCCGTGAGGAAAATGTTACGGACTGCTCGAGCT TAACCACCCAGCTCT A CTCGGCGGTGACCAGTGGCTCGTCAGGA GGAGCCGTCTCCCTGAAGGGGAAGGACTCCTC	5602
	CCGCCGAGTAGAGCTGG	5603
	CCAGCTCT A CTCGGCGG	5604

White leaves Immutans <i>Oryza sativa</i> Trp37Term TGG-TGA	CTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCAC CGCCGAGGAGAGCTGAGTGGTTAAGCTCGAGCAGTCCGTGAACA TTTTCTCACGGAGTCAGTCATCACGATACTT	5605
	AAGTATCGTGATGACTGACTCCGTGAGGAAAATGTTACGGACTG CTCGAGCTTAACCACTCAGCTCTCCTCGGCGGTGACCAGTGGCTC GTCAGGAGGAGCCGTCTCCCTGAAGGGGAAG	5606
	GAGAGCTGAGTGGTTAA	5607
	TTAACCACCTCAGCTCTC	5608
White leaves Immutans <i>Triticum aestivum</i> Trp22Term TGG-TGA	TCCGGAGGAGGAAGGGGGATTTCGACGAGGAGCTCACCCTCGCCG GCGAGGACGGCGACTGAGTCGTGAGATTTCGAGCAGTCCTTCAAC GTATTCCTCACGGATACTGTCATCTTTATACTC	5609
	GAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTG CTCGAATCTGACGACTCAGTCGCCGTCTCGCCGGCGAGGGTGA GCTCCTCGTGAATCCCCCTTCCTCCTCCGGA	5610
	GGCGACTGAGTCGTGAG	5611
	CTGACGACTCAGTCGCC	5612
White leaves Immutans <i>Triticum aestivum</i> Arg25Term AGA-TGA	GAGGAAGGGGGATTTCGACGAGGAGCTCACCCTCGCCGGCGAGG ACGGCGACTGGGTCGTCTGATTTCGAGCAGTCCTTCAACGTATTCC TCACGGATACTGTCATCTTTATACTCGATATTC	5613
	GAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAA GGACTGCTCGAATCAGACGACCCAGTCGCCGTCTCGCCGGCGA GGGTGAGCTCCTCGTGAATCCCCCTTCCTC	5614
	GGGTCGTCTGATTTCGAG	5615
	CTCGAATCAGACGACCC	5616
White leaves Immutans <i>Triticum aestivum</i> Glu27Term GAG-TAG	GGGGGATTTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCG ACTGGGTCGTGAGATTCTAGCAGTCCTTCAACGTATTCTCACGGA TACTGTCATCTTTATACTCGATATTCTGTATC	5617
	GATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATAC GTTGAAGGACTGCTAGAATCTGACGACCCAGTCGCCGTCTCGCC GGCGAGGGTGAGCTCCTCGTGAATCCCCC	5618
	TCAGATTCTAGCAGTCC	5619
	GGACTGCTAGAATCTGA	5620
White leaves Immutans <i>Triticum aestivum</i> Gln28Term CAG-TAG	GGATTTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTG GGTCGTGAGATTTCGAGTAGTCCTTCAACGTATTCTCACGGATACT GTCATCTTTATACTCGATATTCTGTATCGTG	5621
	CACGATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAA TACGTTGAAGGACTACTCGAATCTGACGACCCAGTCGCCGTCTC GCCGGCGAGGGTGAGCTCCTCGTGAATCC	5622
	GATTTCGAGTAGTCCTTC	5623
	GAAGGACTACTCGAATC	5624

White leaves Immutans <i>Triticum aestivum</i> Tyr46Term TAT-TAG	CGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATA CTCGATATTCTGTAGCGTGACCGCGACTACGCAAGGTTCTTCGTG CTCGAGACCATCGCCAGGGTGCCCTATTTTC	5625
	GAAATAGGGCACCCCTGGCGATGGTCTCGAGCACGAAGAACCTTG CGTAGTCGCGGTCACGCTACAGAATATCGAGTATAAAGATGACAG TATCCGTGAGGAATACGTTGAAGGACTGCTCG	5626
	ATTCTGTAGCGTGACCG	5627
	CGGTCACGCTACAGAAT	5628

Example 30

Altering amino acid content of plants

[255] Another aim of biotechnology is to generate plants, especially crop plants, with added value traits. An example of such a trait is improved nutritional quality in food crops. For example, lysine, tryptophan and threonine, which are essential amino acids in the diet of humans and many animals, are limiting nutrients in most cereal crops. Consequently, grain-based diets, such as those based on corn, barley, wheat, rice, maize, millet, sorghum, and the like, must be supplemented with more expensive synthetic amino acids or amino-acid-containing oilseed protein meals. Increasing the lysine content of these grains or of any of the feed component crops would result in significant added value.

[256] Naturally occurring mutants of plants that have different levels of particular essential amino acids have been identified. However, these mutants are generally not the result of increased free amino acid, but are instead the result of shifts in the overall protein profile of the grain. For example, in maize, reduced levels of lysine-deficient endosperm proteins (prolamines) are complemented by elevated levels of more lysine-rich proteins (albumins, globulins and glutelins). While nutritionally superior, these mutants are associated with reduced yields and poor grain quality, limiting their agronomic usefulness.

[257] An alternative approach is to generate plants with mutations that render key amino acid biosynthetic enzymes insensitive to feedback inhibition. Many such mutations are known and mutation results in increased free amino acid. The increased production can optionally be coupled to increased expression of an abundant storage protein comprising the chosen amino acid. Alternatively, a normally abundant protein can be engineered to contain more of the target amino acid.

[258] The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that remove feedback inhibition in plant amino acid biosynthetic enzymes.

Table 37
Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS <i>Arabidopsis thaliana</i> Arg77His CGT-CAT	TATCCTCCAGGATCTTAAGATTTCTCCTAATTTGTCCTCAGCT GAGCATTAAAGCCCATAGAAACTGTAGCAACATCGGTGTTGCACA GATCGTGGCGGCTAAGTGGTCCAACAACCC	5629
	GGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACCGAT GTTGCTACAGTTTCTATGGGCTTTAATGCTCAGCTGACGGACGAA ATTAGGAGGAAATCTTAAGATCCTGGAGGATA	5630
	TAAAGCCCATAGAAACT	5631
	AGTTTCTATGGGCTTTA	5632
Met Overproduction CGS <i>Arabidopsis thaliana</i> Ser81Asn AGC-AAC	TCTTAAGATTTCTCCTAATTTGTCCTCAGCTGAGCATTAAAGC CCGTAGAAACTGTAAACAACATCGGTGTTGCACAGATCGTGGCGG CTAAGTGGTCCAACAACCCATCCTCCGCGTT	5633
	AACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTG TGCAACACCGATGTTGTACAGTTTCTACGGGCTTTAATGCTCAGC TGACGGACGAAATTAGGAGGAAATCTTAAGA	5634
	AAACTGTAAACAACATCG	5635
	CGATGTTGTACAGTTT	5636
Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Ser GGT-AGT	TTTCCTCCTAATTTGTCCTCAGCTGAGCATTAAAGCCCGTAGAA ACTGTAGCAACATCAGTGTTGCACAGATCGTGGCGGCTAAGTGGT CCAACAACCCATCCTCCGCGTTACCTTCGG	5637
	CCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCC ACGATCTGTGCAACACATGATGTTGCTACAGTTTCTACGGGCTTTAA TGCTCAGCTGACGGACGAAATTAGGAGGAAA	5638
	GCAACATCAGTGTTGCA	5639
	TGCAACACATGATGTTGC	5640
Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Asp GGT-GAT	TTCCTCCTAATTTGTCCTCAGCTGAGCATTAAAGCCCGTAGAAA CTGTAGCAACATCGATGTTGCACAGATCGTGGCGGCTAAGTGGTC CAACAACCCATCCTCCGCGTTACCTTCGGC	5641
	GCCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGC CACGATCTGTGCAACATCGATGTTGCTACAGTTTCTACGGGCTTTA ATGCTCAGCTGACGGACGAAATTAGGAGGAA	5642
	CAACATCGATGTTGCAC	5643
	GTGCAACATCGATGTTG	5644

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS <i>Fragraria vesca</i> Arg73His CGC-CAC	TATCGTCACTCATCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGC TCAGCACCAAGGCCCACCGCAACTGCAGCAACATCGGCGTCGCG CAGATCGTCGCGGCTTCGTGGTCCAACAAAGA	5645
	TCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGCCGAT GTTGCTGCAGTTGCGGTGGGCCTTGGTGCTGAGCTGGCGGACGA AGTTGGGAGGGAAGCGGAGGATGAGTGACGATA	5646
	CAAGGCCCCACCGCAACT	5647
	AGTTGCGGTGGGCCTTG	5648
Met Overproduction CGS <i>Fragraria vesca</i> Ser77Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGG CCCGCCGCAACTGCAACAACATCGGCGTCGCGCAGATCGTCGCG GCTTCGTGGTCCAACAAAGACTCCGACCTTTC	5649
	GAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTG CGCGACGCCGATGTTGTGTCAGTTGCGGCGGGCCTTGGTGCTGA GCTGGCGGACGAAGTTGGGAGGGAAGCGGAGGA	5650
	CAACTGCAACAACATCG	5651
	CGATGTTGTGTCAGTTG	5652
Met Overproduction CGS <i>Fragraria vesca</i> Gly80Ser GGC-AGC	TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG CAACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCGGCTTCGT GGTCCAACAAAGACTCCGACCTTTCGGCGGTGC	5653
	GCACCGCCGAAAGGTGCGAGTCTTTGTTGGACCACGAAGCCGCG ACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGGGCCTT GGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAA	5654
	GCAACATCAGCGTCGCG	5655
	CGCGACGCTGATGTTGC	5656
Met Overproduction CGS <i>Fragraria vesca</i> Gly80Asp GGC-GAC	TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG AACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCGGCTTCGTG GTCCAACAAAGACTCCGACCTTTCGGCGGTGCC	5657
	GGCACCGCCGAAAGGTGCGAGTCTTTGTTGGACCACGAAGCCGC GACGATCTGCGCGACGCTCGATGTTGCTGCAGTTGCGGCGGGCCT TGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAA	5658
	CAACATCAGCGTCGCGC	5659
	GCGCGACGCTCGATGTTG	5660
Met Overproduction CGS <i>Glycine max</i> Arg68His CGC-CAC	TCTCCTCCCTCATCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGC TAAGCACCAAGGCGAGCCGCAACTGCAGCAACATCGGCGTCGCG CAAATCGTCGCCGCTTCGTGGTCAACAACAG	5661
	CTGTTGTTGACCACGAAGCGGCGACGATTTGCGCGACGCCGAT GTTGCTGCAGTTGCGGCTCGCCTTGGTGCTTAGCTGGCGCTGGA AGTTGGGAGGGAAGCGGAGGATGAGGGAGGAGA	5662
	CCAAGGCGAGCCGCAAC	5663
	GTTGCGGCTCGCCTTG	5664

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS <i>Glycine max</i> Ser72Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGG CGCGCCGCAACTGCAACAACATCGGCGTCGCGCAAATCGTCGCC GCTTCGTGGTTCGAACAACAGCGACAACCTCTCC	5665
	GGAGAGTTGTCGCTGTTGTTTCGACCACGAAGCGGCGACGATTTG CGCGACGCCGATGTTGTTGTCAGTTGCGGCGCGCCTTGGTGCTTA GCTGGCGCTGGAAGTTGGGAGGGAAGCGGAGGA	5666
	CAACTGCAACAACATCG	5667
	CGATGTTGTTGTCAGTTG	5668
Met Overproduction CGS <i>Glycine max</i> Gly75Ser GGC-AGC	TTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCG CAACTGCAGCAACATCAGCGTCGCGCAAATCGTCGCCGCTTCGT GGTCGAACAACAGCGACAACCTCTCCGGCCGCCG	5669
	CGGCGGCCGGAGAGTTGTCGCTGTTGTTTCGACCACGAAGCGGCG ACGATTTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGCGCCTT GGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA	5670
	GCAACATCAGCGTCGCG	5671
	CGCGACGCTGATGTTGC	5672
Met Overproduction CGS <i>Glycine max</i> Gly75Asp GGC-GAC	TCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCGC AACTGCAGCAACATCAGCGTCGCGCAAATCGTCGCCGCTTCGTG GTCGAACAACAGCGACAACCTCTCCGGCCGCCG	5673
	CCGGCGGCCGGAGAGTTGTCGCTGTTGTTTCGACCACGAAGCGGC GACGATTTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGCGCCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGA	5674
	CAACATCAGCGTCGCGC	5675
	GCGCGACGCTGATGTTG	5676
Met Overproduction CGS <i>Solanum tuberosum</i> Arg70His AGG-CAC	TGTCTTCTCTGATTTTCAGGTTTCTCCTAATTTCTGAGGCAGCT AAGCATTAAAGGCTCACAGGAATTGCAGCAATATTGGCGTGGCTCA AGTTGTGGCGGCTTCTGGTCTAACAACCA	5677
	TGGTTGTTAGACCAGGAAGCCGCCACAACCTTGAGCCACGCCAATA TTGCTGCAATTCCTGTGAGCCTTAATGCTTAGCTGCCTCACGAAAT TAGGAGGAAACCTGAAATCAGAGAAGACA	5678
	TAAGGCTCACAGGAATT	5679
	AATTCCTGTGAGCCTTA	5680
Met Overproduction CGS <i>Solanum tuberosum</i> Ser74Asn AGC-AAC	TTTCAGGTTTCTCCTAATTTCTGAGGCAGCTAAGCATTAAAGG TAGGAGGAATTGCAACAATATTGGCGTGGCTCAAGTTGTGGCGG CTTCCTGGTCTAACAACCAAGCCGGTCTGA	5681
	TCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCCACAACCTTG AGCCACGCCAATATTGTTGCAATTCCTCCTAGCCTTAATGCTTAGC TGCCTCACGAAATTAGGAGGAAACCTGAAAA	5682
	GAATTGCAACAATATTG	5683
	CAATATTGTGCAATTC	5684

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS <i>Solanum tuberosum</i> Gly77Ser GGC-AGC	TTTCCTCCTAATTTCTGAGGCAGCTAAGCATTAAAGGCTAGGAGG AATTGCAGCAATATTAGCGTGGCTCAAGTTGTGGCGGCTTCCTGG TCTAACAACCAAGCCGGTCCTGAATTCCTC	5685
	GAGTGAATTCAGGACCGGCTTGTTGTTAGACCAGGAAGCCGCC ACAACCTTGAGCCACGCTAATATTGCTGCAATTCCTCCTAGCCTTAA TGCTTAGCTGCCTCACGAAATTAGGAGGAAA	5686
	GCAATATTAGCGTGGCT	5687
	AGCCACGCTAATATTGC	5688
Met Overproduction CGS <i>Solanum tuberosum</i> Gly77Asp GGC-GAC	TTCCTCCTAATTTCTGAGGCAGCTAAGCATTAAAGGCTAGGAGGA ATTGCAGCAATATTGACGTGGCTCAAGTTGTGGCGGCTTCCTGGT CTAACAACCAAGCCGGTCCTGAATTCCTC	5689
	GGAGTGAATTCAGGACCGGCTTGTTGTTAGACCAGGAAGCCGC CACAACCTTGAGCCACGCTCAATATTGCTGCAATTCCTCCTAGCCTTA ATGCTTAGCTGCCTCACGAAATTAGGAGGAA	5690
	CAATATTGACGTGGCTC	5691
	GAGCCACGCTCAATATTG	5692
Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Arg73His CGC-CAC	CTTCCTCTCTTATCCTTCGCTTTCTCCCAACTTTGTCCGTCAGCT CAGCACCAAGGCTCGCCACAACCTGCAGCAACATTGGTGTGCGAC AGGTCGTCGCTGCCTCCTGGTCCAACAACCTC	5693
	GAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACACCAAT GTTGCTGCAGTTGTGGCGAGCCTTGGTGCTGAGCTGACGGACAA AGTTGGGAGGAAAGCGAAGGATAAGAGAGGAAG	5694
	GGCTCGCCACAACCTGCA	5695
	TGCAGTTGTGGCGAGCC	5696
Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Ser77Asn AGC-AAC	TCCTTCGCTTTCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGG CTCGCCGCAACTGCAACAACATTGGTGTGCGACAGGTCGTCGCT GCCTCCTGGTCCAACAACCTCCGATGCCGGCGC	5697
	GCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCT GTGCGACACCAATGTTGTGTCAGTTGCGGCGAGCCTTGGTGCTG AGCTGACGGACAAAGTTGGGAGGAAAGCGAAGGA	5698
	CAACTGCAACAACATTG	5699
	CAATGTTGTGTCAGTTG	5700
Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Gly80Ser GGT-AGT	TTTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGC AACTGCAGCAACATTAGTGTGCGACAGGTCGTCGCTGCCTCCTG GTCCAACAACCTCCGATGCCGGCGCCACCTCTT	5701
	AAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGC GACGACCTGTGCGACACTAATGTTGCTGCAAGTTGCGGCGAGCCT TGGTGCTGAGCTGACGGACAAAGTTGGGAGGAAA	5702
	GCAACATTAGTGTGCGCA	5703

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCGACACTAATGTTGC	5704
Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Gly80Asp GGT-GAT	TTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGCA ACTGCAGCAACATTGATGTGCGCACAGGTCGTGCTGCCTCCTGGT CCAACAACCTCCGATGCCGGCGCCACCTCTTG	5705
	CAAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAG CGACGACCTGTGCGACATCAATGTTGCTGCAGTTGCGGCGAGCC TTGGTGCTGAGCTGACGGACAAAGTTGGGAGGAA	5706
	CAACATTGATGTGCGCAC	5707
	GTGCGACATCAATGTTG	5708
Met Overproduction CGS <i>Zea mays</i> Arg41His CGC-CAC	CCTCTGCTACCATCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGC TTAGCACCAAGGCACACCGCAACTGCAGCAACATCGGCGTCGCG CAGATCGTCGCCGCCGCGTGGTCCGACTGCCC	5709
	GGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGCCGA TGTTGCTGCAGTTGCGGTGTGCTTGGTGCTAAGCTGGCGGACA AAGTTTGGCGGAAAGCGGAGGATGGTAGCAGAGG	5710
	CAAGGCACACCGCAACT	5711
	AGTTGCGGTGTGCTTG	5712
Met Overproduction CGS <i>Zea mays</i> Ser45Asn AGC-AAC	TCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGG CACGCCGCAACTGCAACAACATCGGCGTCGCGCAGATCGTCGCC GCCGCGTGGTCCGACTGCCCCGCCGCTCGCCC	5713
	GGGCGAGCGGCGGGGCGAGTCGGACCACGCGGCGGCGACGATCT GCGCGACGCCGATGTTGTGTCAGTTGCGGCGTGCTTGGTGCTA AGCTGGCGGACAAAGTTTGGCGGAAAGCGGAGGA	5714
	CAACTGCAACAACATCG	5715
	CGATGTTGTGTCAGTTG	5716
Met Overproduction CGS <i>Zea mays</i> Gly48Ser GGC-AGC	TTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGC AACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCCGCCGCGTG GTCCGACTGCCCCGCCGCTCGCCCCCACTTAG	5717
	CTAAGTGGGGGCGAGCGGCGGGGCGAGTCGGACCACGCGGCGG CGACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGTGCC TTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAA	5718
	GCAACATCAGCGTCGCG	5719
	CGCGACGCTGATGTTGC	5720
Met Overproduction CGS <i>Zea mays</i> Gly48Asp GGC-GAC	TTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGCA ACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCCGCCGCGTG TCCGACTGCCCCGCCGCTCGCCCCCACTTAG	5721
	CCTAAGTGGGGGCGAGCGGCGGGGCGAGTCGGACCACGCGGCG GCGACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGTG CTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAA	5722
	CAACATCAGCGTCGCGC	5723

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCGCGACG <u>I</u> CGATGTTG	5724
Met Overproduction TS <i>Arabidopsis thaliana</i> Leu205Arg CTT-CGT	GTATGAATGATCTGTGGGTGAAACACTGTGGGATTAGTCATACAG GAAGTTTCAAGGATC <u>G</u> TGGAATGACTGTTTTGGTTAGTCAAGTTAA TCGTCTGAGAAAGATGAAACGACCTGTGGT	5725
	ACCACAGGTCGTTTCATCTTTCTCAGACGATTAACCTTGACTAACCA AAACAGTCATTCCA <u>C</u> GATCCTTGAACTTCCTGTATGACTAATCCC ACAGTGTTTCACCCACAGATCATTACATAC	5726
	CAAGGATC <u>G</u> TGGAATGA	5727
	TCATTCCA <u>C</u> GATCCTTG	5728
Met Overproduction TS <i>Solanum tuberosum</i> Leu198Arg CTT-CGT	GCATGACTGATTTGTGGGTCAAACACTGTGGGATTAGCCATACTG GTAGTTTTAAGGATC <u>G</u> TGGGATGACTGTTTTGGTGAGTCAAGTTAA TCGCTTGCGGAAAATGCATAAACCGTTGT	5729
	ACAACCGGTTTATGCATTTTCCGCAAGCGATTAACCTTGACTCACCA AAACAGTCATCCCA <u>C</u> GATCCTTAAACTACCAGTATGGCTAATCCC ACAGTGTTTGACCCACAAATCAGTCATGC	5730
	TAAGGATC <u>G</u> TGGGATGA	5731
	TCATCCCA <u>C</u> GATCCTTA	5732
Lys Overproduction DHPS <i>Zea mays</i> Ser157Asn AGC-AAC	TCATTGGGCACACAGTGAACCTGCTTTGGCTCTAGAATCAAAGTGA TAGGCAACACAGGAA <u>A</u> CAACTCAACCAGAGAAGCCGTCACGCA ACAGAACAGGGATTTGCTGTTGGCATGCATGC	5733
	GCATGCATGCCAACAGCAAATCCCTGTTCTGTTGCGTGGACGGCT TCTCTGGTTGAGTTG <u>I</u> TTCTGTGTTGCCTATCACTTTGATTCTAG AGCCAAAGCAGTTCACTGTGTGCCCAATGA	5734
	CACAGGAA <u>A</u> CAACTCAA	5735
	TTGAGTTG <u>I</u> TTCTGTG	5736
Lys Overproduction DHPS <i>Zea mays</i> Ala166Val GCA-GAA	GCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACCA GAGAAGCCGTCCACG <u>A</u> AACAGAACAGGGATTTGCTGTTGGCATG CATGCGGCTCTCCACATCAATCCTTACTACGG	5737
	CCGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGC AATCCCTGTTCTGTT <u>I</u> CGTGGACGGCTTCTCTGGTTGAGTTGCTT CCTGTGTTGCCTATCACTTTGATTCTAGAGC	5738
	CGTCCACG <u>A</u> AACAGAAC	5739
	GTTCTGTT <u>I</u> CGTGGACG	5740
Lys Overproduction DHPS <i>Zea mays</i> Ala166Thr GCA-ACA	GGCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACC AGAGAAGCCGTCCAC <u>A</u> CAACAGAACAGGGATTTGCTGTTGGCAT GCATGCGGCTCTCCACATCAATCCTTACTACG	5741
	CGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGCA AATCCCTGTTCTGTTG <u>I</u> GTGGACGGCTTCTCTGGTTGAGTTGCTT CTGTGTTGCCTATCACTTTGATTCTAGAGCC	5742

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGTCCAC <u>A</u> CAACAGAA	5743
	TTCTGTTG <u>I</u> GTGGACGG	5744
Lys Overproduction DHPS <i>Oryza sativa</i> Ser124Asn AGT-AAT	TTATTGGGCATACAGTTAACTGCTTTGGCACTAAAATTAAAGTGGT CGGCAACACAGGAA <u>A</u> TA ACTCAACAAGGGAGGCTATTACGCAAC TGAGCAGGGATTGCTGTAGGTATGCACGC	5745
	GCGTGCATACCTACAGCGAATCCCTGCTCAGTTGCGTGAATAGCC TCCCTTGTTGAGTTA <u>TT</u> CCTGTGTTGCCGACCACTTTAATTTTAGT GCCAAAGCAGTTAACTGTATGCCCAATAA	5746
	CACAGGAA <u>A</u> TA ACTCAA	5747
	TTGAGTTA <u>TT</u> CCTGTG	5748
Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Val GCA-GTA	GCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTA ACTCAACAA GGGAGGCTATTACG <u>I</u> A ACTGAGCAGGGATTGCTGTAGGTATG CACGCGGCTCTCCACATCAATCCTTACTACGG	5749
	CCGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGC GAATCCCTGCTCAGTT <u>A</u> CGTGAATAGCCTCCCTTGTTGAGTTACTT CCTGTGTTGCCGACCACTTTAATTTTAGTGC	5750
	TATTCACG <u>I</u> A ACTGAGC	5751
	GCTCAGTT <u>A</u> CGTGAATA	5752
Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Thr GCA-ACA	GGCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTA ACTCAACA AGGGAGGCTATTAC <u>A</u> CA ACTGAGCAGGGATTGCTGTAGGTAT GCACGCGGCTCTCCACATCAATCCTTACTACG	5753
	CGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGCG AATCCCTGCTCAGTTG <u>I</u> GTGAATAGCCTCCCTTGTTGAGTTACTTC CTGTGTTGCCGACCACTTTAATTTTAGTGCC	5754
	CTATTCAC <u>A</u> CA ACTGAG	5755
	CTCAGTTG <u>I</u> GTGAATAG	5756
Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ser165Asn AGT-AAT	TCATCGGGCATACTGTTAACTGCTTTGGAGCCAACATTAAAGTGAT AGGCAACACGGGAA <u>A</u> TA ACTCAACCAGAGAAGCTGTTACGCGA CAGAGCAGGGATTGCTGTTGGCATGCATGC	5757
	GCATGCATGCCAACAGCAAATCCCTGCTCTGTGCGGTGAACAGCT TCTCTGGTTGAGTTA <u>TT</u> CCCCGTGTTGCCTATCACTTAATGTTGG CTCCAAAGCAGTTAACAGTATGCCCGATGA	5758
	CACGGGAA <u>A</u> TA ACTCAA	5759
	TTGAGTTA <u>TT</u> CCCCGTG	5760
Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Val GCG-GTG	GAGCCAACATTAAAGTGATAGGCAACACGGGAAGTA ACTCAACCA GAGAAGCTGTTACG <u>I</u> GACAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTTCATGTCAATCCTTACTACGG	5761

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTCA A CGTGAACAGCTTCTCTGGTTGAGTTACTTC CCGTGTTGCCTATCACTTTAATGTTGGCTC	5762
	TGTTACAGT I GACAGAGC	5763
	GCTCTGTC A CGTGAACA	5764
Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Thr GCG-ACG	GGAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACC AGAGAAGCTGTTACAC A CGACAGAGCAGGGATTTGCTGTTGGCAT GCATGCAGCTCTTCATGTCAATCCTTACTACG	5765
	CGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTCTG T GTGAACAGCTTCTCTGGTTGAGTTACTTCC CGTGTTGCCTATCACTTTAATGTTGGCTCC	5766
	CTGTTACAC A CGACAGAG	5767
	CTCTGTCTG T GTGAACAG	5768
Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ser154Asn AGT-AAT	TCATCGGGCACACTGTTAACTGCTTTGGAACAACTAAAGTGAT AGGCAACACGGGAA A TAACTCAACTAGAGAAGCGATTACAGCTTC AGAGCAGGGATTTGCTGTTGGCATGCATGC	5769
	GCATGCATGCCAACAGCAAATCCCTGCTCTGAAGCGTGAATCGCT TCTCTAGTTGAGTTA I TTCCCGTGTTGCCTATCACTTTAATGTTAGT TCCAAAGCAGTTAACAGTGTGCCCGATGA	5770
	CACGGGAA A TAACTCAA	5771
	TTGAGTTA I TTCCCGTG	5772
Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Val GCT-GTT	GAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACTA GAGAAGCGATTACAG T TTCAGAGCAGGGATTTGCTGTTGGCATGC ATGCAGCTCTCCATGTCAATCCTTACTATGG	5773
	CCATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGAA A CGTGAATCGCTTCTCTAGTTGAGTTACTTC CCGTGTTGCCTATCACTTTAATGTTAGTTC	5774
	GATTCAG T TTTACAGAGC	5775
	GCTCTGAA A CGTGAATC	5776
Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Thr GCT-ACT	GGAATAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACT AGAGAAGCGATTACAC A CTTCAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTCCATGTCAATCCTTACTATG	5777
	CATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGAAG T GTGAATCGCTTCTCTAGTTGAGTTACTTCC CGTGTTGCCTATCACTTTAATGTTAGTTC	5778
	CGATTACAC A CTTCAGAG	5779
	CTCTGAAG T GTGAATCG	5780

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ser154Asn AGT-AAT	CTCATTGGGCATACTGTGAACTGCTTTGGCTCTAGAATTAAAGTGA TAGGCAACACAGGAAATAACTCAACCAGAGAAGCTGTTACAGCAA CAGAGCAGGGATTTGCTGTTGGCATGCATG	5781
	CATGCATGCCAACAGCAAATCCCTGCTCTGTTGCGTGAACAGCTT CTCTGGTTGAGTTATTTCTGTGTTGCCTATCACTTTAATTCTAGA GCCAAAGCAGTTCACAGTATGCCCAATGAG	5782
	CACAGGAAATAACTCAA	5783
	TTGAGTTATTTCTGTG	5784
Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Val GCA-GTA	GCTCTAGAATTAAAGTGATAGGCAACACAGGAAGTAACTCAACCA GAGAAGCTGTTACAGTAACAGAGCAGGGATTTGCTGTTGGCATGC ATGCAGCTCTCCACATCAATCCTTACTATGG	5785
	CCATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTTACGTGAACAGCTTCTCTGGTTGAGTTACTTC CTGTGTTGCCTATCACTTTAATTCTAGAGC	5786
	TGTTACAGTAACAGAGC	5787
	GCTCTGTTACGTGAACA	5788
Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Thr GCA-ACA	GGCTCTAGAATTAAAGTGATAGGCAACACAGGAAGTAACTCAACC AGAGAAGCTGTTACACAACAACAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTCCACATCAATCCTTACTATG	5789
	CATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTTGTGTGAACAGCTTCTCTGGTTGAGTTACTTCC TGTGTTGCCTATCACTTTAATTCTAGAGCC	5790
	CTGTTACACAACAACAGAG	5791
	CTCTGTTGTGTGAACAG	5792
Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ser136Asn AGC-AAC	TCATTGGTCACACAGTCAATTGTTTTGGAGGGTCCATCAAAGTCAT CGGGAACACTGGAAACAACCTCCACAAGGGAAGCAATCCATGCAA CTGAACAGGGATTTGCTGTAGGTATGCATGC	5793
	GCATGCATACCTACAGCAAATCCCTGTTGAGTTGCATGGATTGCTT CCCTTGTGGAGTTGTTCCAGTGTTCCCGATGACTTTGATGGACC CTCCAAAACAATTGACTGTGTGACCAATGA	5794
	CACTGGAAACAACCTCCA	5795
	TGGAGTTGTTCCAGTG	5796
Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Val GCA-GTA	GAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCACAA GGGAAGCAATCCATGTAAGTGAACAGGGATTTGCTGTAGGTATGC ATGCAGCTCTTCACATTAATCCCTACTATGG	5797
	CCATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCA AATCCCTGTTGAGTTACATGGATTGCTTCCCTTGTGGAGTTGCTTC CAGTGTTCCCGATGACTTTGATGGACCCTC	5798
	AATCCATGTAAGTGAAC	5799

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTCAGTT <u>A</u> CATGGATT	5800
Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Thr GCA-ACA	GGAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCAC AAGGGAAGCAATCCAT <u>A</u> CAACTGAACAGGGATTGCTGTAGGTAT GCATGCAGCTCTTCACATTAATCCCTACTATG	5801
	CATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCAA ATCCCTGTTCAAGTTG <u>T</u> ATGGATTGCTTCCCTTGTGGAGTTGCTTCC AGTGTTCCCGATGACTTTGATGGACCCTCC	5802
	CAATCCAT <u>A</u> CAACTGAA	5803
	TTCAGTTG <u>T</u> ATGGATTG	5804
Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ser142Asn AGC-AAC	TTATAGGCCATACCGTTAACTGTTTTGGCGGAAGCATCAAAGTCAT TGGAACACTGGAA <u>A</u> CAATTGACTAGAGAAGCAATCCACGCGAC TGAACAAGGATTGCGGGTTGGAATGCATGC	5805
	GCATGCATTCCAACCGCGAATCCTTGTTCAAGTCGCGTGGATTGCT TCTCTAGTCGAATTG <u>T</u> TTCCAGTGTTTCCAATGACTTTGATGCTTC CGCCAAAACAGTTAACGGTATGGCCTATAA	5806
	CACTGGAA <u>A</u> CAATTGCA	5807
	TCGAATTG <u>T</u> TTCCAGTG	5808
Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Val GCG-GTG	GCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACTA GAGAAGCAATCCACG <u>T</u> GACTGAACAAGGATTCGCGGTTGGAATG CATGCTGCTCTTCATATAAACCCCTTACTATGG	5809
	CCATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCG AATCCTTGTTCAAGTC <u>A</u> CGTGGATTGCTTCTCTAGTCGAATTGCTTC CAGTGTTTCCAATGACTTTGATGCTTCCGC	5810
	AATCCACG <u>T</u> GACTGAAC	5811
	GTTCAGTC <u>A</u> CGTGGATT	5812
Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Thr GCG-ACG	GGCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACT AGAGAAGCAATCCAC <u>A</u> CGACTGAACAAGGATTCGCGGTTGGAAT GCATGCTGCTCTTCATATAAACCCCTTACTATG	5813
	CATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCGA ATCCTTGTTCAAGTCG <u>T</u> GTGGATTGCTTCTCTAGTCGAATTGCTTCC AGTGTTTCCAATGACTTTGATGCTTCCGCC	5814
	CAATCCAC <u>A</u> CGACTGAA	5815
	TTCAGTCG <u>T</u> GTGGATTG	5816
Lys Overproduction DHPS <i>Glycine max</i> Ser103Asn AGC-AAC	TTATTGCTCATACAGTCAACTGTTTTGGTGGGAAAATTAAGGTTAT TGGAATACTGGAA <u>A</u> CAACTCCACCAGGGAAGCAATTCATGCCAC TGAGCAGGGTTTTGCTGTTGGAATGCATGC	5817
	GCATGCATTCCAACAGCAAAACCCTGCTCAGTGGCATGAATTGCT TCCCTGGTGGAGTTG <u>T</u> TTCCAGTATTTCCAATAACCTTAATTTTCC CACCAAAACAGTTGACTGTATGAGCAATAA	5818

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TACTGGAA <u>A</u> CAACTCCA	5819
	TGGAGTTG <u>I</u> TTCCAGTA	5820
Lys Overproduction DHPS <i>Glycine max</i> Ala112Val GCC-GTC	GTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACCA GGGAAGCAATTCATG <u>T</u> CACTGAGCAGGGTTTTGCTGTTGGAATGC ATGCTGCCCTTCACATAAACCCCTTACTATGG	5821
	CCATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCA AAACCCTGCTCAGTG <u>A</u> CATGAATTGCTTCCCTGGTGGAGTTGCTT CCAGTATTTCCAATAACCTTAATTTTCCCAC	5822
	AATTCATG <u>I</u> CACTGAGC	5823
	GCTCAGTG <u>A</u> CATGAATT	5824
Lys Overproduction DHPS <i>Glycine max</i> Ala112Thr GCC-ACC	GGTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACC AGGGAAGCAATTCAT <u>A</u> CCACTGAGCAGGGTTTTGCTGTTGGAATG CATGCTGCCCTTCACATAAACCCCTTACTATG	5825
	CATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCAA AACCCCTGCTCAGTGGT <u>A</u> TGAATTGCTTCCCTGGTGGAGTTGCTTC CAGTATTTCCAATAACCTTAATTTTCCCACC	5826
	CAATTCAT <u>A</u> CCACTGAG	5827
	CTCAGTGGT <u>A</u> TGAATTG	5828
Trp Overproduction AS <i>Arabidopsis thaliana</i> Asp341Asn GAC-AAC	CTTGCAGGAGACATATTTTCAAGTCGTGCTGAGTCAACGTTTTGAG CGGCGAACATTTGCA <u>A</u> ACCCCTTTGAAGTTTATAGAGCACTAAGA GTTGTGAATCCAAGTCCGTATATGGGTTATT	5829
	AATAACCCATATACGGACTTGGATTCACAACTCTTAGTGCTCTATA AACTTCAAAGGGGTT <u>I</u> TGCAAATGTTGCGCGCTCAAAACGTTGACT CAGCACGATCTGAAATATGTCTCCTGCAAG	5830
	CATTTGCA <u>A</u> ACCCCTTT	5831
	AAAGGGGT <u>I</u> TGCAAATG	5832
Trp Overproduction AS <i>Nicotiana tabacum</i> Asp326Asn GAC-AAC	GCTGCAGGAGACATATTTCAAATCGTTTTAAGTCAACGCTTTGAGA GAAGAACATTTGCT <u>A</u> ACCCATTTGAAGGTACAGAGCATTGAAGAAT TGTGAATCCAAGCCCATATATGACTTACA	5833
	TGTAAGTCATATATGGGCTTGGATTCACAATTCTTAATGCTCTGTA CACTTCAAATGGGT <u>I</u> AGCAAATGTTCTTCTCTCAAAGCGTTGACTT AAAACGATTTGAAATATGTCTCCTGCAGC	5834
	CATTTGCT <u>A</u> ACCCATTT	5835
	AAATGGGT <u>I</u> AGCAAATG	5836
Trp Overproduction AS <i>Oryza sativa</i> Asp323Asn GAC-AAC	CTAGCTGGTGACATTTTTCAAGTAGTCTTAAGCCAGCGTTTTGAGA GGCGTACATTTGCT <u>A</u> ACCCCTTTGAGGTGTACCGTGCAATTGCGTA TTGTCAATCCTAGTCCTTATATGGCCTATC	5837

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GATAGGCCATATAAGGACTAGGATTGACAATACGCAATGCACGGT ACACCTCAAAGGGGT <u>T</u> AGCAAATGTACGCCTCTCAAACGCTGGC TTAAGACTACTTGAAAAATGTCACCAGCTAG	5838
	CATTTGCT <u>A</u> ACCCCTTT	5839
	AAAGGGGT <u>T</u> AGCAAATG	5840
Trp Overproduction AS <i>Ruta graveolens</i> Asp354Asn GAC-AAC	CTTGCTGGTGACATATTCCAGATCGTACTAAGTCAGCGTTTTGAAA GGCGAACGTTTCGCA <u>A</u> ACCCATTTGAAATCTATAGATCACTGAGGA TTGTTAATCCAAGCCCATATATGACTTATT	5841
	AATAAGTCATATATGGGCTTGGATTAACAATCCTCAGTGATCTATA GATTTCAAATGGGT <u>T</u> TGCGAACGTTTCGCCTTTCAAACGCTGACTT AGTACGATCTGGAATATGTCACCAGCAAG	5842
	CGTTTCGCA <u>A</u> ACCCATTT	5843
	AAATGGGT <u>T</u> TGCGAACG	5844
Trp Overproduction AS <i>Catharanthus roseus</i> Asp354Asn GAT-AAT	CTGGCTGGGGACATATTCCAGCTTGTCTAAGTCAGCGTTTTGAA CGGCGAACATTTGCA <u>A</u> ATCCATTTGAAGTCTACCGAGCATTGAGA ATTGTCAACCCAAGTCCATATATGACTTATT	5845
	AATAAGTCATATATGGACTTGGGTTGACAATTCTCAATGCTCGGTA GACTTCAAATGGAT <u>T</u> TGCAAATGTTGCCGTTCAAACGCTGACTT AGGACAAGCTGGAATATGTCCCCAGCCAG	5846
	CATTTGCA <u>A</u> ATCCATTT	5847
	AAATGGAT <u>T</u> TGCAAATG	5848

Example 31

Production of modified starch in plants

[259] A principal aim of biotechnology is the improvement of crop plants for food value, agriculture, and to produce a range of plant-derived raw materials. Along with oils, fats and proteins, polysaccharides constitute the main raw materials derived from plants, and apart from cellulose, the storage polymer starch is the most important polysaccharide raw material. Starch is derived from a range of plants, but maize is the most important cultivated plant for the production of starch.

[260] The polysaccharide starch is a polymer made up of glucose molecules. However, starch is not a homogeneous raw material and is, in fact, a highly complex mixture of various types of molecules which differ from each other, for example, in their degree of polymerization and in the degree of branching of the glucose chains. For example, amylose-starch is a basically non-branched polymer made up of α -1,4-glycosidically branched glucose molecules, and amylopectin-starch is a complex mixture of variously branched glucose chains. The branching results from additional α -1,6-glycosidic linkages. In plants from which starch is typically isolated, for example maize or potato, the starch is approximately 25% amylose-starch and 75% amylopectin-starch.

[261] In maize, various mutants in starch metabolism are known, for example *waxy*, *sugary*, *shrunk* and *opaque-2*. In addition to producing a modified starch, these mutations greatly improve grain quality in maize, and thus expand the use of maize not only as the food but also for the important industrial materials in food chemistry. It would therefore be advantageous to be able readily to obtain mutants in these genes in particular maize genotypes as well as other plants. Such plants can be obtained, for example, using traditional breeding methods and through specific genetic modification by means of recombinant DNA techniques.

[262] The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 38
Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Ala99Lys GCA-AAA	GAAC TTGAGACTGAGAAAAGGGATCCAAGGACAGTTGCTTCCATT ATTCTTGGAGGTGGA AA AGGAACTCGACTCTTTCCTCTCACAAAA CGCCGCGCCAAGCCTGCCGTTCTATCGGGG	5849
	CCCCGATAGGAACGGCAGGCTTGGCGCGGCGTTTTGTGAGAGGA AAGAGTCGAGTTCCTTTCCACCTCCAAGAATAATGGAAGCAACT GTCCTTGGATCCCTTTCTCAGTCTCAAGTTC	5850
	GAGGTGGA AA AGGAACT	5851
	AGTTCCTTTCCACCTC	5852
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro127Leu CCA-CTA	CAAAACGCGCGCCAAGCCTGCCGTTCTATCGGGGGAGCCTAT AGGTTGATAGATGTACTAATGAGCAATTGTATTACAGCGGAATCA ACAAAGTCTACATACTCACACAATATAACTC	5853
	GAGTTATATTGTGTGAGTATGTAGACTTTGTTGATTCCGCTGTAA TACAATTGCTCATTAGTACATCTATCAACCTATAGGCTCCCCCGAT AGGAACGGCAGGCTTGGCGCGGCGTTTTG	5854
	AGATGTACTAATGAGCA	5855
	TGCTCATTAGTACATCT	5856
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAT	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC TTACAACCTCCAAT AAT CTTGGCTTTGGAGATGGCTATGTTGAGGTT CTTGCGGCCACTCAAACGCCAGGAGAATC	5857
	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAAAGCCAAG ATT ATTGGAGTTGTAAGCACGGGCTAAATGC CTGTTCAATGATGCTGAGTTATATTGTGTGA	5858
	CTCCAAT AAT CTTGGCT	5859
	AGCCAAG ATT ATTGGAG	5860
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAC	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC TTACAACCTCCAAT AAC CTTGGCTTTGGAGATGGCTATGTTGAGGTT CTTGCGGCCACTCAAACGCCAGGAGAATC	5861
	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAAAGCCAAG GTT ATTGGAGTTGTAAGCACGGGCTAAATGC CTGTTCAATGATGCTGAGTTATATTGTGTGA	5862
	CTCCAAT AAC CTTGGCT	5863
	AGCCAAG GTT ATTGGAG	5864

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Asn100Lys AAT-AAA	GTTTGAGAGAAGAAAGGTAGACCCGCAAAATGTGGCTGCAATCAT TCTAGGAGGAGGCAAAGGAGCTAAACTCTTCCCTCTTACAATGAG AGCCGCAACACCAGCTGTAAATATTCATCTT	5865
	AAGATGAATATTTACAGCTGGTGTTCGGCTCTCATTGTAAGAGG GAAGAGTTTAGCTCCTTTGCCTCCTCCTAGAATGATTGCAGCCAC ATTTTGCGGGTCTACCTTTCTTCTCTCAAAC	5866
	GGAGGCAAAGGAGCTAA	5867
	TTAGCTCCTTTGCCTCC	5868
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro128Leu CCG-CTG	CTTGTGTCTTCAAATTATGTTAGGTTCTGTTGGTGGATGCTACAG GCTGATCGATATCCTGATGAGTAACTGTATTAACAGCTGCATCAAC AAGATATTTGTGCTGACACAGTTCAACTC	5869
	GAGTTGAAGTGTGTCAGCACAAATATCTTGTGATGCAGCTGTTAA TACAGTTACTCATCAGGATATCGATCAGCCTGTAGCATCCACCAA CAGGAACCTAACATAATTTGAAGACACAAG	5870
	CGATATCCTGATGAGTA	5871
	TACTCATCAGGATATCG	5872
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAT	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC TTATTTTGGGAATAAATAAACTTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	5873
	GCTGAGAGTTATTATTGTCATAGTGTTTGTACCTCTACGAAACCAC CTCCAAAGTTTATATTATTCCCAAATAAGTTTCGTGCTAAATGTCTG ATTAAGGGAAGCTGAGTTGAACTGTGTCA	5874
	TGGGAATAAATAAACT	5875
	AGTTTATATTATTCCCA	5876
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAC	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC TTATTTTGGGAATAACATAAACTTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	5877
	GCTGAGAGTTATTATTGTCATAGTGTTTGTACCTCTACGAAACCAC CTCCAAAGTTTATGTTATTCCCAAATAAGTTTCGTGCTAAATGTCTG ATTAAGGGAAGCTGAGTTGAACTGTGTCA	5878
	TGGGAATAACATAAACT	5879
	AGTTTATGTTATTCCCA	5880
Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Val94Lys GTT-AAA	TTGAGGAACAACCAACGGCAGATCCAAAAGCTGTTGCCTCTGTCA TTCTAGGTGGTGGTAAAGGAACTCGTCTTTTCTCTTACAAGCA GAAGAGCTAAACCAGCTGTTCTATTGGTGG	5881
	CCACCAATAGGAACAGCTGGTTTAGCTCTTCTGCTTGTAAGAGGA AAAAGACGAGTTCCCTTACCACCACCTAGAATGACAGAGGCAACA GCTTTTGGATCTGCCGTTGGTTGTTCTCTCAA	5882
	TGGTGGTAAAGGAACTC	5883

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAGTTCCTTTACCACCA	5884
Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Pro122Leu CCA-CAA	CAAGCAGAAGAGCTAAACCAGCTGTTCTATTGGTGGTTGTTACC GGCTAATTGATGTACAATGAGTAACTGCATTAACAGTGGCATA GGAAAATTTTCATCTTAACACAGTTCAATTC	5885
	GAATTGAACTGTGTTAAGATGAAAATTTTCCGTATGCCACTGTTAA TGCAGTTACTCATTGTACATCAATTAGCCGGTAACAACCACCAAT AGGAACAGCTGGTTTAGCTCTTCTGCTTG	5886
	TGATGTACAATGAGTA	5887
	TACTCATTGTACATCA	5888
Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Gly158Asn GGA-AAT	CACAGTTCAATTCCTTTCCCTCAATCGTCACCTTGCCCGCACGTA TAATTTTGAAATATGTGGGTTTTGGAGATGGATTTGTGGAGGTT TTAGCTGCAACCCAGACTCCAGGGGATGC	5889
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA TCTCCAAAACCCACATTATTTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAACTGTG	5890
	TGGAAATATGTGGGTT	5891
	AACCCACATTATTTCCA	5892
Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Gly158Asn GGA-AAC	CACAGTTCAATTCCTTTCCCTCAATCGTCACCTTGCCCGCACGTA TAATTTTGAAATAACGTGGGTTTTGGAGATGGATTTGTGGAGGT TTTAGCTGCAACCCAGACTCCAGGGGATGC	5893
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA TCTCCAAAACCCACGTTATTTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAACTGTG	5894
	TGGAAATAACGTGGGTT	5895
	AACCCACGTTATTTCCA	5896
Increased Starch ADPGPP <i>Cicer arietinum</i> Ala101Lys GCT-AAA	ACGTAGATTTGGAAAAAGAGACCCAAGTACAGTTGTAGCAATTAT ACTAGGTGGAGGTAAAGGAAGTCTCTCTTCCCTCTCACCAAGCG ACGAGCCAAGCCTGCTGTTCCAATTGGAGG	5897
	CCTCCAATTGGAACAGCAGGCTTGGCTCGTCTGCTTGGTGAGAGG GAAGAGACGAGTTCTTTACCTCCACCTAGTATAATTGCTACAAC GTACTTGGGTCTCTTTTTTCCAAATCTACGT	5898
	TGGAGGTAAAGGAAGTCT	5899
	GAGTTCCTTTACCTCCA	5900
Increased Starch ADPGPP <i>Cicer arietinum</i> Pro129Leu CCA-CTA	CCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGGTGCTTATA GGCTGATAGATGTACTAATGAGTAACTGCATCAATAGTGGGATCA ACAAAGTATACATTCTCACTCAATTTAATTC	5901

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAATTAAATTGAGTGAGAATGTATACTTTGTTGATCCCACTATTGA TGCAGTTACTCATTAGTACATCTATCAGCCTATAAGCACCTCCAAT TGGAACAGCAGGCTTGGCTCGTCGCTTGG	5902
	AGATGTACTAATGAGTA	5903
	TACTCATTAGTACATCT	5904
Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAT	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAACTCTGGTACTAATGTCACCTTTTGGAGATGGCTATGTTGAGGTT CTTGCAAGCAACTCAAACCTCCAGGGGAGCA	5905
	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACATTAGTACCAGAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAATTGAG	5906
	TGGTACTAATGTCACCT	5907
	AAGTGACATTAGTACCA	5908
Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAC	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAACTCTGGTACTAACGTCACTTTTGGAGATGGCTATGTTGAGGTT CTTGCAAGCAACTCAAACCTCCAGGGGAGCA	5909
	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACGTTAGTACCAGAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAATTGAG	5910
	TGGTACTAACGTCACTT	5911
	AAGTGACGTTAGTACCA	5912
Increased Starch ADPGPP <i>Ipomoea batatas</i> Ala94Lys GCA-AAA	ATATTGGAGAGGCGTCGGGGCAAACCCTAAGAATGTGGCTGCAATC ATACTGCCAGGCGGTAAAGGGACACACCTATTCCCTCTCACC AAT CGAGCTGCAACCCCTGCTGTTCCACTTGGAG	5913
	CTCCAAGTGGAAACAGCAGGGGTTGCAGCTCGATTGGTGAGAGGG AATAGGTGTGTCCCTTTACCGCCTGGCAGTATGATTGCAGCCACA TTCTTAGGGTTTGCCCGACGCCTCTCCAATAT	5914
	CAGGCGGTAAAGGGACA	5915
	TGTCCCTTTACCGCCTG	5916
Increased Starch ADPGPP <i>Ipomoea batatas</i> Pro122Leu CCA-CTA	CCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAGGATGCTATA GGTTGATCGACATTCTAATGAGCAACTGCATCAACAGCGGGGTTA ACAAGATCTTTGTGCTGACCCAGTTCAATTC	5917
	GAATTGAACTGGGTGAGCACAAGATCTTGTTAACCCCGCTGTTG ATGCAGTTGCTCATTAGAATGTGATCAACCTATAGCATCCTCCAA GTGGAACAGCAGGGGTTGCAGCTCGATTGG	5918
	CGACATTCTAATGAGCA	5919
	TGCTCATTAGAATGTGCG	5920

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAT	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC CGTCTTTGGCAAT <u>AAT</u> GTGAGCTTCGGAGATGGATTTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	5921
	GTTTCCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCAC <u>ATT</u> ATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACTGGGTCA	5922
	TGGCAAT <u>AAT</u> GTGAGCT	5923
	AGCTCAC <u>ATT</u> ATTGCCA	5924
Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAC	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC CGTCTTTGGCAAT <u>AAC</u> GTGAGCTTCGGAGATGGATTTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	5925
	GTTTCCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCAC <u>GTT</u> ATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACTGGGTCA	5926
	TGGCAAT <u>AAC</u> GTGAGCT	5927
	AGCTCAC <u>GTT</u> ATTGCCA	5928
Increased Starch ADPGPP <i>Oryza sativa</i> Thr96Lys ACC-AAA	CATTCCGGAGGAACTTTGCGGATCCAAATGAGGTTGCTGCTGTTA TATTGGGTGGTGGCA <u>AA</u> GGGACTCAACTTTTTCTCTCACAAGCA CAAGGGCCACGCCTGCTGTTCTATTGGAGG	5929
	CCTCCAATAGGAACAGCAGGCGTGGCCCTTGTGCTTGTGAGAGG AAAAAGTTGAGTCCCTTTGCCACCACCCAATATAACAGCAGCAAC CTCATTTGGATCCGCAAAGTTCCTCCGGAATG	5930
	TGGTGGCA <u>AA</u> GGGACTC	5931
	GAGTCCCTTTGCCACCA	5932
Increased Starch ADPGPP <i>Oryza sativa</i> Pro124Leu CCC-CTC	CAAGCACAAGGGCCACGCCTGCTGTTCTATTGGAGGATGCTATA GGCTTATCGATATCC <u>T</u> CATGAGCAACTGTTTCAACAGTGGCATAAA CAAGATATTCATAATGACTCAATTCAACTC	5933
	GAGTTGAATTGAGTCATTATGAATATCTTGTTTATGCCACTGTTGA AACAGTTGCTCATG <u>A</u> GGATATCGATAAGCCTATAGCATCCTCCAAT AGGAACAGCAGGCGTGGCCCTTGTGCTTG	5934
	CGATATCC <u>T</u> CATGAGCA	5935
	TGCTCATG <u>A</u> GGATATCG	5936
Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAT	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGGTGGT <u>AAT</u> ATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC	5937
	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGAT <u>ATT</u> ACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA	5938
	TGGTGGT <u>AAT</u> ATCAACT	5939

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AGTTGAT <u>ATT</u> ACCACCA	5940
Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAC	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGGTGGT <u>AAC</u> ATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC	5941
	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGAT <u>GTT</u> ACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA	5942
	TGGTGGT <u>AAC</u> ATCAACT	5943
	AGTTGAT <u>GTT</u> ACCACCA	5944
Increased Starch ADPGPP <i>Triticum aestivum</i> Thr80Lys ACC-AAA	GTCCTTCAGGAGGATTAAGCGATCCGAACGAGGTTGCGGCCGTC ATACTCGGCGGCGGCA <u>AA</u> GGGACTCAGCTCTTCCCACTCACGAG CACAAGGGCCACACCTGCTGTTCTATTGGAGG	5945
	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTCGTGAGTGG GAAGAGCTGAGTCCCT <u>TTT</u> GCCGCCGCCGAGTATGACGGCCGCAA CCTCGTTCCGATCGCTTAATCCTCCTGAAGGAC	5946
	CGGCGGCA <u>AA</u> GGGACTC	5947
	GAGTCCCT <u>TTT</u> GCCGCCG	5948
Increased Starch ADPGPP <i>Triticum aestivum</i> Pro108Leu CCC-CTC	CGAGCACAAGGGCCACACCTGCTGTTCTATTGGAGGATGTTACA GGCTCATCGACATTCTCATGAGCAACTGCTTCAACAGTGGCATCA ACAAGATATTCGTCATGACCCAGTTCAACTC	5949
	GAGTTGAAGTGGGTCATGACGAATATCTTGTGATGCCACTGTTG AAGCAGTTGCTCATG <u>AGA</u> ATGTCGATGAGCCTGTAACATCCTCCA ATAGGAACAGCAGGTGTGGCCCTTGTGCTCG	5950
	CGACATTCTCATGAGCA	5951
	TGCTCATG <u>AGA</u> ATGTGCG	5952
Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAT	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG <u>AAT</u> ATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5953
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGAT <u>ATT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	5954
	CGGCGGG <u>AAT</u> ATCAATT	5955
	AATTGAT <u>ATT</u> CCCGCCG	5956
Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAC	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG <u>AAC</u> ATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5957
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGAT <u>GTT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	5958

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGGCGGG <u>AAC</u> ATCAATT	5959
	AATTGAT <u>GTT</u> CCCGCCG	5960
Increased Starch ADPGPP <i>Oryza sativa</i> Thr95Lys ACT-AAA	CCTCCCGAAAGAATTATGCTGATGCAAGCCACGTTTCTGCTGTCA TTTTGGGTGGAGGCA <u>AA</u> GGAGTTCAACTCTTCTCTGACAAGCA CAAGGGCTACCCCCGCTGTTCTGTTGGAGG	5961
	CCTCCAACAGGAACAGCGGGGGTAGCCCTTGCTTGTGAGAGG AAAGAGTTGAACTCCTTGCCTCCACCCAAAATGACAGCAGAAAC GTGGCTTGCATCAGCATAATTCTTTCGGGAGG	5962
	TGGAGGCA <u>AA</u> GGAGTTC	5963
	GAACTCCTTGCCTCCA	5964
Increased Starch ADPGPP <i>Oryza sativa</i> Pro123Leu CCT-CTT	CAAGCACAAGGGCTACCCCCGCTGTTCTGTTGGAGGATGTTACA GGCTTATTGACATCCTTATGAGCAATTGCTTCAATAGCGGAATAAA TAAATATTTGTGATGACTCAGTTCAATTC	5965
	GAATTGAACTGAGTCATCACAATATTTTATTATTCGGCTATTGAA GCAATTGCTCATA <u>AG</u> GATGTCAATAAGCCTGTAACATCCTCCAACA GGAACAGCGGGGGTAGCCCTTGCTTG	5966
	TGACATCCTTATGAGCA	5967
	TGCTCATA <u>AG</u> GATGTCA	5968
Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAT	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATACA TACCTTGGTGGG <u>AAT</u> ATCAACTTTACTGATGGGTCTGTGCAGGTA TTGGCTGCTACACAAATGCCTGACGAACC	5969
	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGAT <u>ATT</u> CCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGAACTGAGTCA	5970
	TGGTGGG <u>AAT</u> ATCAACT	5971
	AGTTGAT <u>ATT</u> CCCACCA	5972
Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAC	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATACA TACCTTGGTGGG <u>AAC</u> ATCAACTTTACTGATGGGTCTGTGCAGGTA TTGGCTGCTACACAAATGCCTGACGAACC	5973
	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGAT <u>GTT</u> CCCACCAAGGTATGTATGATGGATATGG CGATTAAGAGAAGCAGAATTGAACTGAGTCA	5974
	TGGTGGG <u>AAC</u> ATCAACT	5975
	AGTTGAT <u>GTT</u> CCCACCA	5976
Increased Starch ADPGPP <i>Triticum aestivum</i> Thr99Lys ACC-AAA	CCTTCGCGAGGAATTACGCCGATCCGAACGAGGTCGCGGCCGTC ATACTCGGCGGTGGCA <u>AA</u> GGGACTCAGCTCTTCCCTCTCACAAG CACAAGGGCCACACCTGCTGTTCTATTGGAGG	5977

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTTGTGAGAGG GAAGAGCTGAGTCCC TT TGCCACCGCCGAGTATGACGGCCGCGA CCTCGTTCGGATCGGCGTAATTCCTGCGGAAGG	5978
	CGGTGGCA AA GGGACTC	5979
	GAGTCCCT TT TGCCACCG	5980
Increased Starch ADPGPP <i>Triticum aestivum</i> Pro127Leu CCC-CTC	CAAGCACAAGGGCCACACCTGCTGTTCTATTGGAGGATGTTACA GGCTCATCGATATT CT CATGAGCAACTGCTTCAATAGTGGCATCAA CAAGATATTCGTCATGACGCAGTTCAACTC	5981
	GAGTTGAACTGCGTCATGACGAATATCTTGTTGATGCCACTATTGA AGCAGTTGCTCATG AGA AATATCGATGAGCCTGTAACATCCTCCAA TAGGAACAGCAGGTGTGGCCCTTGTGCTTG	5982
	CGATATT CT CATGAGCA	5983
	TGCTCATG AGA AATATCG	5984
Increased Starch ADPGPP <i>Triticum aestivum</i> Gly162Asn GGA-AAT	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG AA TATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCCGGGGAGGC	5985
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGAT ATT CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	5986
	CGGCGGG AA TATCAATT	5987
	AATTGAT ATT CCCGCCG	5988
Increased Starch ADPGPP <i>Triticum aestivum</i> Gly162Asn GGA-AAC	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG AA CATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCCGGGGAGGC	5989
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGAT GTT CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	5990
	CGGCGGG AA CATCAATT	5991
	AATTGAT GTT CCCGCCG	5992
Increased Starch ADPGPP <i>Zea mays</i> Thr96Lys ACC-AAA	CTTTTCGGAGGAATTATGCTGATCCTAATGAAGTCGCTGCCGTCA TTTTGGGTGGTGGTA AA GGGACTCAGCTTTCCCTCTCACAAGCA CAAGGGCCACCCCTGCTGTTCTATTGGAGG	5993
	CCTCCAATAGGAACAGCAGGGGTGGCCCTTGTGCTTGTGAGAGG GAAAAGCTGAGTCCC TTT TACCACCACCCAAAATGACGGCAGCGAC TTCATTAGGATCAGCATAATTCCTCCGAAAAG	5994
	TGGTGGTA AA GGGACTC	5995
	GAGTCCCT TTT TACCACCA	5996

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP <i>Zea mays</i> Pro124Leu CCC-CTC	CAAGCACAAGGGCCACCCCTGCTGTTCTATTGGAGGATGTTACA GGCTTATTGATATCC <u>I</u> CATGAGCAACTGTTTCAACAGTGGCATAAA CAAGATATTTGTTATGACTCAGTTCAACTC	5997
	GAGTTGAACTGAGTCATAACAAATATCTTGTTTATGCCACTGTTGA AACAGTTGCTCATG <u>A</u> GGATATCAATAAGCCTGTAACATCCTCCAAT AGGAACAGCAGGGGTGGCCCTTGTGCTTG	5998
	TGATATCC <u>I</u> CATGAGCA	5999
	TGCTCATG <u>A</u> GGATATCA	6000
Increased Starch ADPGPP <i>Zea mays</i> Gly159Asn GGG-AAT	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC CTATCTTGGTGGG <u>A</u> ATATCAACTTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC	6001
	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGAT <u>ATT</u> CCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	6002
	TGGTGGG <u>A</u> ATATCAACT	6003
	AGTTGAT <u>ATT</u> CCCACCA	6004
Increased Starch ADPGPP <i>Zea mays</i> Gly159Asn GGG-AAC	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC CTATCTTGGTGGG <u>A</u> ACATCAACTTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC	6005
	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGAT <u>GTT</u> CCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	6006
	TGGTGGG <u>A</u> ACATCAACT	6007
	AGTTGAT <u>GTT</u> CCCACCA	6008
Increased Starch ADPGPP <i>Solanum tuberosum</i> Ala58Lys GCG-AAG	CTTGAGAGGCAAAAGAAGGGCGATGCAAGGACAGTAGTAGCAAT CATTCTAGGAGGGGG <u>A</u> AGGGGAAGTCTGCTTTTCCCCCTCACCAA ACGTCGTGCTAAGCCTGCCGTTCCAATGGGAG	6009
	CTCCCATTTGGAACGGCAGGCTTAGCACGACGTTTGGTGAGGGGG AAAAGACGAGTTCCCT <u>TT</u> CCCCCTCCTAGAATGATTGCTACTACTG TCCTTGCATCGCCCTTCTTTTGCCTCTCAAG	6010
	GAGGGGG <u>A</u> AGGGGAAGT	6011
	AGTTCCC <u>TT</u> CCCCCTC	6012
Increased Starch ADPGPP <i>Solanum tuberosum</i> Pro86Leu CCA-CTA	CCAAACGTCTGTGCTAAGCCTGCCGTTCCAATGGGAGGAGCATATA GGCTAATTGATGTACT <u>I</u> AATGAGCAACTGTATTAACAGTGGCATCAA CAAAGTATACATTCTCACTCAATTCAACTC	6013
	GAGTTGAATTGAGTGAGAATGTATACTTTGTTGATGCCACTGTTAA TACAGTTGCTCATT <u>A</u> GTACATCAATTAGCCTATATGCTCCTCCCAT TGGAACGGCAGGCTTAGCACGACGTTTGG	6014
	TGATGTACT <u>I</u> AATGAGCA	6015

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCTCATT <u>AG</u> TACATCA	6016
Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAT	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAAT <u>AAT</u> GTCACATTGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6017
	AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCA CTCTCGAATGTGAC <u>ATT</u> ATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTAAAGTGAGGCTGAGTTGAATTGAG	6018
	TGGCAAT <u>AAT</u> GTCACAT	6019
	ATGTGAC <u>ATT</u> ATTGCCA	6020
Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAC	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAAT <u>AAC</u> GTCACATTGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6021
	AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCA CTCTCGAATGTGAC <u>GTT</u> ATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTAAAGTGAGGCTGAGTTGAATTGAG	6022
	TGGCAAT <u>AAC</u> GTCACAT	6023
	ATGTGAC <u>GTT</u> ATTGCCA	6024
Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAA	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGT <u>AAAG</u> GGACTCGCCTCTTTCCTCTTACTAGCAG GAGAGCTAAGCCAGCAGTGCCAATTGGAGG	6025
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCC <u>TTT</u> ACCACCACCCAGCACAAATTGCAGCCACA TTTTTTGGGTCAGCTTTTGGAGATTCAAATA	6026
	TGGTGGT <u>AAAG</u> GGACTC	6027
	GAGTCCC <u>TTT</u> ACCACCA	6028
Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAC	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGT <u>AAC</u> GGGACTCGCCTCTTTCCTCTTACTAGCAG GAGAGCTAAGCCAGCAGTGCCAATTGGAGG	6029
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCC <u>GTT</u> ACCACCACCCAGCACAAATTGCAGCCAC ATTTTTGGGTCAGCTTTTGGAGATTCAAATA	6030
	TGGTGGT <u>AAC</u> GGGACTC	6031
	GAGTCCC <u>GTT</u> ACCACCA	6032
Increased Starch ADPGPP <i>Beta vulgaris</i> Pro126Leu CCT-CTT	CTAGCAGGAGAGCTAAGCCAGCAGTGCCAATTGGAGGGTGTAC AGGCTGATTGATGTGCT <u>T</u> ATGAGCAACTGCATCAACAGTGGCATT AGAAAGATTTTCAATTCTTACCCAGTTCAATTC	6033
	GAATTGAAGTGGGTAAGAATGAAAATCTTTCTAATGCCACTGTTGA TGCAGTTGCTCATA <u>AG</u> CACATCAATCAGCCTGTAACACCCTCCAA TTGGCACTGCTGGCTTAGCTCTCCTGCTAG	6034

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATGTGCTTATGAGCA	6035
	TGCTCATAAGCACATCA	6036
Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAT	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTTGGAGATAATGTGAATTTGGGGATGGCTTTGTGGAGGTT TTTGCTGCTACACAAACACCTGGAGAATC	6037
	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATTCACATTATCTCCAAAATTATAGGTTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG	6038
	TGGAGATAATGTGAATT	6039
	AATTCACATTATCTCCA	6040
Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAC	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTTGGAGATAACGTGAATTTGGGGATGGCTTTGTGGAGGT TTTGCTGCTACACAAACACCTGGAGAATC	6041
	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATTCACGTTATCTCCAAAATTATAGGTTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG	6042
	TGGAGATAACGTGAATT	6043
	AATTCACGTTATCTCCA	6044

Table 39
Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser12Term TCA-TGA	GAATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTT CTTCTAACTTTGTGTGAAGAACTTCACTTTTCAACAATCATGGTGCT TCTTCATGCTCTGATGTCGCTCAGATTAC	6045
	GTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTG AAAAGTGAAGTTCTTACACAAAGTTAGAAGAAGCAGTCACAGTTG CCATTATGAACTACCCGTTTACCTGGATTG	6046
	CTTTGTGTGAAGAACTT	6047
	AAGTTCTTACACAAAG	6048
Waxy starch GBSS <i>Arabidopsis thaliana</i> Arg13Term AGA-TGA	ATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTT CTAACTTTGTGTCACTGAAGTTCCTTTTCAACAATCATGGTGCTTCT TCATGCTCTGATGTCGCTCAGATTACCT	6049
	AGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGT TGAAAAGTGAAGTTCAATGACACAAAGTTAGAAGAAGCAGTCACAGT TGCCATTATGAACTACCCGTTTACCTGGAT	6050
	TTGTGTCACTGAAGTTC	6051
	TGAAGTTCAATGACACAA	6052
Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA	TAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTTCTAACTT TGTGTCAAGAAGTGAAGTTCCTTTTCAACAATCATGGTGCTTCTTCATGCT CTGATGTCGCTCAGATTACCTTAAAAGG	6053
	CCTTTTAAGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCAT GATTGTTGAAAAGTCAAGTTCTTGACACAAAGTTAGAAGAAGCAGT CACAGTTGCCATTATGAACTACCCGTTTA	6054
	AAGAAGTGAAGTTCCTTTTCA	6055
	TGAAAAGTCAAGTTCTT	6056
Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser24Term TCA-TGA	TGACTGCTTCTTCTAACTTTGTGTCAAGAAGTTCCTTTTCAACAAT CATGGTGCTTCTTGATGCTCTGATGTCGCTCAGATTACCTTAAAAG GCCAATCCTTGACTCATTGTGGGTTAAG	6057
	CTTAACCCACAATGAGTCAAGGATTGGCCTTTTAAGGTAATCTGAG CGACATCAGAGCATCAAGAAGCACCATGATTGTTGAAAAGTGAAG TTCTTGACACAAAGTTAGAAGAAGCAGTCA	6058
	TGCTTCTTGATGCTCTG	6059
	CAGAGCATCAAGAAGCA	6060

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Arabidopsis thaliana</i> Cys25Term TGC-TGA	TGCTTCTTCTAACTTTGTGTCAAGAACTTCACTTTTCAACAATCATG GTGCTTCTTCATGATCTGATGTCGCTCAGATTACCTTAAAAGGCCA ATCCTTGACTCATTGTGGGTTAAGGTCA	6061
	TGACCTTAACCCACAATGAGTCAAGGATTGGCCTTTTAAGGTAATC TGAGCGACATCAGATCATGAAGAAGCACCATGATTGTTGAAAAGT GAAGTTCTTGACACAAAGTTAGAAGAAGCA	6062
	TCTTCATGATCTGATGT	6063
	ACATCAGATCATGAAGA	6064
Waxy starch GBSS <i>Antirrhinum majus</i> Lys24Term AAA-TAA	GTAACAGCTTCACAGTTGGTGTACATGTCCATGGTGGAGCAACG TCTTCACCGGATACTTAAACAACTTGGCCCAGGTTGGCCTCAGG AACCAGCAATTCACCTCACAATGGGTTGAGAT	6065
	ATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGAGGCCAACCTG GGCCAAGTTTGTTTAAGTATCCGGTGAAGACGTTGCTCCACCATG GACATGTGACACCAACTGTGAAGCTGTTAC	6066
	CGGATACTTAAACAAAC	6067
	GTTTGTTTAAGTATCCG	6068
Waxy starch GBSS <i>Antirrhinum majus</i> Leu27Term TTG-TAG	CACAGTTGGTGTACATGTCCATGGTGGAGCAACGTCTTCACCGG ATACTAAACAACTAGGCCAGGTTGGCCTCAGGAACCAGCAAT TCACTCACAATGGGTTGAGATCAATAAACAT	6069
	ATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGA GGCCAACCTGGGCCAGTTTGTTTAGTATCCGGTGAAGACGTTG CTCCACCATGGACATGTGACACCAACTGTG	6070
	AACAACTAGGCCAGG	6071
	CCTGGGCCAGTTTGT	6072
Waxy starch GBSS <i>Antirrhinum majus</i> Gln29Term CAG-TAG	TTGGTGTACATGTCCATGGTGGAGCAACGTCTTCACCGGATACT AAAACAACTTGGCCAGGTTGGCCTCAGGAACCAGCAATTCAT CACAATGGGTTGAGATCAATAAACATGGTTG	6073
	CAACCATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGT CCTGAGGCCAACCTAGGCCAAGTTTGTTTAGTATCCGGTGAAGA CGTTGCTCCACCATGGACATGTGACACCAA	6074
	ACTTGGCCAGGTTGGC	6075
	GCCAACCTAGGCCAAGT	6076
Waxy starch GBSS <i>Antirrhinum majus</i> Gln35Term CAG-TAG	GGTGGAGCAACGTCTTCACCGGATACTAAACAACTTGGCCCAG GTTGGCCTCAGGAAGTAGCAATTCATCACAATGGGTTGAGATCA ATAAACATGGTTGATAAGCTTCAAATGAGGA	6077
	TCCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCATTG TGAGTGAATTGCTAGTTCCTGAGGCCAACCTGGGCCAAGTTTGT TAGTATCCGGTGAAGACGTTGCTCCACC	6078

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCAGGAAC <u>T</u> AGCAATTC	6079
	GAATTGCT <u>A</u> GTTCTGA	6080
Waxy starch GBSS <i>Antirrhinum majus</i> Gln36Term CAA-TAA	GGAGCAACGTCCTTCACCGGATACTAAAACAACTTGGCCCAGGTT GGCCTCAGGAACCAG <u>T</u> AATTCACACCAATGGGTTGAGATCAATAA ACATGGTTGATAAGCTTCAAATGAGGAACA	6081
	TGTTCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCA TTGTGAGTGAATT <u>A</u> CTGGTTCCTGAGGCCAACCTGGGCCAAGTTT GTTTTAGTATCCGGTGAAGACGTTGCTCC	6082
	GGAACCAG <u>T</u> AATTCAC	6083
	AGTGAATT <u>A</u> CTGGTTC	6084
Waxy starch GBSS <i>Ipomoea batatas</i> Gly20Term GGA-TGA	GTGATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTG GGGGTGCCACTTCT <u>T</u> GAGAATCAAAGTGGGGTTGGGTCAATTAG CCCTGAGGAGCCAAGCTGTGACTCACAATG	6085
	CATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACC CCACTTTTGATTCTC <u>A</u> AGAAGTGGCACCCCCACAGACATGAGAAA CAAAGTGTGAGGCAGTTATAGTCGCCATCAC	6086
	CCACTTCT <u>T</u> GAGAATCA	6087
	TGATTCTC <u>A</u> AGAAGTGG	6088
Waxy starch GBSS <i>Ipomoea batatas</i> Glu21Term GAA-TAA	ATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGG GTGCCACTTCTGGAT <u>A</u> ATCAAAGTGGGGTTGGGTCAATTAGCCC TGAGGAGCCAAGCTGTGACTCACAATGGGT	6089
	ACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCA ACCCCACTTTTGATT <u>A</u> TCCAGAAGTGGCACCCCCACAGACATGAG AAACAAAGTGTGAGGCAGTTATAGTCGCCAT	6090
	CTTCTGGAT <u>A</u> ATCAAAA	6091
	TTTTGATT <u>A</u> TCCAGAAG	6092
Waxy starch GBSS <i>Ipomoea batatas</i> Ser22Term TCA-TGA	CGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGC CACTTCTGGAGAAT <u>G</u> AAAAGTGGGGTTGGGTCAATTAGCCCTGAG GAGCCAAGCTGTGACTCACAATGGGTTGAG	6093
	CTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGA CCCAACCCCACTTTT <u>C</u> ATTCTCCAGAAGTGGCACCCCCACAGACAT GAGAAACAAAGTGTGAGGCAGTTATAGTCG	6094
	TGGAGAAT <u>G</u> AAAAGTGG	6095
	CCACTTTT <u>C</u> ATTCTCCA	6096

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Ipomoea batatas</i> Lys23Term AAA-TAA	ACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCA CTTCTGGAGAATCATAAGTGGGGTTGGGTCAATTAGCCCTGAGGA GCCAAGCTGTGACTCACAATGGGTTGAGAC	6097
	GTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATT GACCCAACCCCACTTATGATTCTCCAGAAGTGGCACCCCCACAGA CATGAGAAACAAAGTGTGAGGCAGTTATAGT	6098
	GAGAATCATTAAGTGGGG	6099
	CCCCACTTATGATTCTC	6100
Waxy starch GBSS <i>Ipomoea batatas</i> Leu26Term TTG-TAG	CCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGAGA ATCAAAAGTGGGGTAGGGTCAATTAGCCCTGAGGAGCCAAGCTGT GACTCACAATGGGTTGAGACCTGTGAACAA	6101
	TTGTTACAGGTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCA GGGCTAATTGACCCCTACCCCACTTTTGATTCTCCAGAAGTGGCACC CCCACAGACATGAGAAACAAAGTGTGAGG	6102
	AGTGGGGTAGGGTCAAT	6103
	ATTGACCCCTACCCCACT	6104
Waxy starch GBSS <i>Astragalus membranaeus</i> Tyr8Term TAT-TAG	CATCGGCGATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACG GTGACGGGGTCTTAGGTGGTGTGCGAGAAGCGCGTGCTTCAATTCC CAGGGAAGAACAGAAGCCAAAGTGAATTCA	6105
	TGAATTCACCTTTGGCTTCTGTTCTTCCCTGGGAATTGAAGCACGCG CTTCTCGACACCACCTAAGACCCCGTCACCGTTGCCATTCTGTGA GAGAGCAGTAAGGAGCAACAATCGCCGATG	6106
	GGGTCTTAGGTGGTGTC	6107
	GACACCACCTAAGACCC	6108
Waxy starch GBSS <i>Astragalus membranaeus</i> Ser11Term TCG-TAG	ATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGG GGTCTTATGTGGTGTAGAGAAGCGCGTGCTTCAATTCCCAGGGAA GAACAGAAGCCAAAGTGAATTCACCTCAGAA	6109
	TTCTGAGGTGAATTCACCTTTGGCTTCTGTTCTTCCCTGGGAATTGA AGCACGCGCTTCTCTACACCACATAAGACCCCGTCACCGTTGCCA TTCTGTGAGAGAGCAGTAAGGAGCAACAAT	6110
	TGTGGTGTAGAGAAGCG	6111
	CGCTTCTCTACACCACA	6112

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Astragalus membranaeus</i> Arg12Term AGA-TGA	TGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGGGG TCTTATGTGGTGTCTGAAGCGCGTGCTTCAATTCCCAGGGAAGA ACAGAAGCCAAAGTGAATTCACCTCAGAAGA	6113
	TCTTCTGAGGTGAATTCACCTTTGGCTTCTGTTCTTCCCTGGGAATT GAAGCACGCGCTTCAACGACACCACATAAGACCCCGTCACCGTTGC CATTCTGTGAGAGAGCAGTAAGGAGCAACA	6114
	TGGTGTCTGGAAGCGCG	6115
	CGCGCTTCAACGACACCA	6116
Waxy starch GBSS <i>Astragalus membranaeus</i> Cys15Term TGC-TGA	ACTGCTCTCTCACAGAATGGCAACGGTGACGGGGTCTTATGTGGT GTCGAGAAGCGCGTGAATTCAATTCCCAGGGAAGAACAGAAGCCAA AGTGAATTCACCTCAGAAGATAAATCTCAAT	6117
	ATTGAGATTTATCTTCTGAGGTGAATTCACCTTTGGCTTCTGTTCTTC CCTGGGAATTGAATCACGCGCTTCTCGACACCACATAAGACCCCG TCACCGTTGCCATTCTGTGAGAGAGCAGT	6118
	AGCGCGTGAATTCAATTC	6119
	GAATTGAATCACGCGCT	6120
Waxy starch GBSS <i>Astragalus membranaeus</i> Gln19Term CAG-TAG	CACAGAATGGCAACGGTGACGGGGTCTTATGTGGTGTGCGAGAAG CGCGTGCTTCAATTCCTAGGGAAGAACAGAAGCCAAAGTGAATTC ACCTCAGAAGATAAATCTCAATAGCCAAGCAT	6121
	ATGCTTGGCTATTGAGATTTATCTTCTGAGGTGAATTCACCTTTGGCT TCTGTTCTTCCCTAGGAATTGAAGCACGCGCTTCTCGACACCACAT AAGACCCCGTCACCGTTGCCATTCTGTG	6122
	TCAATTCCTAGGGAAGA	6123
	TCTTCCCTAGGAATTGA	6124
Waxy starch GBSS <i>Solanum tuberosum</i> Ser7Term TCA-TGA	TGTAGCTTGGTAGATTCCCCTTTTTGTAGACCACACATCACATGGC AAGCATCACAGCTTGACACCACTTTGTGTCAAGAAGCCAAACTTCA CTAGACACCAAATCAACCTTGTACAGAT	6125
	ATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTTGGCTTCTTG ACACAAAGTGGTGTCAAGCTGTGATGCTTGCCATGTGATGTGTGG TCTACAAAAGGGGAATCTACCAAGCTACA	6126
	CACAGCTTGACACCACT	6127
	AGTGGTGTCAAGCTGTG	6128
Waxy starch GBSS <i>Solanum tuberosum</i> Ser12Term TCA-TGA	TCCCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTC ACACCACTTTGTGTGAAGAAGCCAAACTTCACTAGACACCAAATCA ACCTTGTCACAGATAGGACTCAGGAACCA	6129
	TGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGTG AAGTTTGGCTTCTTCACACAAAGTGGTGTGAAGCTGTGATGCTTGC CATGTGATGTGTGGTCTACAAAAGGGGA	6130

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTTTGTGTGAAGAAGCC	6131
	GGCTTCTTCACACAAAG	6132
Waxy starch GBSS <i>Solanum tuberosum</i> Arg13Term AGA-TGA	CCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTCAC ACCACTTTGTGTCAATGAAGCCAACTTCACTAGACACCAAATCAAC CTTGTCACAGATAGGACTCAGGAACCATA	6133
	TATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAG TGAAGTTTGGCTTCAATGACACAAAGTGGTGTGAAGCTGTGATGCTT GCCATGTGATGTGTGGTCTACAAAAGGG	6134
	TTGTGTCATGAAGCCAA	6135
	TTGGCTTCAATGACACAA	6136
Waxy starch GBSS <i>Solanum tuberosum</i> Gln15Term CAA-TAA	TTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACT TTGTGTCAAGAAGCTAAACTTCACTAGACACCAAATCAACCTTGTC ACAGATAGGACTCAGGAACCATACTCTGA	6137
	TCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGT GTCTAGTGAAGTTTAGCTTCTTGACACAAAGTGGTGTGAAGCTGTG ATGCTTGCCATGTGATGTGTGGTCTACAA	6138
	CAAGAAGCTAAACTTCA	6139
	TGAAGTTTAGCTTCTTG	6140
Waxy starch GBSS <i>Solanum tuberosum</i> Ser17Term TCA-TGA	CCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTC AAGAAGCCAACTTGACTAGACACCAAATCAACCTTGTCACAGATA GGAATCAGGAACCATACTCTGACTCACAA	6141
	TTGTGAGTCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTG ATTTGGTGTCTAGTCAAGTTTGGCTTCTTGACACAAAGTGGTGTGA AGCTGTGATGCTTGCCATGTGATGTGTGG	6142
	CCAACTTGACTAGACA	6143
	TGTCTAGTCAAGTTTGG	6144
Waxy starch GBSS <i>Pisum sativum</i> Gly6Term GGA-TGA	GTCGATCACTCTTCTCTCACCGCCGAAACAGATTTTGACACAAAA TGGCAACAATAACGTGATCTTCAATGCCGACGAGAACCGCGTGCT TCAATTACCAAGGAAGATCAGCAGAGTCTA	6145
	TAGACTCTGCTGATCTTCTTGGTAATTGAAGCACGCGGTTCTCGT CGGCATTGAAGATCACGTTATTGTTGCCATTTTTGTGTCAAATCT GTTTCGGCGGTGAGAGAAGAGTGATCGAC	6146
	CAATAACGTGATCTTCA	6147
	TGAAGATCACGTTATTG	6148

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Pisum sativum</i> Ser8Term TCA-TGA	ACTCTTCTCTCACC GCCGAAACAGATTTTGACACAAAAATGGCAAC AATAACGGGATCTTGAATGCCGACGAGAACCGCGTGCTTCAATTA CCAAGGAAGATCAGCAGAGTCTAAACTGAA	6149
	TTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGG TTCTCGTCGGCATTCAAGATCCCGTTATTGTTGCCATTTTGTGTCA AAATCTGTTTCGGCGGTGAGAGAAGAGT	6150
	GGGATCTTGAATGCCGA	6151
	TCGGCATTCAAGATCCC	6152
Waxy starch GBSS <i>Pisum sativum</i> Arg12Term AGA-TGA	ACCGCCGAAACAGATTTTGACACAAAAATGGCAACAATAACGGGA TCTTCAATGCCGACGTGAACCGCGTGCTTCAATTACCAAGGAAGA TCAGCAGAGTCTAAACTGAATTTGCCTCAGA	6153
	TCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATT GAAGCACGCGGTTCAAGTCGGCATTGAAGATCCCGTTATTGTTGC CATTTTTGTGTCAAATCTGTTTCGGCGGT	6154
	TGCCGACGTGAACCGCG	6155
	CGCGGTTCACGTCGGCA	6156
Waxy starch GBSS <i>Pisum sativum</i> Cys15Term TGC-TGA	AGATTTTGACACAAAAATGGCAACAATAACGGGATCTTCAATGCCG ACGAGAACCGCGTGATTCAATTACCAAGGAAGATCAGCAGAGTCT AAACTGAATTTGCCTCAGATACACTTCAAT	6157
	ATTGAAGTGTATCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTT CCTTGGTAATTGAATCACGCGGTTCTCGTCGGCATTGAAGATCCC GTTATTGTTGCCATTTTGTGTCAAATCT	6158
	ACCGCGTGATTCAATTA	6159
	TAATTGAATCACGCGGT	6160
Waxy starch GBSS <i>Pisum sativum</i> Tyr18Term TAC-TAG	CACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACGAGAAC CGCGTGCTTCAATTAGCAAGGAAGATCAGCAGAGTCTAAACTGAA TTTGCCTCAGATACACTTCAATAACAACCAA	6161
	TTGGTTGTTATTGAAGTGTATCTGAGGCAAATTCAGTTTAGACTCT GCTGATCTTCCTTGCTAATTGAAGCACGCGGTTCTCGTCGGCATTG AAGATCCCGTTATTGTTGCCATTTTGTG	6162
	TTCAATTAGCAAGGAAG	6163
	CTTCCTTGCTAATTGAA	6164
Waxy starch GBSS <i>Manihot esculenta</i> Ser14Term TCA-TGA	TCTACACCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATT TCGTTTCCAGGAGCTGACACTTGAGCATCCATGCATTAGAGACTAA GGCTAATAATTTGTCTCACTGGACCCTG	6165
	CAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTAATGCAT GGATGCTCAAGTGTAGCTCCTGGAAACGAAATGTGCAGCTATTA CAGTTGCCATGGTGCTCTCTCCGGTGTAGA	6166

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAGGAGCTGACACTTGA	6167
	TCAAGTGTGAGCTCCTG	6168
Waxy starch GBSS <i>Manihot esculenta</i> Leu16Term TTG-TAG	CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTGTTTT CCAGGAGCTCACACTAGAGCATCCATGCATTAGAGACTAAGGCTA ATAATTTGTCTCACACTGGACCCTGGACCCA	6169
	TGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTA ATGCATGGATGCTCTAGTGTGAGCTCCTGGAAACGAAATGTGCAG CTATTACAGTTGCCATGGTGCTCTCTCCGG	6170
	CTCACACTAGAGCATCC	6171
	GGATGCTCTAGTGTGAG	6172
Waxy starch GBSS <i>Manihot esculenta</i> Leu21Term TTA-TGA	TGGCAACTGTAATAGCTGCACATTTGTTTTCCAGGAGCTCACACTT GAGCATCCATGCATGAGAGACTAAGGCTAATAATTTGTCTCACACT GGACCCTGGACCCAACTATCACTCCCAA	6173
	TTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAATTA TTAGCCTTAGTCTCTCATGCATGGATGCTCAAGTGTGAGCTCCTGG AAACGAAATGTGCAGCTATTACAGTTGCCA	6174
	CCATGCATGAGAGACTA	6175
	TAGTCTCTCATGCATGG	6176
Waxy starch GBSS <i>Manihot esculenta</i> Glu22Term GAG-TAG	GCAACTGTAATAGCTGCACATTTGTTTTCCAGGAGCTCACACTTGA GCATCCATGCATTATAGACTAAGGCTAATAATTTGTCTCACACTGG ACCCTGGACCCAACTATCACTCCCAATG	6177
	CATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAAT TATTAGCCTTAGTCTATAATGCATGGATGCTCAAGTGTGAGCTCCT GGAAACGAAATGTGCAGCTATTACAGTTGC	6178
	ATGCATTATAGACTAAG	6179
	CTTAGTCTATAATGCAT	6180
Waxy starch GBSS <i>Manihot esculenta</i> Lys24Term AAG-TAG	GTAATAGCTGCACATTTGTTTTCCAGGAGCTCACACTTGAGCATCC ATGCATTAGAGACTTAGGCTAATAATTTGTCTCACACTGGACCCTG GACCCAACTATCACTCCCAATGGTTTAA	6181
	TTAAACCATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAG ACAAATTATTAGCCTAAGTCTCTAATGCATGGATGCTCAAGTGTGA GCTCCTGGAAACGAAATGTGCAGCTATTAC	6182
	TAGAGACTTAGGCTAAT	6183
	ATTAGCCTAAGTCTCTA	6184

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Phaseolus vulgaris</i> Ser12Term TCA-TGA	ACAACTCCTCCGTCACCGGTATAAGCATGGCAACGGTATCGATGG CATCGTGCGTGGCGTGAAAAGGCGCGTGGAGTACAGAGACAAAA GTGAAATCTTCGGGTCAGATGAGCCTGAACCG	6185
	CGGTTCAGGCTCATCTGACCCGAAGATTTCACTTTTGTCTCTGTAC TCCACGCGCCTTTTACGCCACGCACGATGCCATCGATACCGTTG CCATGCTTATACCGGTGACGGAGGAGTTGT	6186
	CGTGCGCGTAAAAGGCG	6187
	CGCCTTTTACGCCACG	6188
Waxy starch GBSS <i>Phaseolus vulgaris</i> Trp16Term TGG-TGA	CACCGGTATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGC GTCAAAGGCGCGTGAGTACAGAGACAAAAGTGAATCTTCGGG TCAGATGAGCCTGAACCGTCATGAATTGAAA	6189
	TTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATTTCACT TTTGTCTCTGTACTTACGCGCCTTTTGACGCCACGCACGATGCCA TCGATACCGTTGCCATGCTTATACCGGTG	6190
	GGCGCGTGAGTACAGA	6191
	TCTGTACTTACGCGCC	6192
Waxy starch GBSS <i>Phaseolus vulgaris</i> Glu19Term GAG-TAG	ATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAA GGCGCGTGGAGTACATAGACAAAAGTGAATCTTCGGGTCAGATG AGCCTGAACCGTCATGAATTGAAATACGATG	6193
	CATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGA TTTCACTTTTGTCTATGTACTCCACGCGCCTTTTGACGCCACGCAC GATGCCATCGATACCGTTGCCATGCTTAT	6194
	GGAGTACATAGACAAA	6195
	TTTTGTCTATGTACTCC	6196
Waxy starch GBSS <i>Phaseolus vulgaris</i> Lys21Term AAA-TAA	ATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAGGCGC GTGGAGTACAGAGACATAAGTGAAATCTTCGGGTCAGATGAGCCT GAACCGTCATGAATTGAAATACGATGGGTTGA	6197
	TCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACC CGAAGATTTCACTTATGTCTCTGTACTCCACGCGCCTTTTGACGCC ACGCACGATGCCATCGATACCGTTGCCAT	6198
	CAGAGACATAAGTGAAA	6199
	TTTCACTTATGTCTCTG	6200
Waxy starch GBSS <i>Phaseolus vulgaris</i> Lys23Term AAA-TAA	ACGGTATCGATGGCATCGTGCGTGGCGTCAAAGGCGCGTGGAG TACAGAGACAAAAGTGTAATCTTCGGGTCAGATGAGCCTGAACCG TCATGAATTGAAATACGATGGGTTGAGATCTC	6201
	GAGATCTCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCAT CTGACCCGAAGATTACACTTTTGTCTCTGTACTCCACGCGCCTTTT GACGCCACGCACGATGCCATCGATACCGT	6202

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAAAAGTG <u>I</u> AATCTTCG	6203
	CGAAGATT <u>A</u> CACCTTTG	6204
Waxy starch GBSS <i>Triticum aestivum</i> Tyr7Term TAT-TAG	GCGCCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGG GTTCCATTCTTAATTAGTGTCTTATCAAACAAACAGTGTTGGTTCA CTGAAACTGTCGCCTCACATCCAATTCCAG	6205
	CTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACTGTT TGTTTGATAAGAACA <u>C</u> TAATTAGGAATGGAACCCATTGGTGCAGCC TCTCAATGACGACCTTTTCGAGCTAGGCGC	6206
	CCTAATTAGTGTCTTA	6207
	TAAGAACA <u>C</u> TAATTAGG	6208
Waxy starch GBSS <i>Triticum aestivum</i> Cys8Term TGT-TGA	CCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTT CATTCTTAATTATTGATCTTATCAAACAAACAGTGTTGGTTCACTGA AACTGTCGCCTCACATCCAATTCCAGCAA	6209
	TTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACT GTTTGTTTGATAAGATCAATAATTAGGAATGGAACCCATTGGTGCA GCCTCTCAATGACGACCTTTTCGAGCTAGG	6210
	AATTATTGATCTTATCA	6211
	TGATAAGATCAATAATT	6212
Waxy starch GBSS <i>Triticum aestivum</i> Tyr10Term TAT-TAG	TCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCC TAATTATTGTTCTTAGCAAACAAACAGTGTTGGTTCACTGAACTGT CGCCTCACATCCAATTCCAGCAATCTTGT	6213
	ACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACC AACACTGTTTGTTTGCTAAGAACAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTTCGA	6214
	TGTTCTTAGCAAACAAA	6215
	TTTGTTTGCTAAGAACA	6216
Waxy starch GBSS <i>Triticum aestivum</i> Gln11Term CAA-TAA	CGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCT AATTATTGTTCTTATTAAACAAACAGTGTTGGTTCACTGAACTGTC GCCTCACATCCAATTCCAGCAATCTTGTA	6217
	TACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAAC CAACACTGTTTGTTTAATAAGAACAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTTCG	6218
	GTTCTTATTAAACAAAC	6219
	GTTTGTTTAATAAGAAC	6220

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Triticum aestivum</i> Ser17Term TCA-TGA	AGGCTGCACCAATGGGTTCCATTCTAATTATTGTTCTTATCAAACA AACAGTGTGGTTGACTGAACTGTCGCCTCACATCCAATTCCAGC AATCTTGTAACAATGAAGTTATGTTCT	6221
	AGGAACATAACTTCATTGTTACAAGATTGCTGGAATTGGATGTGAG GCGACAGTTTCAGTCAACCAACACTGTTTGTGGATAAGAACAATA ATTAGGAATGGAACCCATTGGTGCAGCCT	6222
	TGTTGGTTGACTGAAAC	6223
	GTTTCAGTCAACCAACA	6224
Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTCTAGGGCGTGAGGCCCGGAGCCCGGCG GATGCGGCTCTCGGCATGAGGACCGTCGGAGCTA	6225
	TAGCTCCGACGGTCTCATGCCGAGAGCCGCATCCGCCGGGCTC CGGGGCCTCACGCCCTAGAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6226
	CAGGTTTCTAGGGCGTG	6227
	CACGCCCTAGAAACCTG	6228
Waxy starch GBSS <i>Triticum aestivum</i> Gly46Term GGA-TGA	GGTTTCCAGGGCGTGAGGCCCGGAGCCCGGCGGATGCGGCTCT CGGCATGAGGACCGTCTAGAGCTAGCGCCGCCCAACGCAAAGCC GGAAAGCGCACCGCGGGACCCGGCGGTGCCTCT	6229
	AGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGCGTT GGGGCGGCGCTAGCTCAGACGGTCTCATGCCGAGAGCCGCATC CGCCGGGCTCCGGGGCCTCACGCCCTGAAACC	6230
	GGACCGTCTGAGCTAGC	6231
	GCTAGCTCAGACGGTCC	6232
Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA	CGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCGGAG CTAGCGCCGCCCAACGTAAAGCCGAAAGCGCACCGCGGGACC CGGCGGTGCCTCTCCATGGTGGTGCGCGCCACCG	6233
	CGGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTACGTTGGGGCGGCGCTAGCTCCGACGG TCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCG	6234
	CCCCAACGTAAAGCCGG	6235
	CCGGCTTTACGTTGGGG	6236
Waxy starch GBSS <i>Triticum aestivum</i> Lys56Term AAA-TAA	GCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTAGCGCCGC CCCAACGAAAGCCGGTAAGCGCACCGCGGGACCCGGCGGTGC CTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCG	6237
	CGCCGCTGCCGGTGCGCGCACCACCATGGAGAGGCACCGCCG GGTCCCGCGGTGCGCTTACCGGCTTTGCGTTGGGGCGGCGCTAG CTCCGACGGTCTCATGCCGAGAGCCGCATCCGC	6238

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAGCCGGT <u>A</u> AGCGCAC	6239
	GTGCGCTT <u>A</u> CCGGCTTT	6240
Waxy starch GBSS <i>Triticum aestivum</i> Glu85Term GAG-TAG	CTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCGGCATGAACCT CGTGTTCTGTCGGCGCC <u>T</u> AGATGGCGCCCTGGAGCAAGACCGGCG GCCTCGGCGACGTCTCGGGGGCCTCCCCCAG	6241
	CTGGGGGGAGGCCCCCGAGGACGTGCGCGAGGCGCCGGTCTT GCTCCAGGGCGCCATCT <u>A</u> GGCGCCGACGAACACGAGGTTTCATGC CGCCGCTGCCGGTGCGCGCACCAACCATGGAGAG	6242
	TCGGCGCC <u>T</u> AGATGGCG	6243
	CGCCATCT <u>A</u> GGCGCCGA	6244
Waxy starch GBSS <i>Triticum aestivum</i> Gln8Term CAG-TAG	GTCGTCTCTCGCTGCAGGTAGCCACACCCTGCGCGCGCGATGGC GGCTCTGGTCACGTCTG <u>T</u> AGCTCGCCACCTCCGGCACCGTCTCTCG GCATCACCGACAGGTTCCGGCGTGACAGTTTTTC	6245
	GAAAACCTGCACGCCGGAACCTGTCGGTGATGCCGAGGACGGTG CCGGAGGTGGCGAGCT <u>A</u> CGACGTGACCAGAGCCGCCATCGCGC GCGCAGGGTGTGGCTACCTGCAGCGAGAGACGAC	6246
	TCACGTCTG <u>T</u> AGCTCGCC	6247
	GGCGAGCT <u>A</u> CGACGTGA	6248
Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGACAGTTTTT <u>T</u> AGGGTGTGAGGCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6249
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACACCCT <u>A</u> AAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6250
	CAGGTTTT <u>T</u> AGGGTGTG	6251
	CACACCCT <u>A</u> AAAACCTG	6252
Waxy starch GBSS <i>Triticum aestivum</i> Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGG AGCGAGCGCCGCCCGT <u>T</u> AGCAACAAAGCCGGAAGCGCACCGCG GGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG	6253
	CGCGCACCAACCATGGAGAGGCACCGCCGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCT <u>A</u> CGGGGCGGCGCTCGCTCCGGTAGTCCT CATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6254
	CCGCCCCG <u>T</u> AGCAACAA	6255
	TTGTTGCT <u>A</u> CGGGGCGG	6256

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCCGAAGTAACAAAGCCGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6257
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGGTAGT CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6258
	CCCCGAAGTAACAAAGC	6259
	GCTTTGTTACTTCGGGG	6260
Waxy starch GBSS <i>Triticum aestivum</i> Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAG CGCCGCCCCGAAGCAATAAAGCCGAAAGCGCACCGCGGGACCC GGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6261
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGGT AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6262
	CGAAGCAATAAAGCCGG	6263
	CCGGCTTTATTGCTTCG	6264
Waxy starch GBSS <i>Triticum durum</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGAGGTTTCTAGGGCGTGAGGCCCGGAACCCGGCG GATGCGGCCCTCGTCATGAGGACTATCGGAGCGA	6265
	TCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGCCGGGTTC CGGGGCCCTACGCCCTAGAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6266
	CAGGTTTCTAGGGCGTG	6267
	CACGCCCTAGAAACCTG	6268
Waxy starch GBSS <i>Triticum durum</i> Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGG AGCGAGCGCCGCCCCGTAGCAAAGCCGAAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6269
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGCTACGGGGCGGCGCTCGCTCCGATAGTCCT CATGACGAGGGCCGCATCCGCCGGGTTCGGGG	6270
	CCGCCCCGTAGCAAAGC	6271
	GCTTTGCTACGGGGCGG	6272
Waxy starch GBSS <i>Triticum durum</i> Gln53Term CAA-TAA	CGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGC GAGCGCCGCCCCGAAGTAAGCCGAAAGCGCACCGCGGGAGC CGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6273
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTACTTCGGGGCGGCGCTCGCTCCGATAGT CCTCATGACGAGGGCCGCATCCGCCGGGTTCG	6274

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCCCGAAGTAAAGCCGG	6275
	CCGGCTTTACTTCGGGG	6276
Waxy starch GBSS <i>Triticum durum</i> Lys56Term AAA-TAA	GCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGC CCCGAAGCAAAGCCGGTAAGCGCACCGCGGGAGCCGGCGGTGC CTCTCCATGGTGGTGCGCGCCACGGGCAGCGGCG	6277
	CGCCGCTGCCCCTGGCGCGCACCAACCATGGAGAGGCACCGCCG GCTCCCGCGGTGCGCTTACCGGCTTTGCTTCGGGGCGGCGCTCG CTCCGATAGTCCTCATGACGAGGGCCGCATCCGC	6278
	AAAGCCGGTAAGCGCAC	6279
	GTGCGCTTACCGGCTTT	6280
Waxy starch GBSS <i>Triticum durum</i> Cys64Term TGC-TGA	TATCGGAGCGAGCGCCGCCCGAAGCAAAGCCGGAAAGCGCACCC GCGGGAGCCGGCGGTGACTCTCCATGGTGGTGCGCGCCACGGG CAGCGGCGGCATGAACCTCGTGTTTCGTCGGCGCC	6281
	GGCGCCGACGAACACGAGGTTTCATGCCGCGCTGCCCGTGGCGC GCACCACCATGGAGAGTCACCGCCGGCTCCCGCGGTGCGCTTTC CGGCTTTGCTTCGGGGCGGCGCTCGCTCCGATA	6282
	CGGCGGTGACTCTCCAT	6283
	ATGGAGAGTCACCGCCG	6284
Waxy starch GBSS <i>Triticum turgidum</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGACAGGTTTTTAGGGTGTGAGGCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6285
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACACCCTAAAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6286
	CAGGTTTTTAGGGTGTG	6287
	CACACCCTAAAAACCTG	6288
Waxy starch GBSS <i>Triticum turgidum</i> Lys52Term AAG-TAG	CCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGG AGCGAGCGCCGCCCGTAGCAACAAAGCCGGAAGCGCACCGCG GGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG	6289
	CGCGCACCAACCATGGAGAGGCACCGCCGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCTACGGGGCGGCGCTCGCTCCGGTAGTCCT CATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6290
	CCGCCCGTAGCAACAA	6291
	TTGTTGCTACGGGGCGG	6292

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Triticum turgidum</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCCGAAGTAACAAAGCCGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6293
	TGGCGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGGTAGT CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6294
	CCCCGAAGTAACAAAGC	6295
	GCTTTGTTACTTCGGGG	6296
Waxy starch GBSS <i>Triticum turgidum</i> Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAG CGCCGCCCCGAAGCAATAAAGCCGAAAGCGCACCGCGGGACCC GGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6297
	CCGTGGCGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGGT AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6298
	CGAAGCAATAAAGCCGG	6299
	CCGGCTTTATTGCTTCG	6300
Waxy starch GBSS <i>Triticum turgidum</i> Lys57Term AAA-TAA	GATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCC GAAGCAACAAAGCCGGTAAGCGCACCGCGGGACCCGGCGGTGC CTCTCCATGGTGGTGCGCGCCACGGGCAGCGCCG	6301
	CGGCGCTGCCCCTGGCGCGCACCAACCATGGAGAGGCACCGCCG GGTCCCGCGGTGCGCTTACCGGCTTTGTTGCTTCGGGGCGGCGC TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATC	6302
	AAAGCCGGTAAGCGCAC	6303
	GTGCGCTTACCGGCTTT	6304
Waxy starch GBSS <i>Aegilops speltoides</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGCCACCGTCCTCGGCATCACCGACAGGTTC CGCCATGCAGGTTTCTAGGGCGTGAGGCCCGGAGCCCGGCAGA TGCGCCGCTCGGCATGAGGACTGTCGGAGCGA	6305
	TCGCTCCGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACGCCCTAGAAACCTGCATGGCGGAACCTGTGGT GATGCCGAGGACGGTGCGGAGGTGGCGAGCTG	6306
	CAGGTTTCTAGGGCGTG	6307
	CACGCCCTAGAAACCTG	6308
Waxy starch GBSS <i>Aegilops speltoides</i> Gly46Term GGA-TGA	GTTTTCCAGGGCGTGAGGCCCGGAGCCCGGCAGATGCGCCGCT CGGCATGAGGACTGTCTGAGCGAGCGCCGCCCCGAAGCAACAAA GCCGAAAGCGCACCGCGGGACCCGGCGGTGCC	6309
	GGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTGCTTC GGGGCGGCGCTCGCTCAGACAGTCCTCATGCCGAGCGGCGCATC TGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	6310

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGACTGTC <u>I</u> GAGCGAGC	6311
	GCTCGCTC <u>A</u> GACAGTCC	6312
Waxy starch GBSS <i>Aegilops speltoides</i> Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGG AGCGAGCGCCGCCCGCTAGCAACAAAGCCGAAAGCGCACCGCG GGACCCGGCGGTGCCTCTCGATGGTGGTGC GCG	6313
	CGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCGGTGCGCT TTCCGGCTTTGTTGCT <u>A</u> CGGGGCGGCGCTCGCTCCGACAGTCCTC ATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6314
	CCGCCCCG <u>T</u> AGCAACAA	6315
	TTGTTGCT <u>A</u> CGGGGCGG	6316
Waxy starch GBSS <i>Aegilops speltoides</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAG CGAGCGCCGCCCGAAGTAAACAAAGCCGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCGATGGTGGTGC GCGCCA	6317
	TGGCGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTT <u>A</u> CTTCGGGGCGGCGCTCGCTCCGACAGT CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6318
	CCCCGAAGTAAACAAAGC	6319
	GCTTTGTT <u>A</u> CTTCGGGG	6320
Waxy starch GBSS <i>Aegilops speltoides</i> Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAGCGAG CGCCGCCCGGAAGCAATAAAGCCGAAAGCGCACCGCGGGACCC GGCGGTGCCTCTCGATGGTGGTGC GCGGCCACCG	6321
	CGGTGGCGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTT <u>A</u> TTGCTTCGGGGCGGCGCTCGCTCCGAC AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6322
	CGAAGCAATAAAGCCGG	6323
	CCGGCTTT <u>A</u> TTGCTTCG	6324
Waxy starch GBSS <i>Oryza glaberrima</i> Gln8Term CAG-TAG	AGTGCAGAGATCTTCCACAGCAACAGCTAGACAACCACCATGTCG GCTCTACCACGTCTAGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCTGACAGGTCGGCGCCGTCGTCGCTGC	6325
	GCAGCGACGACGGCGCCGACCTGTCAGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG GTTGTCTAGCTGTTGCTGTGGAAGATCTCTGCACT	6326
	CCACGTCC <u>I</u> AGCTCGCC	6327
	GGCGAGCTAGGACGTGG	6328

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Oryza glaberrima</i> Ser12Term TCG-TAG	TCCACAGCAACAGCTAGACAACCACCATGTCGGCTCTCACCACGT CCCAGCTCGCCACCTAGGCCACCGGCTTCGGCATCGCTGACAGG TCGGCGCCGTCGTCGCTGCTCCGCCACGGTT	6329
	AACCCGTGGCGGAGCAGCGACGACGGCGCCGACCTGTCAGCGAT GCCGAAGCCGGTGGCCTAGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGA	6330
	CGCCACCTAGGCCACCG	6331
	CGGTGGCCTAGGTGGCG	6332
Waxy starch GBSS <i>Oryza glaberrima</i> Ser22Term TCG-TAG	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCTGACAGGTAGGCGCCGTCGTCGCTGCTCCGCCACGG GTTCCAGGGCCTCAAGCCCCGCAGCCCCGCCGG	6333
	CCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACCCGTGGCGGA GCAGCGACGACGGCGCCTACCTGTCAGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6334
	TGACAGGTAGGCGCCGT	6335
	ACGGCGCCTACCTGTCA	6336
Waxy starch GBSS <i>Oryza glaberrima</i> Ser25Term TCG-TAG	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCT GACAGGTGCGGCGCCGTAGTCGCTGCTCCGCCACGGGTTCCAGGG CCTCAAGCCCCGCAGCCCCGCCGGCGGCGACGC	6337
	GCGTCGCCGCGCGGGGCTGCGGGGCTTGAGGCCCTGGAACC CGTGGCGGAGCAGCGACTACGGCGCCGACCTGTCAGCGATGCCG AAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	6338
	GGCGCCGTAGTCGCTGC	6339
	GCAGCGACTACGGCGCC	6340
Waxy starch GBSS <i>Oryza glaberrima</i> Ser26Term TCG-TAG	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCTGAC AGGTGCGGCGCCGTCGTAGCTGCTCCGCCACGGGTTCCAGGGCCT CAAGCCCCGCAGCCCCGCCGGCGGCGACGCGAC	6341
	GTCGCGTCGCCGCGGGGCTGCGGGGCTTGAGGCCCTGGA ACCCGTGGCGGAGCAGCTACGACGGCGCCGACCTGTCAGCGATG CCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	6342
	GCCGTCGTAGCTGCTCC	6343
	GGAGCAGCTACGACGGC	6344
Waxy starch GBSS <i>Oryza sativa</i> Gln8Term CAG-TAG	TCCACAGCAAGAGCTAAACAGCCGACCGTGTGCACCACCATGTG GCTCTCACCACGTCTAGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCCGACAGGTGCGGCGCCGTCGTCGCTGC	6345
	GCAGCGACGACGGCGCCGACCTGTGCGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG GTGCACACGGTCGGCTGTTAGCTCTTGCTGTGGA	6346

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCACGTCC <u>T</u> AGCTCGCC	6347
	GGCGAGCT <u>A</u> GGACGTGG	6348
Waxy starch GBSS <i>Oryza sativa</i> Ser12Term TCG-TAG	CTAAACAGCCGACCGTGTGCACCACCATGTCTGGCTCTCACCACGT CCCAGCTCGCCACCT <u>A</u> GGCCACCGGCTTCGGCATCGCCGACAGG TCGGCGCCGTCGTCGCTGCTTCGCCACGGGT	6349
	AACCCGTGGCGAAGCAGCGACGACGGCGCCGACCTGTCTGGCGAT GCCGAAGCCGGTGGCC <u>T</u> AGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTGCACACGGTCGGCTGTTTAG	6350
	CGCCACCT <u>A</u> GGCCACCG	6351
	CGGTGGCC <u>T</u> AGGTGGCG	6352
Waxy starch GBSS <i>Oryza sativa</i> Ser22Term TCG-TAG	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCCGACAGGT <u>A</u> GGCGCCGTCGTCGCTGCTTCGCCACGG GTTCCAGGGCCTCAAGCCCCGTAGCCACAGCCGG	6353
	CCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCCGTGGCGAA GCAGCGACGACGGCGCC <u>T</u> ACCTGTCTGGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6354
	CGACAGGT <u>A</u> GGCGCCGT	6355
	ACGGCGCC <u>T</u> ACCTGTCTG	6356
Waxy starch GBSS <i>Oryza sativa</i> Ser25Term TCG-TAG	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCC GACAGGTCGGCGCCGT <u>A</u> GTCTGCTTCGCCACGGGTTCCAGGG CCTCAAGCCCCGTAGCCACAGCCGGCGGGGACGC	6357
	GCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCC GTGGCGAAGCAGCGAC <u>T</u> ACGGCGCCGACCTGTCTGGCGATGCCGA AGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	6358
	GGCGCCGT <u>A</u> GTCTGCTGC	6359
	GCAGCGAC <u>T</u> ACGGCGCC	6360
Waxy starch GBSS <i>Oryza sativa</i> Ser26Term TCG-TAG	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCCGAC AGGTCTGGCGCCGTCGT <u>A</u> GTCTTCGCCACGGGTTCCAGGGCCT CAAGCCCCGTAGCCACAGCCGGCGGGGACGCATC	6361
	GATGCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAA CCCGTGGCGAAGCAGC <u>T</u> ACGACGGCGCCGACCTGTCTGGCGATGC CGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	6362
	GCCGTCGT <u>A</u> GTCTGCTTC	6363
	GAAGCAGC <u>T</u> ACGACGGC	6364

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Hordeum vulgare</i> Gln8Term CAG-TAG	GTCTCTCACTGCAGGTAGCCACACCCTGTGCGCGGCGCCATGGC GGCTCTGGCCACGTCC <u>T</u> AGCTCGCCACCTCCGGCACCGTCCTCG GCGTCACCGACAGATTCCGGCGTCCAGGTTTTTC	6365
	GAAAACCTGGACGCCGGAATCTGTCCGTGACGCCGAGGACGGTG CCGGAGGTGGCGAGCT <u>A</u> GGACGTGGCCAGAGCCGCCATGGCGC CGCGCACAGGGTGTGGCTACCTGCAGTGAGAGAC	6366
	CCACGTCC <u>T</u> AGCTCGCC	6367
	GGCGAGCT <u>A</u> GGACGTGG	6368
Waxy starch GBSS <i>Hordeum vulgare</i> Arg21Term AGA-TGA	ATGGCGGCTCTGGCCACGTCCCAGCTCGCCACCTCCGGCACCGT CCTCGGCGTCACCGACT <u>I</u> GATTCCGGCGTCCAGGTTTTTCAGGGCCT CAGGCCCCGGAACCCGGCGGATGCGGCGCTTG	6369
	CAAGCGCCGCATCCGCCGGGTTCCGGGGCCTGAGGCCCTGAAAA CCTGGACGCCGGAATC <u>A</u> GTCCGTGACGCCGAGGACGGTGCCGG AGGTGGCGAGCTGGGACGTGGCCAGAGCCGCCAT	6370
	TCACCGACT <u>I</u> GATTCCGG	6371
	CCGGAATC <u>A</u> GTCCGTGA	6372
Waxy starch GBSS <i>Hordeum vulgare</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCGTCACCGACAGATT CCGGCGTCCAGGTTTTT <u>I</u> AGGGCCTCAGGCCCCGGAACCCGGCGG ATGCGGCGCTTGGTATGAGGACTATCGGAGCAA	6373
	TTGCTCCGATAGTCCTCATACCAAGCGCCGCATCCGCCGGGTTCC GGGGCCTGAGGCCCT <u>A</u> AAAACTGGACGCCGGAATCTGTCCGTG ACGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6374
	CAGGTTTT <u>I</u> AGGGCCTC	6375
	GAGGCCCT <u>A</u> AAAACTG	6376
Waxy starch GBSS <i>Hordeum vulgare</i> Gly46Term GGA-TGA	GGTTTTCAGGGCCTCAGGCCCCGGAACCCGGCGGATGCGGCGCT TGGTATGAGGACTATC <u>I</u> GAGCAAGCGCCGCCCGAAGCAAAGCC GGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCT	6377
	AGAGGCACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTTGCTTC GGGGCGGCGCTTGCTC <u>A</u> GATAGTCCTCATACCAAGCGCCGCATC CGCCGGGTTCCGGGGCCTGAGGCCCTGAAAACC	6378
	GGAATATC <u>I</u> GAGCAAGC	6379
	GCTTGCTC <u>A</u> GATAGTCC	6380
Waxy starch GBSS <i>Hordeum vulgare</i> Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCGGCGCTTGGTATGAGGACTATCGG AGCAAGCGCCGCCCG <u>I</u> AGCAAAGCCGGAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCGTGGTGGTGAAGCGCCA	6381
	TGGCGCTACCACCACGAGAGGCACCGCCGGCTCCCGCGGTGC GCTTTCCGGCTTTGCTC <u>A</u> CGGGGCGGCGCTTGCTCCGATAGTCCTC ATACCAAGCGCCGCATCCGCCGGGTTCCGGGG	6382

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGCCCCG <u>T</u> AGCAAAGC	6383
	GCTTTGCT <u>A</u> CGGGGCGG	6384
Waxy starch GBSS <i>Zea mays</i> Gln8Term CAG-TAG	ACGTCTTTTCTCTCTCTCTCTACGCAGTGGATTAATCGGCATGGCGG CTCTGGCCACGTCTG <u>T</u> AGCTCGTCGCAACGCGCGCCGGCCTGGGC GTCCCGGACGCGTCCACGTTCCGCCGCGGCG	6385
	CGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCCAGGCCGGC GCGCGTTGCGACGAGCT <u>A</u> CGACGTGGCCAGAGCCGCCATGCCGA TTAATCCACTGCGTAGGAGAGAGAGAAAAGACGT	6386
	CCACGTCTG <u>T</u> AGCTCGTC	6387
	GACGAGCT <u>A</u> CGACGTGG	6388
Waxy starch GBSS <i>Zea mays</i> Gln30Term CAG-TAG	GTCGCAACGCGCGCCGGCCTGGGCGTCCCGGACGCGTCCACGTT CCGCCGCGGCGCCGCG <u>T</u> AGGGCCTGAGGGGGGCCCCGGGCGTCG GCGGCGGCGGACACGCTCAGCATGCGGACCAGCG	6389
	CGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGCGACGCCCGG GCCCCCTCAGGCCCT <u>A</u> CGCGGCGCCGCGGCGGAACGTGGACG CGTCCGGGACGCCCAGGCCGCGCGCGTTGCGAC	6390
	GCGCCGCG <u>T</u> AGGGCCTG	6391
	CAGGCCCT <u>A</u> CGCGGCGC	6392
Waxy starch GBSS <i>Zea mays</i> Ser38Term TCG-TAG	TCCCGGACGCGTCCACGTTCCGCCGCGGCGCCGCGCAGGGCCT GAGGGGGGCCCCGGGCGT <u>A</u> GGCGGCGGCGGACACGCTCAGCATG CGGACCAGCGCGCGCGCGGCCCGGCCAGGCACCAGCA	6393
	TGCTGGTGCCTGGGCGCCGCGCGCGCGCTGGTCCGCATGCTGAG CGTGTCCGCCGCGCCCT <u>T</u> ACGCCCGGGCCCCCTCAGGCCCTGCG CGGCGCCGCGGCGGAACGTGGACGCGTCCGGGA	6394
	CCGGGCGT <u>A</u> GGCGGCGG	6395
	CCGCCGCC <u>T</u> ACGCCCGG	6396
Waxy starch GBSS <i>Zea mays</i> Ser57Term CAG-TAG	GCGTCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGC GCGCGGCGCCAGGCACTAGCAGCAGGCGCGCCGCGGGGGCAG GTTCCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCA	6397
	TGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCCCC GCGGCGCGCCTGCTGCT <u>A</u> GTGCCTGGGCGCCGCGCGCGCTG GTCCGCATGCTGAGCGTGTCCGCCGCCGCGGACGC	6398
	CCAGGCACTAGCAGCAG	6399
	CTGCTGCT <u>A</u> GTGCCTGG	6400

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Zea mays</i> Gln58Term CAG-TAG	TCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCG CGGCGCCCAGGCACCAGTAGCAGGCGCGCCGCGGGGGCAGGTT CCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCATGA	6401
	TCATGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCC CCGCGGCGCGCCTGCTACTGGTGCCTGGGCGCCGCGCGCGCGC TGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGA	6402
	GGCACCAGTAGCAGGCG	6403
	CGCCTGCTACTGGTGCC	6404

Example 32

Altering fatty acid content of plants

[263] Improved means to manipulate fatty acid compositions, from biosynthetic or natural plant sources, are needed. For example, oils containing reduced saturated fatty acids are desired for dietary reasons and oils containing increased saturated fatty acids are also needed as alternatives to current sources of highly saturated oil products, such as tropical oils or chemically hydrogenated oils. It would therefore be advantageous to influence directly the production and composition of fatty acids in crop plants.

[264] Higher plants synthesize fatty acids, primarily palmitic, stearic and oleic acids, in the plastids (i.e., chloroplasts, proplastids, or other related organelles) as part of the Fatty Acid Synthase (FAS) complex. Fatty acid synthesis is the result of the three enzymatic activities: acyl-ACP elongase, acyl-ACP desaturase and acyl-ACP thioesterases specific for each of palmitoyl-, stearyl- and oleoyl-ACP.

[265] A variety of enzymes have been identified that influence the relative levels of saturated vs. unsaturated fatty acids in plants. For example, the enzymes stearyl-acyl carrier protein (stearyl-ACP) desaturase, oleoyl desaturase and linoleate desaturase produce unsaturated fatty acids from saturated precursors. Similarly, relative enzymatic activities of the various acyl-ACP thioesterases influences the relative acyl-chain composition of the resultant fatty acids. Consequently a reduction or an increase of the activity of these enzymes can alter the properties of oils produced in a plant. In fact, specific targeting of particular enzymatic activities can results in altered levels of particular fatty acids.

[266] The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes encoding proteins involved in fatty acid biosynthesis.

Table 40
Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser8Term TCG-TAG	TTTGGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGC CACCTCTGCTACGTAGTCATTCTTTCTGTACCATCTTCTTCACTTG ATCCTAATGGAAAAGGCAATAAGATTGG	6405
	CCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATGGTA CAGGAAAGAATGACTACGTAGCAGAGGTGGCCACCATGACGAGG AGATGAAGCGTTCAAAGACACTGCCACCAA	6406
	TGCTACGTAGTCATTCT	6407
	AGAATGACTACGTAGCA	6408
Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser9Term TCA-TGA	GGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGCCA CCTCTGCTACGTGCTGATTCTTTCTGTACCATCTTCTTCACTTGAT CCTAATGGAAAAGGCAATAAGATTGGGTC	6409
	GACCCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATG GTACAGGAAAGAATCACGACGTAGCAGAGGTGGCCACCATGACG AGGAGATGAAGCGTTCAAAGACACTGCCACC	6410
	TACGTGCTGATTCTTTC	6411
	GAAAGAATCACGACGTA	6412
Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser17Term TCA-TGA	ATCTCCTCGTCATGGTGGCCACCTCTGCTACGTCGTCATTCTTTCC TGTACCATCTTCTTGACTTGATCCTAATGGAAAAGGCAATAAGATT GGGTCTACGAATCTTGCTGGACTCAATTC	6413
	GAATTGAGTCCAGCAAGATTCGTAGACCCAATCTTATTGCCTTTTC CATTAGGATCAAGTCAAGAAGATGGTACAGGAAAGAATGACGACG TAGCAGAGGTGGCCACCATGACGAGGAGAT	6414
	ATCTTCTTGACTTGATC	6415
	GATCAAGTCAAGAAGAT	6416
Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Gly22Term GGA-TGA	GTGGCCACCTCTGCTACGTCGTCATTCTTTCTGTACCATCTTCTT CACTTGATCCTAATTGAAAAGGCAATAAGATTGGGTCTACGAATCT TGCTGGACTCAATTCTGCACCTAACTCTG	6417
	CAGAGTTAGGTGCAGAATTGAGTCCAGCAAGATTCGTAGACCCAA TCTTATTGCCTTTTCAATTAGGATCAAGTGAAGAAGATGGTACAGG AAAGAATGACGACGTAGCAGAGGTGGCCAC	6418
	ATCCTAATTGAAAAGGC	6419
	GCCTTTTCAATTAGGAT	6420
Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser8Term TCA-TGA	GCTTGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGC TACTGCCGCCACGTGATCATTCTTTCCGTTGACTTCCCCTTCTGGG GATGCCAAATCGGGCAATCCCGGAAAAGG	6421
	CCTTTTCCGGGATTGCCCGATTGGCATCCCCAGAAGGGGAAGTC AACGGAAAGAATGATCACGTGGCGGCAGTAGCAACCATTGTGGCC ACAATTAACCAATCAGATCACAAATTCAAGC	6422

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCCACGTGATCATTCT	6423
	AGAATGATCACGTGGCG	6424
Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser9Term TCA-TGA	TGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGCTAC TGCCGCCACGTCATGATTCTTTCCGTTGACTTCCCCTTCTGGGGAT GCCAAATCGGGCAATCCCGGAAAAGGGTC	6425
	GACCCTTTTCCGGGATTGCCCGATTGGCATCCCCAGAAGGGGAA GTCAACGGAAAGAATCATGACGTGGCGGCAGTAGCAACCATTGTG GCCACAATTAACCAATCAGATCACAATTCA	6426
	CACGTCATGATTCTTTC	6427
	GAAAGAATCATGACGTG	6428
Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Leu13Term TTG-TAG	CTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGT CATCATTCTTTCCGTAGACTTCCCCTTCTGGGGATGCCAAATCGGG CAATCCCGGAAAAGGGTCGGTGAGTTTTGG	6429
	CCAAACTCACCGACCCTTTTCCGGGATTGCCCGATTGGCATCC CCAGAAGGGGAAGTCTACGGAAAGAATGATGACGTGGCGGCAGT AGCAACCATTGTGGCCACAATTAACCAATCAG	6430
	CTTTCCGTAGACTTCCC	6431
	GGGAAGTCTACGGAAAG	6432
Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Lys21Term AAA-TAA	ATGGTTGCTACTGCCGCCACGTCATCATTCTTTCCGTTGACTTCCC CTTCTGGGGATGCCIAATCGGGCAATCCCGGAAAAGGGTCGGTG AGTTTTGGGTCAATGAAGTCGAAATCCGCGG	6433
	CCGCGGATTTGACTTCATTGACCCAAAACCTCACCGACCCTTTTCC GGGATTGCCCGATTAGGCATCCCCAGAAGGGGAAGTCAACGGAA AGAATGATGACGTGGCGGCAGTAGCAACCAT	6434
	GGGATGCCIAATCGGGC	6435
	GCCCGATTAGGCATCCC	6436
Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser8Term TCG-TAG	GGGATTTGAGCACGAAATTGAAGTTGTTTTTAAAAACCATGGTTGC TACTGCTGTGACATAGGCGTTTTTCCCAGTCACTTCTTACCTGAC TCCTCTGACTCGAAAAACAAGAAGCTCGG	6437
	CCGAGCTTCTTGTTTTTCGAGTCAGAGGAGTCAGGTGAAGAAGTG ACTGGGAAAAACGCCATATGTCACAGCAGTAGCAACCATGGTTTTTA AAAACAACCTTCAATTTCTGTGCTGAAATCCC	6438
	TGTGACATAGGCGTTTT	6439
	AAAACGCCATATGTCACA	6440

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser16Term TCA-TGA	TGTTTTTAAAAACCATGGTTGCTACTGCTGTGACATCGGCGTTTTT CCCAGTCACTTCTTGACCTGACTCCTCTGACTCGAAAAACAAGAAG CTCGGAAGCATCAAGTCGAAGCCATCGGT	6441
	ACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTTTTCGAGT CAGAGGAGTCAGGTCAAGAAGTGACTGGGAAAAACGCCGATGTCA CAGCAGTAGCAACCATGGTTTTTAAAAACA	6442
	CACTTCTTGACCTGACT	6443
	AGTCAGGTCAAGAAGTG	6444
Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser22Term TCG-TAG	TTGCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACC TGACTCCTCTGACTAGAAAAACAAGAAGCTCGGAAGCATCAAGTC GAAGCCATCGGTTTCTTCTGGAAGTTTGCA	6445
	TGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCCG AGCTTCTTGTTTTCTAGTCAGAGGAGTCAGGTGAAGAAGTGACTG GGAAAAACGCCGATGTCACAGCAGTAGCAA	6446
	CTCTGACTAGAAAAACA	6447
	TGTTTTTCTAGTCAGAG	6448
Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Lys23Term AAA-TAA	GCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACCTG ACTCCTCTGACTCGTAAACAAGAAGCTCGGAAGCATCAAGTCGA AGCCATCGGTTTCTTCTGGAAGTTTGCAAG	6449
	CTTGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCC GAGCTTCTTGTTTTACGAGTCAGAGGAGTCAGGTGAAGAAGTGAC TGGGAAAAACGCCGATGTCACAGCAGTAGC	6450
	CTGACTCGTAAACAAG	6451
	CTTGTTTTACGAGTCAG	6452
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Ser14Term TCG-TAG	CTCCCGCTCGTTGAAAGACAATGGTGGCTACCGCTGCAAGCTCTG CATTCTTCCCCGTGTAGTCCCCGGTCACCTCCTCTAGACCAGGAA AGCCCGGAAATGGGTCATCGAGCTTCAGCCC	6453
	GGGCTGAAGCTCGATGACCCATTTCGGGGCTTTCCTGGTCTAGAG GAGGTGACCGGGGACTACACGGGGAAGAATGCAGAGCTTGCAGC GGTAGCCACCATTGTCTTTCAACGAGCGGGAG	6454
	CCCCGTGTAGTCCCCGG	6455
	CCGGGGACTACACGGGG	6456
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Arg21Term AGA-TGA	ATGGTGGCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCC CCGGTCACCTCCTCTGACCAGGAAAGCCCGGAAATGGGTGTCG AGCTTCAGCCCCATCAAGCCCAAATTTGTG	6457
	CGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTT CGGGCTTTCCTGGTCAAGAGGAGGTGACCGGGGACGACACGGG GAAGAATGCAGAGCTTGCAGCGGTAGCCACCAT	6458

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCTCCTCT <u>T</u> GACCAGGA	6459
	TCCTGGTC <u>A</u> AGAGGAGG	6460
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gly23Term GGA-TGA	GCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTC ACCTCCTCTAGACCA <u>T</u> GAAAGCCCGGAAATGGGTCATCGAGCTTC AGCCCCATCAAGCCCAAATTTGTCGCCAATG	6461
	CATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACC CATTTCCGGGCTTTCA <u>T</u> GGTCTAGAGGAGGTGACCGGGGACGAC ACGGGGAAGAATGCAGAGCTTGCAGCGGTAGC	6462
	CTAGACCA <u>T</u> GAAAGCCC	6463
	GGGCTTTC <u>A</u> TGGTCTAG	6464
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG	ACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACC TCCTCTAGACCAGGA <u>T</u> AGCCCGGAAATGGGTCATCGAGCTTCAGC CCCATCAAGCCCAAATTTGTCGCCAATGGCG	6465
	CGCCATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATG ACCCATTTCCGGGCT <u>A</u> TCCTGGTCTAGAGGAGGTGACCGGGGAC GACACGGGGAAGAATGCAGAGCTTGCAGCGGT	6466
	GACCAGGA <u>T</u> AGCCCGGA	6467
	TCCGGGCT <u>A</u> TCCTGGTC	6468
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly23Term GGA-TGA	GCCACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGAC ACCTCCTCTAGGCCG <u>T</u> GAAAGCTCGGAAATGGGTCATCGAGCTTG AGCCCCCTCAAGCCCAAATTTGTCGCCAATG	6469
	CATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACC CATTTCCGAGCTTTCA <u>C</u> GGCCTAGAGGAGGTGTCCGGGGACGGC AGGGGGAAGAATGCAGAACTTGCAGCGGTGGC	6470
	CTAGGCCG <u>T</u> GAAAGCTC	6471
	GAGCTTTC <u>A</u> CGGCCTAG	6472
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Lys24Term AAG-TAG	ACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACC TCCTCTAGGCCGGGA <u>T</u> AGCTCGGAAATGGGTCATCGAGCTTGAGC CCCCTCAAGCCCAAATTTGTCGCCAATGCCG	6473
	CGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGAT GACCCATTTCCGAGCT <u>A</u> TCCCGGCCTAGAGGAGGTGTCCGGGGA CGGCAGGGGGAAGAATGCAGAACTTGCAGCGGT	6474
	GGCCGGGA <u>T</u> AGCTCGGA	6475
	TCCGAGCT <u>A</u> TCCCGGCC	6476

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly26Term GGA-TGA	GCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCT AGGCCGGGAAAGCTCTGAAATGGGTCATCGAGCTTGAGCCCCCT CAAGCCCAAATTTGTCGCCAATGCCGGGTGA	6477
	TCAACCCGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGC TCGATGACCCATTTCAAGAGCTTTCCCGGCCTAGAGGAGGTGTCCG GGGACGGCAGGGGGAAGAATGCAGAACTTGC	6478
	GAAAGCTCTGAAATGGG	6479
	CCCATTTCAGAGCTTTC	6480
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Ser29Term TCA-TGA	CATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGGAA AGCTCGGAAATGGGTGATCGAGCTTGAGCCCCCTCAAGCCCAAAT TTGTCGCCAATGCCGGGTGAAGGTTAAGGC	6481
	GCCTTAACCTTCAACCCGGCATTGGCGACAAATTTGGGCTTGAGG GGGCTCAAGCTCGATCACCCATTTCCGAGCTTTCCCGGCCTAGAG GAGGTGTCCGGGGACGGCAGGGGGAAGAATG	6482
	AAATGGGTGATCGAGCT	6483
	AGCTCGATCACCCATTT	6484
Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Ser9Term TCG-TAG	CGTTTAAGTGGATCGGACATTTAAGTGTTTTAATCATGGTAGCTAT GAGTGCTACTGCGTAGCTGTTTCCGGTTTCTTCCCCAAAACCTCAC TCTGGAGCCAAGACATCTGATAAGCTTGG	6485
	CCAAGCTTATCAGATGTCTTGGCTCCAGAGTGAGGTTTTGGGGAA GAAACCGGAAACAGCTACGCAGTAGCACTCATAGCTACCATGATT AAAACACTTAAATGTCCGATCCACTTAAACG	6486
	TACTGCGTAGCTGTTTC	6487
	GAAACAGCTACGCAGTA	6488
Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys17Term AAA-TAA	AGTGTTTTAATCATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTC CGGTTTCTTCCCCATAACCTCACTCTGGAGCCAAGACATCTGATAA GCTTGGAGGTGAACCAGGTAGTGTTGCTG	6489
	CAGCAACACTACCTGGTTACCTCCAAGCTTATCAGATGTCTTGGC TCCAGAGTGAGGTTATGGGGAAGAAACCGGAAACAGCGACGCAG TAGCACTCATAGCTACCATGATTAAAACACT	6490
	CTTCCCCATAACCTCAC	6491
	GTGAGGTTATGGGGAAG	6492
Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Gly21Term GGA-TGA	ATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCC CAAAACCTCACTCTGAGCCAAGACATCTGATAAGCTTGAGGGTG AACCAGGTAGTGTTGCTGTGCGCGGAATCA	6493
	TGATTCCGCGCACAGCAACACTACCTGGTTACCTCCAAGCTTATC AGATGTCTTGGCTCAAGAGTGAGGTTTTGGGGAAGAAACCGGAAA CAGCGACGCAGTAGCACTCATAGCTACCAT	6494

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTCACTCTT <u>I</u> GAGCCAAG	6495
	CTTGGCTC <u>A</u> AGAGTGAG	6496
Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys23Term AAG-TAG	GCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCCCAAAAC CTCACTCTGGAGCCT <u>I</u> AGACATCTGATAAGCTTGGAGGTGAACCAG GTAGTGTGCTGTGCGCGGAATCAAGACAA	6497
	TTGTCTTGATTCCGCGCACAGCAACACTACCTGGTTTACCTCCAAG CTTATCAGATGTCT <u>A</u> GGCTCCAGAGTGAGGTTTTGGGGAAGAAAC CGGAAACAGCGACGCAGTAGCACTCATAGC	6498
	CTGGAGCCT <u>I</u> AGACATCT	6499
	AGATGTCT <u>A</u> GGCTCCAG	6500
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys21Term AAA-TAA	ATGGTGGCTGCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCC CCAGGAGCCTCCCCT <u>I</u> AACCTGGGAAGTTAGGCAACTGGTCATCG AGTTTGAGCCCTTCTTGAAGCCCAAGTCAA	6501
	TTGACTTGGGCTTCAAGGAAGGGCTCAAACCTCGATGACCAGTTGC CTAACTTCCCAGGTT <u>A</u> AGGGGAGGCTCCTGGGGATGGAACAGGG AAGCATGCAGAACTTGCTGCAGCAGCCACCAT	6502
	CCTCCCCT <u>I</u> AACCTGGG	6503
	CCCAGGTT <u>A</u> AGGGGAGG	6504
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys24Term AAG-TAG	GCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCCCCAGGAGCC TCCCCTAAACCTGGG <u>I</u> AGTTAGGCAACTGGTCATCGAGTTTGAGC CCTTCCTTGAAGCCCAAGTCAATCCCCAATG	6505
	CATTGGGGATTGACTTGGGCTTCAAGGAAGGGCTCAAACCTCGATG ACCAGTTGCCTAACT <u>A</u> CCCAGGTTTAGGGGAGGCTCCTGGGGATG GAACAGGGAAGCATGCAGAACTTGCTGCAGC	6506
	AACCTGGG <u>I</u> AGTTAGGC	6507
	GCCTAACT <u>A</u> CCCAGGTT	6508
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Trp28Term TGG-TGA	TGCATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGG GAAGTTAGGCAACTG <u>A</u> TCATCGAGTTTGAGCCCTTCTTGAAGCC CAAGTCAATCCCCAATGGCGGATTTTCAGGTT	6509
	AACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAAGG GCTCAAACCTCGATGAT <u>C</u> AGTTGCCTAACTTCCCAGGTTTAGGGGA GGCTCCTGGGGATGGAACAGGGAAGCATGCA	6510
	GGCAACTG <u>A</u> TCATCGAG	6511
	CTCGATGAT <u>C</u> AGTTGCC	6512

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Ser29Term TCA-TGA	CATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGGGA AGTTAGGCAACTGGT G ATCGAGTTTGAGCCCTTCCTTGAAGCCCA AGTCAATCCCCAATGGCGGATTT C AGGTAA	6513
	TTAACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAA GGGCTCAA A CTCGAT C ACCAGTTGCCTAACTTCCCAGGTTTAGGG GAGGCTCCTGGGGATGGAACAGGGAAGCATG	6514
	CAACTGGT G ATCGAGTT	6515
	AACTCGAT C ACCAGTTG	6516
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys21Term AAA-TAA	ATGGTGGCTGCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACC CCGGGAATCTCCCCT T AACCCGGGAAGTTCGGTAATGGTGGCTTT CAGGTAAAGGCAAACGCCAATGCCCATCCTA	6517
	TAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGCCACCATTAC CGAACTTCCCGGGTT A AGGGGAGATTCCCGGGGTTGGAACGGAG AAGAATGCAGAACTTGCTGCGGCAGCCACCAT	6518
	TCTCCCCT T AACCCGGG	6519
	CCCGGGTT A AGGGGAGA	6520
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG	GCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACCCCGGGAATC TCCCCTAAACCCGGG T AGTTCCGGTAATGGTGGCTTTCAGGTAAAG GCAAACGCCAATGCCCATCCTAGTCTAAAGT	6521
	ACTTTAGACTAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGC CACCATTACCGAACT A CCCGGGTTTAGGGGAGATTCCCGGGGTTG GAACGGAGAAGAATGCAGAACTTGCTGCGGC	6522
	AACCCGGG T AGTTCCGT	6523
	ACCGAACT A CCCGGGTT	6524
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gln31Term CAG-TAG	TTCTCCGTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTC GGTAATGGTGGCTTT T AGGTAAAGGCAAACGCCAATGCCCATCCT AGTCTAAAGTCTGGCAGCCTCGAGACTGAAG	6525
	CTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGGCATTGG CGTTTGCCTTAACCT A AAAGCCACCATTACCGAACTTCCCGGGTTT AGGGGAGATTCCCGGGGTTGGAACGGAGAA	6526
	GTGGCTTT T AGGTAAAG	6527
	CTTAACCT A AAAGCCAC	6528
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys33Term AAG-TAG	GTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTCGGTAAT GGTGGCTTTCAGGTT T AGGCAAACGCCAATGCCCATCCTAGTCTA AAGTCTGGCAGCCTCGAGACTGAAGATGACA	6529
	TGTCATCTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGG CATTGGCGTTTGCCT A AACCTGAAAGCCACCATTACCGAACTTCCC GGGTTTAGGGGAGATTCCCGGGGTTGGAAC	6530

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTCAGGTT <u>I</u> AGGCAAAC	6531
	GTTTGCCT <u>A</u> AACCTGAA	6532
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Gln21Term CAA-TAA	ATGTTGAAGCTCTCGTGTAATGCGACTGATAAGTTACAGACCCTCT TCTCGCATTCTCAT <u>I</u> AACCGGATCCGGCACACCGGAGAACCGTCT CCTCCGTGTCGTGCTCTCATCTGAGGAAAC	6533
	GTTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCTCCGGT GTGCCGGATCCGGTT <u>A</u> ATGAGAATGCGAGAAGAGGGTCTGTAAC TATCAGTCGCATTACACGAGAGCTTCAACAT	6534
	ATTCTCAT <u>I</u> AACCGGAT	6535
	ATCCGGTT <u>A</u> ATGAGAAT	6536
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Arg28Term AGA-TGA	GCGACTGATAAGTTACAGACCCTCTTCTCGCATTCTCATCAACCGG ATCCGGCACACCGGT <u>G</u> AACCGTCTCCTCCGTGTCGTGCTCTCATC TGAGGAAACCGGTTCTCGATCCTTTGCGAG	6537
	CTCGCAAAGGATCGAGAACCGGTTTCCTCAGATGAGAGCACGACA CGGAGGAGACGGTT <u>C</u> ACCGGTGTGCCGGATCCGGTTGATGAGAA TGCGAGAAGAGGGTCTGTAACCTATCAGTCGC	6538
	CACACCGGT <u>G</u> AACCGTC	6539
	GACGGTTC <u>A</u> CCGGTGTG	6540
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Ser24Term TCG-TAG	CCCTCTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAA CCGTCTCCTCCGTGT <u>A</u> GTGCTCTCATCTGAGGAAACCGGTTCTCG ATCCTTTGCGAGCGATCGTATCTGCTGATCA	6541
	TGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTC CTCAGATGAGAGCACT <u>I</u> ACACGGAGGAGACGGTTCTCCGGTGTGC CGGATCCGGTTGATGAGAATGCGAGAAGAGGG	6542
	CTCCGTGT <u>A</u> GTGCTCTC	6543
	GAGAGCACT <u>I</u> ACACGGAG	6544
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Cys25Term TGC-TGA	CTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAACCGT CTCCTCCGTGTCGTG <u>A</u> TCTCATCTGAGGAAACCGGTTCTCGATCC TTTGCGAGCGATCGTATCTGCTGATCAAGGA	6545
	TCCTTGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGG TTTCCTCAGATGAGAT <u>C</u> ACGACACGGAGGAGACGGTTCTCCGGTG TGCCGGATCCGGTTGATGAGAATGCGAGAAG	6546
	GTGTCGTG <u>A</u> TCTCATCT	6547
	AGATGAGAT <u>C</u> ACGACAC	6548

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Leu2Term TTG-TAG	ATTCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAAGG GCATCAAAAATGTAGAAGCTTTCGTGTAATGTGACTAACAACTTAC ACACCTTCTCCTTCTTCTCCGATTCTC	6549
	GAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCACA TTACACGAAAGCTTCTACATTTTTGATGCCCTTTTTTTTTTATGGTTC CTGAGGTTTTGGTTTATAGAAGAAGAAT	6550
	AAAAATGTAGAAGCTTT	6551
	AAAGCTTCTACATTTTT	6552
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Lys3Term AAG-TAG	TCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAAGGG CATCAAAAATGTTGTAGCTTTCGTGTAATGTGACTAACAACTTACAC ACCTTCTCCTTCTTCTCCGATTCTCCC	6553
	GGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCA CATTACACGAAAGCTACAACATTTTTGATGCCCTTTTTTTTTATGG TTCCTGAGGTTTTGGTTTATAGAAGAAGA	6554
	AAATGTTGTAGCTTTTCG	6555
	CGAAAGCTACAACATTT	6556
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Ser5Term TCG-TAG	CTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAAGGGCATCAAA AATGTTGAAGCTTTAGTGTAAATGTGACTAACAACTTACACACCTTCT CCTTCTTCTCCGATTCTCCCTTTTCAT	6557
	ATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTT GTTAGTCACATTACACTAAAGCTTCAACATTTTTGATGCCCTTTTTT TTTTATGGTTCCTGAGGTTTTGGTTTATAG	6558
	GAAGCTTTAGTGTAAATG	6559
	CATTACACTAAAGCTTC	6560
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Cys6Term TGT-TGA	AAACCAAAACCTCAGGAACCATAAAAAAAAAAAGGGCATCAAAAATG TTGAAGCTTTCGTGAATGTGACTAACAACTTACACACCTTCTCCTT CTTCTCCGATTCTCCCTTTTCATCCCG	6561
	CGGGATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTA AGTTGTTAGTCACATTACAGAAAGCTTCAACATTTTTGATGCCCTT TTTTTTTTATGGTTCCTGAGGTTTTGGTTT	6562
	CTTTCGTGAATGTGAC	6563
	GTCACATTACAGAAAG	6564

Table 41
Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Lys4Term AAG-TAG	GGGAGAGCTCTAGCTCTGTAGAAAAGAAGGATTCATTCATCATATC CAGAAATGGCTCTATAGTTTAAACCCTTTGGTGGCATCTCAGCCTTA CAAATTCCTTCCTCGACTCGTCCGCCAA	6565
	TTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCTGAGATGCC ACCAAAGGGTTAAACTATAGAGCCATTCTGGATATGATGAATGAA TCCTTCTTTTCTACAGAGCTAGAGCTCTCCC	6566
	TGGCTCTATAGTTTAAC	6567
	GTAAACTATAGAGCCA	6568
Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Leu8Term TTG-TAG	CTCTGTAGAAAAGAAGGATTCATTCATCATATCCAGAAATGGCTCT AAAGTTTAAACCCTTAGGTGGCATCTCAGCCTTACAAATTCCTTCC TCGACTCGTCCGCCAACTCCTTCTTTCAG	6569
	CTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTTGTA AGGCTGAGATGCCACCTAAGGGTTAACTTTAGAGCCATTTCTGG ATATGATGAATGAATCCTTCTTTTCTACAGAG	6570
	TAACCCTTAGGTGGCAT	6571
	ATGCCACCTAAGGGTTA	6572
Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Gln12Term CAG-TAG	AGAAGGATTCATTCATCATATCCAGAAATGGCTCTAAAGTTTAAACC CTTTGGTGGCATCTTAGCCTTACAAATTCCTTCCTCGACTCGTCC GCCAACTCCTTCTTTCAGATCTCCCAAGT	6573
	ACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAA GGGAATTTGTAAGGCTAAGATGCCACCAAAGGGTTAACTTTAGA GCCATTTCTGGATATGATGAATGAATCCTTCT	6574
	TGGCATCTTAGCCTTAC	6575
	GTAAGGCTAAGATGCCA	6576
Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Phe14Term TAC-TAG	TCATTCATCATATCCAGAAATGGCTCTAAAGTTTAAACCCTTTGGTG GCATCTCAGCCTTAGAAATTCCTTCCTCGACTCGTCCGCCAACTC CTTCTTTCAGATCTCCCAAGTTCCTCTGC	6577
	GCAGAGGAACCTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAG TCGAGGAAGGGAATTTCTAAGGCTGAGATGCCACCAAAGGGTTAA ACTTTAGAGCCATTTCTGGATATGATGAATGA	6578
	CAGCCTTAGAAATTCCT	6579
	GGGAATTTCTAAGGCTG	6580

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu3Term TTG-TAG	GAGAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAA AAAGAAAATGGCATAGAAGCTTAACCCTTTGGCATCTCAGCCTTAC AAACTCCCTTCCTCGGCTCGTCCGCCAAT	6581
	ATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAAGGCTGAGATGC CAAAGGGTTAAGCTTCTATGCCATTTTCTTTTTTTTGATACGAGGTT TGATGTTCTTTCAGACACGAGCGAGCTCTC	6582
	AATGGCATAGAAGCTTA	6583
	TAAGCTTCTATGCCATT	6584
Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Lys4Term AAG-TAG	GAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAA AGAAAATGGCATTGTAGCTTAACCCTTTGGCATCTCAGCCTTACAA ACTCCCTTCCTCGGCTCGTCCGCCAATCT	6585
	AGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAAGGCTGAGAT GCCAAAGGGTTAAGCTACAATGCCATTTTCTTTTTTTTGATACGAG GTTTGATGTTCTTTCAGACACGAGCGAGCTC	6586
	TGGCATTGTAGCTTAAC	6587
	GTTAAGCTACAATGCCA	6588
Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu8Term TTG-TAG	TCTGAAAGAACATCAAACCTCGTATCAAAAAAAGAAAATGGCATT GAAGCTTAACCCTTAGGCATCTCAGCCTTACAACTCCCTTCCTCG GCTCGTCCGCCAATCTCTACTCTCAGATC	6589
	GATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTTT GTAAGGCTGAGATGCCTAAGGGTTAAGCTTCAATGCCATTTTCTTT TTTTTGATACGAGGTTTGATGTTCTTTCAGA	6590
	TAACCCTTAGGCATCTC	6591
	GAGATGCCTAAGGGTTA	6592
Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Gln11Term CAG-TAG	AACATCAAACCTCGTATCAAAAAAAGAAAATGGCATTGAAGCTTA ACCCTTTGGCATCTTAGCCTTACAACTCCCTTCCTCGGCTCGTCC GCCAATCTCTACTCTCAGATCTCCCAAGT	6593
	ACTTGGGAGATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAA GGGAGTTTGTAAAGGCTAAGATGCCAAAGGGTTAAGCTTCAATGCC ATTTTCTTTTTTTTGATACGAGGTTTGATGTT	6594
	TGGCATCTTAGCCTTAC	6595
	GTAAGGCTAAGATGCCA	6596
Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln27Term CAA-TAA	AACCAAAAGAAAAAGGTAAGAAAAAACAATGGCTCTCAAGCTCA ATCCTTTCCTTCTTAAACCCAAAAGTTACCTTCTTTCGCTCTTCCA CCAATGGCCAGTACCAGATCTCCTAAGT	6597
	ACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAG GTAACTTTTGGGTTTAAAGAAAGGAAAGGATTGAGCTTGAGAGCCAT TGTTTTTTTCTTACCTTTTTCTTTTGTT	6598

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCTTTCTTAAACCCAA	6599
	TTGGGTTTAAAGAAAGGA	6600
Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln29Term CAA-TAA	AAGAAAAAGGTAAGAAAAAAACAATGGCTCTCAAGCTCAATCCTT TCCTTTCTCAAACCTTAAAGTTACCTTCTTTGCTCTTCCACCAATG GCCAGTACCAGATCTCCTAAGTTCTACA	6601
	TGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAAGAGCGA AAGAAGGTAACTTTTAGGTTTGAGAAAGGAAAGGATTGAGCTTGA GAGCCATTGTTTTTTTTCTTACCTTTTTCTT	6602
	CTCAAACCTTAAAGTTA	6603
	TAACTTTTAGGTTTGAG	6604
Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys30Term AAG-TAG	AAAAAGGTAAGAAAAAAACAATGGCTCTCAAGCTCAATCCTTTCC TTTCTCAAACCCAAAGTTACCTTCTTTGCTCTTCCACCAATGGCC AGTACCAGATCTCCTAAGTTCTACATGG	6605
	CCATGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAAGAG CGAAAGAAGGTAACCTATTGGGTTTGAGAAAGGAAAGGATTGAGCT TGAGAGCCATTGTTTTTTTTCTTACCTTTTT	6606
	AAACCCAAAGTTACCT	6607
	AGGTAACCTATTGGGTTT	6608
Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys46Term AAG-TAG	TCTCAAACCCAAAAGTTACCTTCTTTGCTCTTCCACCAATGGCCA GTACCAGATCTCCTTAGTTCTACATGGCCTCTACCCTCAAGTCTGG TTCTAAGGAAGTTGAGAATCTCAAGAAGC	6609
	GCTTCTTGAGATTCTCAACTTCCTTAGAACCAGACTTGAGGGTAGA GGCCATGTAGAACTAAGGAGATCTGGTACTGGCCATTGGTGGAAAG AGCGAAAGAAGGTAACCTTTGGGTTTGAGA	6610
	GATCTCCTTAGTTCTAC	6611
	GTAGAACTAAGGAGATC	6612
Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln11Term CAA-TAA	TCTTCTGATTCATTTAATCTTTACTCATCAATGGCTCTGAGACTGAA CCCTATCCCCACCTTAAACCTTCTCCCTCCCCCAAATGGCCAGTCTC AGATCTCCAGGTTCCGCATGGCCTCTA	6613
	TAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTTGG GGGAGGGAGAAGGTTTAGGTGGGGATAGGGTTCACTCTCAGAGC CATTGATGAGTAAAGATTAAATGAATCAGAAGA	6614
	TCCCCACCTTAAACCTTC	6615
	GAAGGTTTAGGTGGGGA	6616

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln17Term CAA-TAA	CTTTACTCATCAATGGCTCTGAGACTGAACCCTATCCCCACCCAAA CCTTCTCCCTCCCCTAAATGGCCAGTCTCAGATCTCCCAGGTTCC GCATGGCCTCTACCCTCCGCTCCGTTCCA	6617
	TGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGAT CTGAGACTGGCCATTTAGGGGAGGGAGAAGGTTTGGGTGGGGAT AGGGTTCAGTCTCAGAGCCATTGATGAGTAAAG	6618
	CCCTCCCCTAAATGGCC	6619
	GGCCATTTAGGGGAGGG	6620
Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Arg22Term AGA-TGA	GCTCTGAGACTGAACCCTATCCCCACCCAAACCTTCTCCCTCCCC CAAATGGCCAGTCTCTGATCTCCCAGGTTCCGCATGGCCTCTACC CTCCGCTCCGGTTCCAAAGAGGTTGAAAATA	6621
	TATTTTCAACCTCTTTGGAACCGGAGCGGAGGGTAGAGGCCATGC GGAACCTGGGAGATCAGAGACTGGCCATTTGGGGGAGGGAGAAG GTTTGGGTGGGGATAGGGTTCAGTCTCAGAGC	6622
	CCAGTCTCTGATCTCCC	6623
	GGGAGATCAGAGACTGG	6624
Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Lys37Term AAA-TAA	CAAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTACC CTCCGCTCCGGTTCCTAAGAGGTTGAAAATATTAAGAAGCCATTCA CTCCTCCCAGAGAAGTGCATGTTCAAGTAA	6625
	TTACTTGAACATGCACTTCTCTGGGAGGAGTGAATGGCTTCTTAAT ATTTTCAACCTCTTAGGAACCGGAGCGGAGGGTAGAGGCCATGCG GAACCTGGGAGATCTGAGACTGGCCATTTG	6626
	CCGGTTCCTAAGAGGTT	6627
	AACCTCTTAGGAACCGG	6628
Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA	CAACAAGCACACACAAGAACAACATCAACAATGGCGATTTCGCATC AATACGGCGACGTTTTAATCAGACCTGTACCGTTTCATTCGCGTTTC CTCAACCGAAACCTCTCAGATCTCCCAAAT	6629
	ATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATGAAC GGTACAGGTCTGATTAAAACGTCGCCGATTGATGCGAATCGCCA TTGTTGATGTTGTTCTTGTGTGTGCTTGTTG	6630
	CGACGTTTAAATCAGAC	6631
	GTCTGATTAAAACGTCG	6632
Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser12Term TCA-TGA	AAGCACACACAAGAACAACATCAACAATGGCGATTTCGCATCAATAC GGCGACGTTTCAATGAGACCTGTACCGTTTCATTCGCGTTTCCTCAA CCGAAACCTCTCAGATCTCCCAAATTCGC	6633
	GCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAAT GAACGGTACAGGTCTCATTGAAACGTCGCCGATTGATGCGAATC GCCATTGTTGATGTTGTTCTTGTGTGTGCTT	6634

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTTCAAT <u>G</u> AGACCTGT	6635
	ACAGGTCT <u>C</u> ATTGAAAC	6636
Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAC-TAG	AAGAACAACATCAACAATGGCGATTTCGCATCAATACGGCGACGTTT CAATCAGACCTGTAG <u>G</u> CGTTCATTTCGCGTTTCCTCAACCGAAACCTC TCAGATCTCCCAAATTCGCCATGGCTTCC	6637
	GGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGG AAACGCGAATGAACG <u>C</u> TACAGGTCTGATTGAAACGTCGCCGTATT GATGCGAATCGCCATTGTTGATGTTGTTCTT	6638
	GACCTGTAG <u>G</u> CGTTCATT	6639
	AATGAACG <u>C</u> TACAGGTC	6640
Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser17Term TCA-TGA	CAACATCAACAATGGCGATTTCGCATCAATACGGCGACGTTTCAATC AGACCTGTACCGTT <u>G</u> ATTTCGCGTTTCCTCAACCGAAACCTCTCAGA TCTCCCAAATTCGCCATGGCTTCCACCAT	6641
	ATGGTGGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGT TGAGGAAACGCGAAT <u>C</u> AACGGTACAGGTCTGATTGAAACGTCGCC GTATTGATGCGAATCGCCATTGTTGATGTTG	6642
	GTACCGTT <u>G</u> ATTTCGCGT	6643
	ACGCGAAT <u>C</u> AACGGTAC	6644
Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Arg4Term CGA-TGA	ACACACAACACACACTCAATCACACACACATCATCATCTTCTTCATC AACGATGGCGCTTT <u>I</u> GAATGAGTCCGGTGACGCTTCAACGGGAGAT ATATCCTTCATACACTTTTCATCAATCGA	6645
	TCGATTGATGAAAAGTGTATGAAGGATATATCTCCCGTTGAAGCGT CACCGGACTCATT <u>C</u> AAGCGCCATCGTTGATGAAGAAGATGATGA TGTGTGTGTGATTGAGTGTGTGTTGTGTGT	6646
	TGGCGCTTT <u>I</u> GAATGAGT	6647
	ACTCATT <u>C</u> AAGCGCCA	6648
Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA	ACACACACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGA GTCCGGTGACGCTTT <u>I</u> AACGGGAGATATATCCTTCATACACTTTTCA TCAATCGAAAAATCTCAGATCTCCTAAAT	6649
	ATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGG ATATATCTCCCGTT <u>A</u> AAGCGTCACCGGACTCATTGAAGCGCCATC GTTGATGAAGAAGATGATGATGTGTGTGT	6650
	TGACGCTTT <u>I</u> AACGGGAG	6651
	CTCCCGTT <u>A</u> AAGCGTCA	6652

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Glu13Term GAG-TAG	ACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGG TGACGCTTCAACGGTAGATATATCCTTCATACACTTTTCATCAATCG AAAAATCTCAGATCTCCTAAATTCGCGA	6653
	TCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTA TGAAGGATATATCTACCGTTGAAGCGTCACCGGACTCATTGGAAG CGCCATCGTTGATGAAGAAGATGATGATGT	6654
	TTCAACGGTAGATATAT	6655
	ATATATCTACCGTTGAA	6656
Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAT-TAG	ATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTGACGCTT CAACGGGAGATATAGCCTTCATACACTTTTCATCAATCGAAAAATC TCAGATCTCCTAAATTCGCGATGGCTTCC	6657
	GGAAGCCATCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGA AAAGTGTATGAAGGCTATATCTCCCGTTGAAGCGTCACCGGACTC ATTCGAAGCGCCATCGTTGATGAAGAAGAT	6658
	GAGATATAGCCTTCATA	6659
	TATGAAGGCTATATCTC	6660
Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys4Term AAG-TAG	AACTCAGCCAGCTTGCCCCAAACAACAGCGCAGAAAAACCTTCA ACAACAATGGCTCTCTAGCTCAACCCAGTCACCACCTTCCCTTCAA CACGCTCCCTCAACAATTCTCCTCCAGAT	6661
	ATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTTGAAGGGAAGGTG GTGACTGGGTTGAGCTAGAGAGCCATTGTTGTTGAAGGTTTTTCT GCGCTGTTGTTGGGGCAAGCTGGCTGAGTT	6662
	TGGCTCTCTAGCTCAAC	6663
	GTTGAGCTAGAGAGCCA	6664
Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Ser13Term TCA-TGA	GCGCAGAAAAACCTTCAACAACAATGGCTCTCAAGCTCAACCCAG TCACCACCTTCCCTTGAAACACGCTCCCTCAACAATTCTCCTCCAG ATCTCCTCGCACCTTTCTCATGGCTGCTTC	6665
	GAAGCAGCCATGAGAAAGGTGCGAGGAGATCTGGAGGAGAAGTT GTTGAGGGAGCGTGTTCAAGGGAAGGTGGTGACTGGGTTGAGCT TGAGAGCCATTGTTGTTGAAGGTTTTTCTGCGC	6666
	CTTCCCTTGAAACACGCT	6667
	AGCGTGTTCAAGGGAAG	6668
Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Arg23Term AGA-TGA	CTCAAGCTCAACCCAGTCACCACCTTCCCTTCAACACGCTCCCTCA ACAATTCTCCTCTGATCTCCTCGCACCTTTCTCATGGCTGCTTC CACTTTCAATTCCACCTCCACCAAGTAAG	6669
	CTTACTTGGTGGAGGTGGAATTGAAAGTGGAAGCAGCCATGAGAA AGGTGCGAGGAGATCAAGGAGGAGAAGTTGTTGAGGGAGCGTGTT GAAGGGAAGGTGGTGACTGGGTTGAGCTTGAG	6670

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCTCCTCC <u>I</u> GATCTCCT	6671
	AGGAGATC <u>A</u> GGAGGAGA	6672
Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys41Term AAG-TAG	TCCTCCAGATCTCCTCGCACCTTTCTCATGGCTGCTTCCACTTTCA ATTCCACCTCCACCTAGTAAGCATCTCCTCCTCCTCGGAATCTCCG CCGATTTCTTTTAAGCGATTGATCGTAGA	6673
	TCTACGATCAATCGCTTAAAAGAAATCGGCGGAGATTCCGAGGAG GAGGAGATGCTTACTAGGTGGAGGTGGAATTGAAAGTGGAAGCA GCCATGAGAAAGGTGCGAGGAGATCTGGAGGA	6674
	CCTCCACCTAGTAAGCA	6675
	TGCTTACTAGGTGGAGG	6676
Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Arg21Term AGA-TGA	ATGGCACTGAAACTTTGCTTTCCACCCACAAGATGCCTTCCTTCC CCGATGCTCGTATCTGATCTCACAGGGTTTTTCATGGCTTCAACTAT TCATTCTCCTTCTATGGAGGTTCGAAAAG	6677
	CTTTTCCGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAA AACCCTGTGAGATCAGATACGAGCATCGGGGAAGGAAGGCATCTT GTGGGGTGGAAGCAAAGTTTCAGTGCCAT	6678
	CTCGTATCTGATCTCAC	6679
	GTGAGATCAGATACGAG	6680
Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Ser29Term TCA-TGA	CCCACAAGATGCCTTCCTTCCCGATGCTCGTATCAGATCTCACAG GGTTTTCATGGCTTGAAGTATTCTCTCTTCTATGGAGGTTCGGA AAAGTTAAAAAGCCTTTCACGCCTCCACG	6681
	CGTGGAGGCGTGAAAGGCTTTTAACTTTTCCGACCTCCATAGAA GGAGAATGAATAGTTCAAGCCATGAAAACCCTGTGAGATCTGATAC GAGCATCGGGGAAGGAAGGCATCTTGTGGG	6682
	CATGGCTTGAAGTATTC	6683
	GAATAGTTCAAGCCATG	6684
Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Glu37Term GAG-TAG	GATGCTCGTATCAGATCTCACAGGGTTTTTCATGGCTTCAACTATTC ATTCTCCTTCTATGTAGGTTCGAAAAGTTAAAAAGCCTTTCACGCC TCCACGAGAGGTACATGTTCAAGTAACCC	6685
	GGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAGGCTTTT TAACTTTTCCGACCTACATAGAAGGAGAATGAATAGTTGAAGCCAT GAAAACCCTGTGAGATCTGATACGAGCATC	6686
	CTTCTATGTAGGTTCGGA	6687
	TCCGACCTACATAGAAG	6688

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Gly39Term GGA-TGA	CGTATCAGATCTCACAGGGTTTTTCATGGCTTCAACTATTTCATTCTC CTTCTATGGAGGTCTGAAAAGTTAAAAAGCCTTTCACGCCTCCACG AGAGGTACATGTTCAAGTAACCCATTCT	6689
	AGGAATGGGTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAG GCTTTTAACTTTTCAAGACCTCCATAGAAGGAGAATGAATAGTTGA AGCCATGAAAACCCTGTGAGATCTGATACG	6690
	TGGAGGTCTGAAAAGTT	6691
	AACTTTTCAAGACCTCCA	6692
Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys4Term AAA-TAA	TTCTCGTTTTTGTCGTCCCCTCTGCTCTCTCTCTATCAGGCACG GAGAAATGGCACTGTAACTCAGTCCAGTCATGTTTCAATCTCAGAA GCTTCCATTTCTTGCCCTCCTATCCGCCTT	6693
	AAGGCGGATAGGAGGCAAGAAATGGAAGCTTCTGAGATTGAAACA TGAAGGACTGAGTTAAGTGCCTTTCTCCGTGCCTGATAGAGA GAGAGAGCAGAGGGGACGACAAAACGAGAA	6694
	TGGCACTGTAACTCAGT	6695
	ACTGAGTTAAGTGCCA	6696
Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln11Term CAA-TAA	CTGCTCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCA GTCCAGTCATGTTTAAATCTCAGAAGCTTCCATTTCTTGCCCTCCTAT CCGCCTTCCAATCTCAGATCTCCGAGGG	6697
	CCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAAT GGAAGCTTCTGAGATTAAACATGACTGGACTGAGTTTCAGTGCC ATTTCTCCGTGCCTGATAGAGAGAGAGAGCAG	6698
	TCATGTTTAAATCTCAG	6699
	CTGAGATTAAACATGA	6700
Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln13Term CAG-TAG	TCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCA GTCATGTTTCAATCTTAGAAGCTTCCATTTCTTGCCCTCCTATCCGCC TTCCAATCTCAGATCTCCGAGGGTTTTCA	6701
	TGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAA GAAATGGAAGCTTCTAAGATTGAAACATGACTGGACTGAGTTTCAG TGCCATTTCTCCGTGCCTGATAGAGAGAGA	6702
	TTCAATCTTAGAAGCTT	6703
	AAGCTTCTAAGATTGAA	6704
Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys14Term AAG-TAG	CTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTC ATGTTTCAATCTCAGTAGCTTCCATTTCTTGCCCTCCTATCCGCCTTC CAATCTCAGATCTCCGAGGGTTTTCATGG	6705
	CCATGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAG GCAAGAAATGGAAGCTACTGAGATTGAAACATGACTGGACTGAGT TTCAGTGCCATTTCTCCGTGCCTGATAGAGAG	6706

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCTCAG <u>I</u> AGCTTCCA	6707
	TGGAAGCT <u>A</u> CTGAGATT	6708
Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Tyr12Term TAC-TAG	CCCCGAGATCTCGCTGCCGCTGCTCATGGCGTTCGCGGCGTCCC ACACCGCATCGCCGTA <u>G</u> TCCTGCGGCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCTGAAGATGGTGGCCATGGCC	6709
	GGCCATGGCCACCATCTTCGACATCCCATTGCTCCTCCTCTGCGC CACGCCGCCGAGGAC <u>T</u> ACGGCGATGCGGTGTGGGACGCCGCG AACGCCATGAGCAGCGGCAGCGAGATCTCGGGG	6710
	TCGCCGTA <u>G</u> TCCTGCGG	6711
	CCGCAGGA <u>C</u> TACGGCGA	6712
Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Gln19Term CAG-TAG	CTGCTCATGGCGTTCGCGGCGTCCCACACCGCATCGCCGTA <u>C</u> CTCC TGCGGCGGCGTGGCGT <u>I</u> AGAGGAGGAGCAATGGGATGTCTGAAGAT GGTGGCCATGGCCTCCACCATCAACAGGGTCA	6713
	TGACCCTGTTGATGGTGGAGGCCATGGCCACCATCTTCGACATCC CATTGCTCCTCCTCT <u>A</u> CGCCACGCCGCCGAGGAGTACGGCGAT GCGGTGTGGGACGCCGGAACGCCATGAGCAG	6714
	GCGTGGCG <u>I</u> AGAGGAGG	6715
	CCTCCTCT <u>A</u> CGCCACGC	6716
Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Ser26Term TCG-TAG	CCCACACCGCATCGCCGTA <u>C</u> CTGCGGCGGCGTGGCGCAGAGG AGGAGCAATGGGATGT <u>A</u> GAAGATGGTGGCCATGGCCTCCACCAT CAACAGGGTCAAGACTGCTAAGAAGCCCTACAC	6717
	GTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGGCC ATGGCCACCATCTTCT <u>I</u> ACATCCCATTGCTCCTCCTCTGCGCCACGC CGCCGCAGGAGTACGGCGATGCGGTGTGGG	6718
	TGGGATGT <u>A</u> GAAGATGG	6719
	CCATCTTCT <u>I</u> ACATCCCA	6720
Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Lys27Term AAG-TAG	CACACCGCATCGCCGTA <u>C</u> CTGCGGCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCTG <u>I</u> AGATGGTGGCCATGGCCTCCACCATCAA CAGGGTCAAGACTGCTAAGAAGCCCTACACTC	6721
	GAGTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGG CCATGGCCACCATCT <u>A</u> CGACATCCCATTGCTCCTCCTCTGCGCCA CGCCGCCGAGGAGTACGGCGATGCGGTGTG	6722
	GGATGTCTG <u>I</u> AGATGGTG	6723
	CACCATCT <u>A</u> CGACATCC	6724

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Leu3Term TTG-TAG	TTCTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGA GAGAAGCAATGGCGTGAAGCTTCACCACACGGCCTTCAATCCTT CCATGGCGGTTACCTCTTCGGGACTTCCTCG	6725
	CGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAGGC CGTGTGGTGAAGCTTACGCCATTGCTTCTCTCTCCTAAGTGCTT CTGTTGGTAACCGCTCAACCTAGAGAGAGAA	6726
	AATGGCGTGAAGCTTC	6727
	GAAGCTTCTACGCCATT	6728
Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Lys4Term AAG-TAG	CTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGAGA GAAGCAATGGCGTTGTAGCTTCACCACACGGCCTTCAATCCTTCC ATGGCGGTTACCTCTTCGGGACTTCCTCGAT	6729
	ATCGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTACAACGCCATTGCTTCTCTCTCCTAAGTG CTTCTGTTGGTAACCGCTCAACCTAGAGAGAG	6730
	TGGCGTTGTAGCTTCAC	6731
	GTGAAGCTACAACGCCA	6732
Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Ser19Term TCG-TAG	AAGCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCAT GGCGGTTACCTCTTAGGGACTTCCTCGATCGTATCACCTCAGATCT CACCGCGTTTTTCATGGCTTCTTCTACAAT	6733
	ATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGATAC GATCGAGGAAGTCCCTAAGAGGTAACCGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTTCAACGCCATTGCTT	6734
	TACCTCTTAGGGACTTC	6735
	GAAGTCCCTAAGAGGTA	6736
Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Gly20Term GGA-TGA	GCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCATG GCGGTTACCTCTTCGTGACTTCCTCGATCGTATCACCTCAGATCTC ACCGCGTTTTTCATGGCTTCTTCTACAATTG	6737
	CAATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGAT ACGATCGAGGAAGTCAAGAAGAGGTAACCGCCATGGAAGGATTG AAGGCCGTGTGGTGAAGCTTCAACGCCATTGC	6738
	CCTCTTCGTGACTTCCT	6739
	AGGAAGTCAAGAAGAGG	6740
Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Ser21Term TCA-TGA	TGGCTCTGAATCTCAACCCCGTTTCCACACCATTTAGTGTCGTG ATTGCCGTCTTTCTGACCTCGTCAAACGCCTTCTCGCAGATCTCCC AAATTCTTCATGGCTTCACTCTCAGCAG	6741
	CTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATCTGCGAGAA GGCGTTTGACGAGGTGAGAAAGACGGCAATCGACGACACTGAAAT GGTGTGGAAACGGGGTTGAGATTGAGAGCCA	6742

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTCTTTCT <u>G</u> ACCTCGTC	6743
	GACGAGGT <u>C</u> AGAAAGAC	6744
Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Gln24Term CAA-TAA	AATCTCAACCCCGTTTCCACACCATTTCAGTGTCGTCGATTGCCGT CTTTCTCACCTCGT <u>T</u> AAACGCCTTCTCGCAGATCTCCCAAATTCTT CATGGCTTCCACTCTCAGCAGCTCTTCTC	6745
	GAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATC TGCGAGAAGGCGTTT <u>A</u> ACGAGGTGAGAAAGACGGCAATCGACGA CACTGAAATGGTGTGGAACGGGGTTGAGATT	6746
	CACCTCGT <u>T</u> AAACGCCT	6747
	AGGCGTTT <u>A</u> ACGAGGTG	6748
Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Arg29Term AGA-TGA	TCCACACCATTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTC AAACGCCTTCTCGC <u>I</u> GATCTCCCAAATTCTTCATGGCTTCCACTCT CAGCAGCTCTTCTCCTAAGGAAGCGGAAA	6749
	TTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGGAAGCCATGA AGAATTTGGGAGATC <u>A</u> GCGAGAAGGCGTTTGACGAGGTGAGAAA GACGGCAATCGACGACACTGAAATGGTGTGGA	6750
	CTTCTCGC <u>I</u> GATCTCCC	6751
	GGGAGATC <u>A</u> GCGAGAAG	6752
Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Lys32Term AAA-TAA	TTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTCAAACGCCTT CTCGCAGATCTCCCT <u>I</u> AATTCTTCATGGCTTCCACTCTCAGCAGCTC TTCTCCTAAGGAAGCGGAAAGCCTGAAGA	6753
	TCTTCAGGCTTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGG AAGCCATGAAGAATT <u>A</u> GGGAGATCTGCGAGAAGGCGTTTGACGAG GTGAGAAAGACGGCAATCGACGACACTGAAA	6754
	GATCTCCC <u>I</u> AATTCTTC	6755
	GAAGAATT <u>A</u> GGGAGATC	6756
Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu10Term TTA-TGA	AAATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATAT CAATGGGGTGTCGT <u>G</u> AAAATCTCACAAAATGTTACCATTTCTTGT TCTTCAGCCAGATCTGAGCGAGTTTTTCAT	6757
	ATGAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAAC ATTTTGTGAGATTTT <u>C</u> ACGACACCCCATTGATATTCAGTGCCATTGT TGATGCTCTGTTTTTACCTCGACTATTT	6758
	GGTGTCGT <u>G</u> AAAATCTC	6759
	GAGATTTT <u>C</u> ACGACACC	6760

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys11Term AAA-TAA	ATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCA ATGGGGTGTCTGTTATAATCTCACAAAATGTTACCATTTCCTTGTTCT TCAGCCAGATCTGAGCGAGTTTTCATGG	6761
	CCATGAAAACCTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTA ACATTTTGTGAGATTATAACGACACCCCATTTGATATTCAGTGCCATT GTTGATGCTCTGTTTTTCACCTCGACTAT	6762
	TGTCGTTATAATCTCAC	6763
	GTGAGATTATAACGACA	6764
Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys14Term AAA-TAA	GTGAAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTG TCGTTAAATCTCACTAAATGTTACCATTTCCTTGTTCTTCAGCCAG ATCTGAGCGAGTTTTCATGGCTTCAACCA	6765
	TGTTGAAGCCATGAAAACCTCGCTCAGATCTGGCTGAAGAACAAG GAAATGGTAACATTTAGTGAGATTTTAACGACACCCCATTTGATATT CAGTGCCATTGTTGATGCTCTGTTTTTCAC	6766
	AATCTCACTAAATGTTA	6767
	TAACATTTAGTGAGATT	6768
Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu16Term TTA-TGA	ACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCTGTTAAA ATCTCACAAAATGTGACCATTTCCTTGTTCTTCAGCCAGATCTGAG CGAGTTTTTCATGGCTTCAACCATTTCATCG	6769
	CGATGAATGGTTGAAGCCATGAAAACCTCGCTCAGATCTGGCTGAA GAACAAGGAAATGGTCACATTTTGTGAGATTTTAACGACACCCCAT TGATATTCAGTGCCATTGTTGATGCTCTGT	6770
	CAAAATGTGACCATTTC	6771
	GAAATGGTCACATTTTG	6772
Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser21Term TCA-TGA	TGGCTCTGAGGCTGAACCCTAACCTTCACAGAAGCTCTTTCTCTC TCCTTCTTCATCATGATCTTCTTCTTCTTCATCGTTCTCGCTTCCTC AAATGGCTAGCCTCAGATCTCCAAGGT	6773
	AACCTTGAGATCTGAGGCTAGCCATTTGAGGAAGCGAGAACGAT GAAGAAGAAGAAGATCATGATGAAGAAGGAGAGAGAAAGAGCTTC TGTGAAGGGTTAGGGTTCAGCCTCAGAGCCA	6774
	TTCATCATGATCTTCTT	6775
	AAGAAGATCATGATGAA	6776
Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser26Term TCA-TGA	ACCCTAACCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCA TCTTCTTCTTCTTGATCGTTCTCGCTTCCTCAAATGGCTAGCCTCA GATCTCCAAGGTTCCGCATGGCCTCCAC	6777
	GTGGAGGCCATGCGGAACCTTGAGATCTGAGGCTAGCCATTTGA GGAAGCGAGAACGATCAAGAAGAAGAAGATGATGATGAAGAAGGA GAGAGAAAGAGCTTCTGTGAAGGGTTAGGGT	6778

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTCTTCTT <u>G</u> ATCGTTCT	6779
	AGAACGAT <u>C</u> AAGAAGAA	6780
Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser27Term TCG-TAG	CTAACCCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCT TCTTCTTCTTCAT <u>A</u> GTTCTCGCTTCCTCAAATGGCTAGCCTCAGAT CTCCAAGGTTCCGCATGGCCTCCACCCT	6781
	AGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCAT TTGAGGAAGCGAGAAC <u>T</u> ATGAAGAAGAAGAAGATGATGATGAAGA AGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAG	6782
	TTCTTCAT <u>A</u> GTTCTCGC	6783
	GCGAGAACT <u>A</u> TGAAGAA	6784
Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser29Term TCG-TAG	CTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCTTCTTCT TCTTCATCGTTCT <u>A</u> GCTTCCTCAAATGGCTAGCCTCAGATCTCCAA GGTTCCGCATGGCCTCCACCCTCCGCAC	6785
	GTGCGGAGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCT AGCCATTTGAGGAAGCT <u>A</u> GAAACGATGAAGAAGAAGAAGATGATGA TGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAG	6786
	ATCGTTCT <u>A</u> GCTTCCTC	6787
	GAGGAAGCT <u>A</u> GAAACGAT	6788
Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Leu3Term TTG-TAG	AAAGTTAAAGCCGTCCAAAACCCAAACCAGGAAAGGCAAACGAA AAGAAAAATGGCTT <u>A</u> GAAATTTAATGCCATCGCCTCGAAATCTCA GAAGCTCCCTTGCTTTGCTCTTCCACCAA	6789
	TTTGGTGAAGAGCAAAGCAAGGGAGCTTCTGAGATTTGAGGGCG ATGGCATTAAATTCT <u>A</u> AGCCATTTTTCTTTTCGTTTGCCTTTCCT GGTTTGGGTTTTGGACGGCTTTTAACTTT	6790
	AATGGCTT <u>A</u> GAAATTTA	6791
	TAAAATTCT <u>A</u> AGCCATT	6792
Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Ser1-Term TCG-TAG	CCCAAACCAGGAAAGGCAAACGAAAAGAAAAATGGCTTTGAATTT TAATGCCATCGCCT <u>A</u> GAAATCTCAGAAGCTCCCTTGCTTTGCTCTT CCACCAAAGGCCACCCTTAGATCTCCCAA	6793
	TTGGGAGATCTAAGGGTGGCCTTTGGTGAAGAGCAAAGCAAGG GAGCTTCTGAGATTTCT <u>A</u> GGCGATGGCATTAAATTCAAAGCCATT TTTTCTTTTCGTTTGCCTTTCCTGGTTTGGG	6794
	CATCGCCT <u>A</u> GAAATCTC	6795
	GAGATTTCT <u>A</u> GGCGATG	6796

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Lys11Term AAA-TAA	CAAACCAGGAAAGGCCAAACGAAAAGAAAAAATGGCTTTGAATTTTA ATGCCATCGCCTCGTAATCTCAGAAGCTCCCTTGCTTTGCTCTTCC ACCAAAGGCCACCCTTAGATCTCCCAAGT	6797
	ACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAAGAGCAAAGCAAG GGAGCTTCTGAGATTACGAGGCGATGGCATTAAAATTCAAAGCCA TTTTTCTTTTCGTTTGCCTTTCCTGGTTTG	6798
	TCGCCTCGTAATCTCAG	6799
	CTGAGATTACGAGGCGA	6800
Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Gln13Term CAG-TAG	AGGAAAGGCCAAACGAAAAGAAAAAATGGCTTTGAATTTTAATGCCA TCGCCTCGAAATCTTAGAAGCTCCCTTGCTTTGCTCTTCCACCAAA GGCCACCCTTAGATCTCCCAAGTTTTCCA	6801
	TGGAAAACCTGGGAGATCTAAGGGTGGCCTTTGGTGGAAAGAGCAA AGCAAGGGAGCTTCTAAGATTTTCGAGGCGATGGCATTAAAATTCA AAGCCATTTTTCTTTTCGTTTGCCTTTCCT	6802
	CGAAATCTTAGAAGCTC	6803
	GAGCTTCTAAGATTTTCG	6804

Table 42
Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser4Term TCG-TAG	AATAGAACGACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGC TCCAATGGCGAGCTAGGTTTTATCAGAATGTGGTTTTAGACCTCTC CCCAGATTCTACCCTAAACACACAACCTC	6805
	GAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTAAAACCA CATTCTGATAAAACCTAGCTCGCCATTGGAGCCTCTTCCCAAGAAG AAAAGAGGAAAAAGTCTCTGTCTGTTCTATT	6806
	GGCGAGCTTGGTTTTAT	6807
	ATAAAACCAGCTCGCC	6808
Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Leu6Term TTA-TGA	ACGACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAAT GGCGAGCTCGGTTTTGATCAGAATGTGGTTTTAGACCTCTCCCCAG ATTCTACCCTAAACACACAACCTCTTTTGC	6809
	GCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTA AAACCACATTCTGATCAAACCGAGCTCGCCATTGGAGCCTCTTCCC AAGAAGAAAAGAGGAAAAAGTCTCTGTCTGT	6810
	CTCGGTTTGATCAGAAT	6811
	ATTCTGATCAAACCGAG	6812
Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser7Term TCA-TGA	ACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAATGGC GAGCTCGGTTTTATGAGAATGTGGTTTTAGACCTCTCCCCAGATTCT TACCCTAAACACACAACCTCTTTTGCCTC	6813
	GAGGCCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGT CTAAAACCACATTCTCATAAAACCGAGCTCGCCATTGGAGCCTCTT CCCAAGAAGAAAAGAGGAAAAAGTCTCTGT	6814
	GGTTTTATGAGAATGTG	6815
	CACATTCTCATAAAACC	6816
Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Glu8Term GAA-TAA	AGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAATGGCGA GCTCGGTTTTATCATTAATGTGGTTTTAGACCTCTCCCCAGATTCTA CCCTAAACACACAACCTCTTTTGCCTCTA	6817
	TAGAGGCCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAG GTCTAAAACCACATTATGATAAAACCGAGCTCGCCATTGGAGCCTC TTCCAAGAAGAAAAGAGGAAAAAGTCTCT	6818
	TTTTATCATTAATGTGGT	6819
	ACCACATTATGATAAAA	6820

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu4Term TTG-TAG	TCATCATCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTC TAGCAATGGCGAACTAGGTCTTATCCGAATGTGGCATAAGACCTC TCCCCAGAATCTACACCACACCCAGATCCAC	6821
	GTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCA CATTCGGATAAGACCTAGTTCGCCATTGCTAGAGCTCTTTTGTCTCT CTCTCTCTCCCCAGAAGAAGAAGATGATGA	6822
	GGCGAACTAGGTCTTAT	6823
	ATAAGACCTAGTTCGCC	6824
Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu6Term TTA-TGA	TCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAA TGCGGAACCTGGTCTGATCCGAATGTGGCATAAGACCTCTCCCCA GAATCTACACCACACCCAGATCCACTTTTCT	6825
	AGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTT ATGCCACATTTCGGATCAGACCAAGTTCGCCATTGCTAGAGCTCTTT TGCTCTCTCTCTCTCCCCAGAAGAAGAAGA	6826
	CTTGGTCTGATCCGAAT	6827
	ATTCGGATCAGACCAAG	6828
Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Glu8Term GAA-TAA	TTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCG AACTTGGTCTTATCCTAATGTGGCATAAGACCTCTCCCCAGAATCT ACACCACACCCAGATCCACTTTCTCTCCA	6829
	TGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGA GGTCTTATGCCACATTAGGATAAGACCAAGTTCGCCATTGCTAGA GCTCTTTTGTCTCTCTCTCTCTCCCCAGAAGAA	6830
	TCTTATCCTAATGTGGC	6831
	GCCACATTAGGATAAGA	6832
Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Cys9Term TGT-TGA	CTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACT TGGTCTTATCCGAATGAGGCATAAGACCTCTCCCCAGAATCTACAC CACACCCAGATCCACTTTCTCTCCAACACC	6833
	GGTGTGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGG GGAGAGGTCTTATGCCCTCATTTCGGATAAGACCAAGTTCGCCATTG CTAGAGCTCTTTTGTCTCTCTCTCTCTCCCCAG	6834
	TCCGAATGAGGCATAAG	6835
	CTTATGCCCTCATTTCGGA	6836
Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Trp5Term TGG-TGA	ATAACAGAATTGCTGAATTCTTGCATTTTAGCTTCTGGGTTTTCAA TGGCTGCTGGTTGAGTATTATCAGAATGTGGTTTAAGGCCTCTCCC AAGAATCTACTCACGACCCAGAATTGGT	6837
	ACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACC ACATTCTGATAATACTCAACCAGCAGCCATTGAAAACCCAGAAGCT AAAAATGCAAGAATTCAGCAATTCTGTTAT	6838

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCTGGTTGAGTATTATC	6839
	GATAATACTCAACCAGC	6840
Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Leu7Term TTA-TGA	AGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTGGTTGGGTATGATCAGAATGTGGTTTAAGGCCTCTCCCAAGAATCTACTCACGACCCAGAATTGGTTTTAC	6841
	GTAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACCACATTCTGATCATAACCAACCAGCAGCCATTGAAAACCCAG AAGCTAAAAATGCAAGAATTCAGCAATTCT	6842
	TTGGGTATGATCAGAAT	6843
	ATTCTGATCATAACCAA	6844
	ATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTGGTTGGGTATTATGAGAATGTGGTTTAAGGCCTCTCCCAAGAATCT ACTCACGACCCAGAATTGGTTTTACATC	6845
Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Ser8Term TCA-TGA	GATGTAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACCACATTCTCATAATACCAACCAGCAGCCATTGAAAACC CAGAAGCTAAAAATGCAAGAATTCAGCAAT	6846
	GGTATTATGAGAATGTG	6847
	CACATTCTCATAATACC	6848
	TGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTG GTTGGGTATTATCAATGTGGTTTAAGGCCTCTCCCAAGAATCTA CTCACGACCCAGAATTGGTTTTACATCGA	6849
Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Glu9Term GAA-TAA	TCGATGTAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAG GCCTTAAACCACATTATGATAATACCAACCAGCAGCCATTGAAAA CCCAGAAGCTAAAAATGCAAGAATTCAGCA	6850
	TATTATCAATGTGGT	6851
	ACCACATTATGATAATA	6852
	GCAAGTTGGGTTTTATCAGAATGTGGTCTTAGACCACTCCCAAGAA TCTACCCTAAGCCCTGAACTGGGGCAGCCACTTCTGCCTCCTCTC ACATTAAGTTGAGAATTCACGTACAGATC	6853
Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg22Term AGA-TGA	GATCTGTACGTGAAATTCTCAACTTAATGTGAGAGGAGGCAGAAGT GGCTGCCCCAGTTCAAGGGCTTAGGGTAGATTCTTGGGAGTGGTCT AAGACCACATTCTGATAAAACCAACTTGC	6854
	CTAAGCCCIGAAGTGGG	6855
	CCCAGTTCAGGGCTTAG	6856

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Lys34Term AAG-TAG	CTCCCAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCT GCCTCCTCTCACATTAGTTGAGAATTTACGTACAGATCTGAGTG GTTCTGCAATTTCTTTGTCTAATACTAATA	6857
	TATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACG TGAAATTCTCAACTAATGTGAGAGGAGGCAGAAGTGGCTGCCCC AGTTCTGGGCTTAGGGTAGATTCTTGGGAG	6858
	CTCACATTAGTTGAGA	6859
	TCTCAACTAATGTGAG	6860
Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Leu35Term TTG-TAG	CAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCT CCTCTCACATTAAGTAGAGAATTTACGTACAGATCTGAGTGGTTC TGCAATTTCTTTGTCTAATACTAATAAAGA	6861
	TCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGT ACGTGAAATTCTCTACTTAATGTGAGAGGAGGCAGAAGTGGCTGC CCCAGTTCTGGGCTTAGGGTAGATTCTTG	6862
	CATTAAGTAGAGAATTT	6863
	AAATTCTCTACTTAATG	6864
Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg36Term AGA-TGA	AGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCC TCTCACATTAAGTTGTGAATTTACGTACAGATCTGAGTGGTTCTG CAATTTCTTTGTCTAATACTAATAAAGAGA	6865
	TCTCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCT GTACGTGAAATTCACAACTTAATGTGAGAGGAGGCAGAAGTGGCT GCCCCAGTTCTGGGCTTAGGGTAGATTCT	6866
	TTAAGTTGTGAATTTCA	6867
	TGAAATTCACAACTTAA	6868
Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Arg22Term AGA-TGA	GCGAGTTGGGTTTTATCAGAATGTGGTCTGAGGCCACTCCCGAGG GTCTATCCTAAGCCATGAAGTGGCCACCCTTTGTTGAATTTCAATC CCACAAAGCTGAGATTTTCAAGAACAGATC	6869
	GATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTCAACAA AGGGTGGCCAGTTCTATGGCTTAGGATAGACCCTCGGGAGTGGCC TCAGACCACATTCTGATAAAACCCAACTCGC	6870
	CTAAGCCATGAAGTGGC	6871
	GCCAGTTCATGGCTTAG	6872
Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu27Term TTG-TAG	CAGAATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAA GAAGTGGCCACCCTTAGTTGAATTTCAATCCCACAAAGCTGAGATT TTCAAGAACAGATCTTGAAATGGTTCTTC	6873
	GAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGTGG GATTGGAATTCACAAAGGGTGGCCAGTTCTTGGCTTAGGATAGA CCCTCGGGAGTGGCCTCAGACCACATTCTG	6874

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCACCCTT <u>A</u> GTTGAATT	6875
	AATTCAACT <u>A</u> AGGGTGG	6876
Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu28Term TTG-TAG	AATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGT <u>A</u> GAATTCCAATCCCACAAAGCTGAGATTTTC AAGAACAGATCTTGGAATGGTTCTTCATT	6877
	AATGAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGT GGGATTGGAATTC <u>T</u> ACAAAGGGTGGCCAGTTCTTGGCTTAGGATA GACCCTCGGGAGTGGCCTCAGACCACATT	6878
	CCCTTTGT <u>A</u> GAATTCCA	6879
	TGGAATTC <u>T</u> ACAAAGGG	6880
Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Lys34Term AAG-TAG	CTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGTTG AATTCCAATCCCACAT <u>A</u> GCTGAGATTTCAAGAACAGATCTTGGAATGTTCTTCATTCTGTTTGTGAGTGGGA	6881
	TCCCACTCGACAAACAGAATGAAGAACCATTTCCAAGATCTGTTCT TGAAAATCTCAGCT <u>A</u> TGTGGGATTGGAATTCAACAAAGGGTGGCC AGTTCTTGGCTTAGGATAGACCCTCGGGAG	6882
	ATCCCACAT <u>A</u> GCTGAGA	6883
	TCTCAGCT <u>A</u> TGTGGGAT	6884
Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Tyr3Term TAC-TAG	CATCAGAGCGGCGATACCTAAGCATTGCTGGGTAAAGAATCCATG GAAGTCTATGAGTTA <u>G</u> GTCGTCAGAGAGCTAGCCATCGTGTTGCGC ACTAGCTGCTGGAGCTGCTTACCTCAACAAT	6885
	ATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGC TAGCTCTCTGACGAC <u>C</u> TAAGTCTATAGACTTCCATGGATTCTTAACC CAGCAATGCTTAGGTATCGCCGCTCTGATG	6886
	ATGAGTTA <u>G</u> GTCGTCAG	6887
	CTGACGAC <u>C</u> TAAGTCTAT	6888
Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Arg6Term AGA-TGA	GCGGCGATACCTAAGCATTGCTGGGTAAAGAATCCATGGAAGTCT ATGAGTTACGTCGTC <u>I</u> GAGAGCTAGCCATCGTGTTGCGACTAGCT GCTGGAGCTGCTTACCTCAACAATTGGCTTG	6889
	CAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACA CGATGGCTAGCTCTC <u>A</u> GACGACGTAAGTCTATAGACTTCCATGGATT CTTAACCCAGCAATGCTTAGGTATCGCCGC	6890
	ACGTCGTC <u>I</u> GAGAGCTA	6891
	TAGCTCTC <u>A</u> GACGACGT	6892

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Glu7Term GAG-TAG	GCGATACCTAAGCATTGCTGGGTAAAGAATCCATGGAAGTCTATGA GTTACGTCGTCAGATAGCTAGCCATCGTGTTTCGCACTAGCTGCTG GAGCTGCTTACCTCAACAATTGGCTTGTTT	6893
	AAACAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGA ACACGATGGCTAGCTATCTGACGACGTAACCTCATAGACTTCCATG GATTCTTAACCCAGCAATGCTTAGGTATCGC	6894
	TCGTCAGATAGCTAGCC	6895
	GGCTAGCTATCTGACGA	6896
Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Gly17Term GGA-TGA	CCATGGAAGTCTATGAGTTACGTCGTCAGAGAGCTAGCCATCGTG TTCGCACTAGCTGCTTGAGCTGCTTACCTCAACAATTGGCTTGTTT GGCCTCTCTATTGGATTGCTCAAGGAACCA	6897
	TGTTTCCTTGAGCAATCCAATAGAGAGGCCAAACAAGCCAATTGTT GAGGTAAGCAGCTCAAGCAGCTAGTGCGAACACGATGGCTAGCT CTCTGACGACGTAACCTCATAGACTTCCATGG	6898
	TAGCTGCTTGAGCTGCT	6899
	AGCAGCTCAAGCAGCTA	6900
Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg22Term AGA-TGA	GCAAGTTGGGTCTATCAGAATGTGGTCTTAGACCACTACCAAGAA TATACCCAAAGCCCTGAATAGGGTCTTCTTCCGTTTGCGCCACCAA TTTAAATCTGAGAAGAATTTACCTTCAC	6901
	GTGAAGGTGAAATCTTCTCAGATTTAAATTGGTGGCGCAAACGGA AGAAGACCCTATTCAAGGGCTTTGGGTATATTCTTGGTAGTGGTCTA AGACCACATTCTGATAGAACCCAACTTGC	6902
	CAAAGCCCTGAATAGGG	6903
	CCCTATTCAGGGCTTTG	6904
Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Cys29Term TGC-TGA	TGGTCTTAGACCACTACCAAGAATATACCCAAAGCCCAGAATAGG GTCTTCTTCCGTTTGAGCCACCAATTTAAATCTGAGAAGAATTTCA CCTTCACCTATACGAACAGATCGGAATTGT	6905
	ACAATTCCGATCTGTTCTGATAGGTGAAGGTGAAATCTTCTCAGA TTTAAATTGGTGGCTCAAACGGAAGAAGACCCTATTCTGGGCTTTG GGTATATTCTTGGTAGTGGTCTAAGACCA	6906
	TCCGTTTGAGCCACCAA	6907
	TTGGTGGCTCAAACGGA	6908
Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Leu33Term TTA-TGA	CACTACCAAGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGT TTGCGCCACCAATTGAAATCTGAGAAGAATTTACCTTCACCTATA CGAACAGATCGGAATTGTTGGGCATTGAG	6909
	CTCAATGCCCAACAATTCCGATCTGTTCTGATAGGTGAAGGTGAAA TTCTTCTCAGATTTCAATTGGTGGCGCAAACGGAAGAAGACCCTAT TCTGGGCTTTGGGTATATTCTTGGTAGTG	6910

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CACCAATTGAAATCTGA	6911
	TCAGATTTCAATTGGTG	6912
Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg36Term AGA-TGA	AGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTGCGCCA CCAATTTAAATCTGTGAAGAATTTACCTTCACCTATACGAACAGAT CGGAATTGTTGGGCATTGAGGGTAAGTG	6913
	CACCTACCCTCAATGCCCAACAATTCCGATCTGTTCGTATAGGTGA AGGTGAAATTCTTCAAGATTTAAATTGGTGGCGCAAACGGAAGAA GACCCTATTCTGGGCTTTGGGTATATTCT	6914
	TAAATCTGTGAAGAATT	6915
	AATTCTTCAAGATTTA	6916
Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Trp4Term TGG-TGA	CTCTTTATTATCCTCCTCTTCTTTGTTTTTTTGAGTTCTGAGTCACC TATGGCAAGTTGAGTGATTTTCAAGATGTGGGCTAAGGCCACTTCC AAGAATCTATGCCAGGCCCAAGAGTGA	6917
	TCCACTTCTGGGCCTGGCATAGATTCTTGAAGTGGCCTTAGCCC ACATTCTGAAATCACTCAACTTGCCATAGGTGACTCAGAACTCAA AAAAACAAAGAAGAGGAGGATAATAAAGAG	6918
	GCAAGTTGAGTGATTTT	6919
	GAAATCACTCAACTTGC	6920
Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Ser7Term TCA-TGA	TATCCTCCTCTTCTTTGTTTTTTTGAGTTCTGAGTCACCTATGGCA AGTTGGGTGATTTGAGAATGTGGGCTAAGGCCACTTCCAAGAATC TATGCCAGGCCCAAGAGTGGAGCTTCATG	6921
	CATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGAAGTGGC CTTAGCCACATTCTCAAATCACCAACTTGCCATAGGTGACTCAG AACTCAAAAAACAAAGAAGAGGAGGATA	6922
	GGTGATTTGAGAATGTG	6923
	CACATTCTCAAATCACC	6924
Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Glu8Term GAA-TAA	TCCTCCTCTTCTTTGTTTTTTTGAGTTCTGAGTCACCTATGGCAAG TTGGGTGATTTCAATATGTGGGCTAAGGCCACTTCCAAGAATCTAT GCCAGGCCCAAGAGTGGAGCTTCATGTT	6925
	AACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGAAGTG GCCTTAGCCACATTATGAAATCACCAACTTGCCATAGGTGACTC AGAACTCAAAAAACAAAGAAGAGGAGGA	6926
	TGATTTCAATATGTGGG	6927
	CCCACATTATGAAATCA	6928

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Cys9Term TGT-TGA	CTCTTCTTTGTTTTTTTGTAGTTCTGAGTCACCTATGGCAAGTTGGG TGATTTCAAGATGAGGGCTAAGGCCACTTCCAAGAATCTATGCCA GGCCCAGAAGTGGAGCTTCATGTTTCAAC	6929
	GTTGAAACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGG AAGTGGCCTTAGCCCTCATTCTGAAATCACCCAACCTGCCATAGGT GACTCAGAACTCAAAAAAACAAAGAAGAG	6930
	TCAGAATGAGGGCTAAG	6931
	CTTAGCCCCCATTCTGA	6932
Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Lys21Term AAA-TAA	ATGAAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTA ATGGTTTTTCATGCTTAAGAAGAAGAAGAAGAGGATTTGACTT AAGCAATCCTCCTCCATTCAATATTGGTC	6933
	GACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTC TTCTTCTTCTTCTTAAGCATGAAAACCATTAAACGCCATTTAGAATTG GGGTGTCTTTGTACTGTTGCTGCTTCAT	6934
	TTCATGCTTAAGAAGAA	6935
	TTCTTCTTAAGCATGAA	6936
Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu22Term GAA-TAA	AAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATG GTTTTTCATGCTAAATAAGAAGAAGAAGAAGAGGATTTGACTTAAG CAATCCTCCTCCATTCAATATTGGTCAGA	6937
	TCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTC TTCTTCTTCTTCTTAATTAGCATGAAAACCATTAAACGCCATTTAGAA TTGGGGTGTCTTTGTACTGTTGCTGCTT	6938
	ATGCTAAATAAGAAGAA	6939
	TTCTTCTTAATTAGCAT	6940
Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu23Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCTAAAGAATAAGAAGAAGAAGAGGATTTGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	6941
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTTAATTCTTTAGCATGAAAACCATTAAACGCCATTTA GAATTGGGGTGTCTTTGTACTGTTGCTG	6942
	CTAAAGAATAAGAAGAA	6943
	TTCTTCTTAATTCTTTAG	6944
Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu24Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCTAAAGAATAAGAAGAAGAAGAGGATTTGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	6945
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTTAATTCTTTAGCATGAAAACCATTAAACGCCATTTA GAATTGGGGTGTCTTTGTACTGTTGCTG	6946

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTAAAGAATAAGAAGAA	6947
	TTCTTCTTATTCTTTAG	6948
Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Tyr21Term TAT-TAG	GGTCCAAGCACAGCCTCTACAACATGTTGGTAATGGTGCAGGGAA AGAAGATCAAGCTTAGTTTGATCCAAGTGCTCCACCACCCTTCAAG ATTGCAAATATCAGAGCAGCAATTCCAAAA	6949
	TTTTGGAATTGCTGCTCTGATATTTGCAATCTTGAAGGGTGGTGGGA GCACTTGGATCAAACTAAGCTTGATCTTCTTCCCTGCACCATTAC CAACATGTTGTAGAGGCTGTGCTTGGACC	6950
	CAAGCTTAGTTTGATCC	6951
	GGATCAAACTAAGCTTG	6952
Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Lys31Term AAG-TAG	GGTAATGGTGCAGGGAAAGAAGATCAAGCTTATTTTGATCCAAGT GCTCCACCACCCTTCTAGATTGCAAATATCAGAGCAGCAATTCCAA AACATTGCTGGGAGAAGAACACATTGAGAT	6953
	ATCTCAATGTGTTCTTCTCCAGCAATGTTTTGGAATTGCTGCTCT GATATTTGCAATCTAGAAGGGTGGTGGAGCACTTGGATCAAATAA GCTTGATCTTCTTCCCTGCACCATTACC	6954
	CACCCTTCTAGATTGCA	6955
	TGCAATCTAGAAGGGTG	6956
Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Arg36Term AGA-TGA	AAAGAAGATCAAGCTTATTTTGATCCAAGTGCTCCACCACCCTTCA AGATTGCAAATATCTGAGCAGCAATTCCAAAACATTGCTGGGAGAA GAACACATTGAGATCTCTGAGTTATGTTT	6957
	GAACATAACTCAGAGATCTCAATGTGTTCTTCTCCAGCAATGTTTT GGAATTGCTGCTCAGATATTTGCAATCTTGAAGGGTGGTGGAGCA CTTGATCAAAATAAGCTTGATCTTCTTT	6958
	CAAATATCTGAGCAGCA	6959
	TGCTGCTCAGATATTTG	6960
Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Leu41Term AAA-TAA	TATTTTGATCCAAGTGCTCCACCACCCTTCAAGATTGCAAATATCA GAGCAGCAATTCCAACATTGCTGGGAGAAGAACACATTGAGAT CTCTGAGTTATGTTCTGAGGGATGTGTTGG	6961
	CCAACACATCCCTCAGAACATAACTCAGAGATCTCAATGTGTTCTT CTCCAGCAATGTTATGGAATTGCTGCTCTGATATTTGCAATCTTG AAGGGTGGTGGAGCACTTGGATCAAAATA	6962
	CAATTCCATAACATTGC	6963
	GCAATGTTATGGAATTG	6964

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Glu8Term GAG-TAG	CATCCACCCGCACCCGCCCCGCTGACGGCGGCAATGGC CCGGCTCGTGCTCTCCTAGTGCTCGGGCCTCGCGCCCGTCCGCC GCCTGCGCGCCGGCCGGGGCGCCATTGCGGGCGC	6965
	GCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGG GCGCGAGGCCCGAGCACTAGGAGAGCACGAGCCGGGCCATTGC CGCCGTCAGCGGGGCGGGTGCGGGTGCGGGTGGATG	6966
	TGCTCTCCTAGTGCTCG	6967
	CGAGCACTAGGAGAGCA	6968
Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Cys9Term TGC-TGA	ACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGG CTCGTGCTCTCCGAGTGATCGGGCCTCGCGCCCGTCCGCCGCCT GCGCGCCGGCCGGGGCGCCATTGCGGCGCGGTCA	6969
	TGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGG ACGGGCGCGAGGCCCGATCACTCGGAGAGCACGAGCCGGGCCA TTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGGGT	6970
	TCCGAGTGATCGGGCCT	6971
	AGGCCCGATCACTCGGA	6972
Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser10Term TCG-TAG	CCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGGCT CGTGCTCTCCGAGTGCTAGGGCCTCGCGCCCGTCCGCCGCCTGC GCGCCGGCCGGGGCGCCATTGCGGCGCGGTCA	6973
	GGTGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGC GGACGGGCGCGAGGCCCTAGCACTCGGAGAGCACGAGCCGGGC CATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGG	6974
	CGAGTGCTAGGGCCTCG	6975
	CGAGGCCCTAGCACTCG	6976
Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser29Term TCA-TGA	GCTCGGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGG CGCCATTGCGGGCGCGGTGACCCCCCGCGCTCTCCGCGGCGCCG CGCCGTCGTCCCGCGTCCGCGTCCATCCACCGCGA	6977
	TCGCGGTGGATGGACGCGGACGCGGGACGACGGCGCGGCGCCG CGGAGAGCGCGGGGGGTACCGCGCCGCAATGGCGCCCCGGCC GGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGAGC	6978
	GGCGCGGTGACCCCCG	6979
	CGGGGGGTACCGCGCC	6980
Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu8Term GAG-TAG	CCCCCTCCCCACGCACACGCACAGATCCATCCGCGGCCATGGC CCCCGCAATGAGGCCGTAGCAGGAGGCGAGCTGCAAGGCCACCG AGGACCACCGCTCCGAGTTCGACGCCGCCAAGC	6981
	GCTTGGCGGCGTCAACTCGGAGCGGTGGTCCTCGGTGGCCTTG CAGCTCGCCTCCTGCTACGGCCTCATTGCGGGGGCCATGGCCGC GGATGGATCTGTGCGTGTGCGTGGGGGAGGGGG	6982

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGAGGCCG <u>T</u> AGCAGGAG	6983
	CTCCTGCT <u>A</u> CGGCCTCA	6984
Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Gln9Term CAG-TAG	CCTCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGGAG <u>T</u> AGGAGGCGAGCTGCAAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGCCGC	6985
	GCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTTGCAGCTCGCCTCCT <u>A</u> CTCCGGCCTCATTGCGGGGGCCATGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGGAGG	6986
	GGCCGGAG <u>T</u> AGGAGGCG	6987
	CGCCTCCT <u>A</u> CTCCGGCC	6988
	CCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGGAGCAG <u>T</u> AGGCGAGCTGCAAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGCCGCCGC	6989
Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu10Term GAG-TAG	GCGGCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTTGCAGCTCGCCT <u>A</u> CTGCTCCGGCCTCATTGCGGGGGCCA	6990
	TGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGG	
	CGGAGCAG <u>T</u> AGGCGAGC	6991
	GCTCGCCT <u>A</u> CTGCTCCG	6992
Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Cys13Term TGC-TGA	ACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGGAGCAGGAGGCGAGCTG <u>A</u> AAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGCCGCCGCCCTTCCGCATC	6993
	GATGCGGAAGGGCGGCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTT <u>T</u> CAGCTCGCCTCCTGCTCCGGCCTCATTGCGGGGGCCATGGCCGCGGATGGATCTGTGCGT	6994
	GCGAGCTG <u>A</u> AAGGCCAC	6995
	GTGGCCTT <u>T</u> CAGCTCGC	6996
	CTTCACAAATCACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATGGCGGCGT <u>A</u> GGCGACCCAGGAGGCCGACTGCAAGGCTTCGAGGACGCCCGTCTCTTCTTCGACGCCGC	
Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Ser4Term TCG-TAG	GCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGCCTTGCAAGTGGCCTCCTGGGTGCGCT <u>A</u> CGCCGCCATTGCCGCCGGGGTGTGCTGGTGGATCTGATTCCGATTTGTGATTTGTGAAG	6998
	GGCGGCGT <u>A</u> GGCGACCC	6999
	GGGTCGCCT <u>A</u> CGCCGCC	7000

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Gln7Term CAG-TAG	ATCACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATG GCGGCGTCGGCGACCTAGGAGGCCGACTGCAAGGCTTCCGAGGA CGCCCGTCTCTTCTTCGACGCCGCCAAGCCCC	7001
	GGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGC CTTGCAATCGGCCTCCTAGGTCGCCGACGCCGCCATTGCCGCCG GGGTGTCGTGGTGGATCTGATTCCGATTTGTGAT	7002
	CGGCGACCTAGGAGGCC	7003
	GGCCTCCTAGGTCGCCG	7004
Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Glu8Term GAG-TAG	ACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATGGC GGCGTCGGCGACCCAGTAGGCCGACTGCAAGGCTTCCGAGGACG CCCGTCTCTTCTTCGACGCCGCCAAGCCCCCGC	7005
	GCGGGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGA AGCCTTGCAATCGGCCTACTGGGTCGCCGACGCCGCCATTGCCG CCGGGGTGTGCTGGTGGATCTGATTCCGATTTGT	7006
	CGACCCAGTAGGCCGAC	7007
	GTCGGCCTACTGGGTCG	7008
Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Cys10Term TGC-TGA	TCAGATCCACCACGACACCCCGGCGGCAATGGCGGCGTCGGCGA CCCAGGAGGCCGACTGAAGGCTTCCGAGGACGCCCGTCTCTTC TTCGACGCCGCCAAGCCCCCGCCCTTCCGCATC	7009
	GATGCGGAAGGGCGGGGGCTTGGCGGCGTCGAAGAAGAGACGG GCGTCCTCGGAAGCCTTCAGTCGGCCTCCTGGGTGCCGACGC CGCCATTGCCGCCGGGGTGTGCTGGTGGATCTGA	7010
	GCCGACTGAAGGCTTC	7011
	GAAGCCTTCAGTCGGC	7012

[267] Although a number of embodiments and features are described herein, it will be understood by those skilled in the art that modification and variations of the described embodiments and features may be made without departing from either the spirit of the invention or the scope of the
5 appended claims. All publications and patents cited herein are incorporated by reference in their entireties.